

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 29, 2002, 10:23:56 : Search time 9 Seconds  
(without alignments)  
27.140 Million cell updates/sec

Title: US-09-580-018-7

Perfect score: 54

Sequence: 1 KMDAEFRHDS 10

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents-AA:\*  
1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PCTUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	18	2	US-08-149-975A-3
2	54	100.0	27	1	US-08-141-324-11
3	54	100.0	27	1	US-08-541-502-11
4	54	100.0	45	1	US-08-462-859A-5
5	54	100.0	45	1	US-08-123-659A-5
6	54	100.0	45	1	US-08-464-247A-5
7	54	100.0	45	1	US-08-464-248A-5
8	54	100.0	53	4	US-09-173-887-5
9	54	100.0	58	1	US-08-371-930-25
10	54	100.0	58	5	PCT-US94-01712-25
11	54	100.0	59	1	US-08-484-969-3
12	54	100.0	59	1	US-08-472-627-3
13	54	100.0	59	1	US-08-388-463-3
14	54	100.0	63	1	US-08-462-859A-3
15	54	100.0	63	1	US-08-462-859A-4
16	54	100.0	63	1	US-08-123-659A-3
17	54	100.0	63	1	US-08-123-659A-4
18	54	100.0	63	1	US-08-464-247A-3
19	54	100.0	63	1	US-08-464-247A-4
20	54	100.0	63	1	US-08-464-248A-3
21	54	100.0	63	1	US-08-464-248A-4
22	54	100.0	103	2	US-08-404-831-2
23	54	100.0	103	2	US-08-612-785B-2
24	54	100.0	103	2	US-08-475-579A-2
25	54	100.0	103	2	US-08-920-162A-2
26	54	100.0	103	2	US-08-339-708A-10
27	54	100.0	103	4	US-09-356-931-2

28	54	100.0	103	4	US-08-703-675C-2	Sequence 2, Appl1
29	54	100.0	103	4	US-08-617-267C-2	Sequence 2, Appl1
30	54	100.0	105	2	US-08-729-345-1	Sequence 1, Appl1
31	54	100.0	117	2	US-08-729-345-3	Sequence 3, Appl1
32	54	100.0	152	6	5187153-4	Patent No. 5187153
33	54	100.0	162	6	5220013-4	Patent No. 5220013
34	54	100.0	162	6	5223482-4	Patent No. 5223482
35	54	100.0	264	1	US-07-990-893-5	Sequence 5, Appl1
36	54	100.0	487	1	US-08-462-859A-9	Sequence 9, Appl1
37	54	100.0	487	1	US-08-123-659A-9	Sequence 9, Appl1
38	54	100.0	487	1	US-08-464-247A-9	Sequence 9, Appl1
39	54	100.0	487	1	US-08-464-248A-9	Sequence 9, Appl1
40	54	100.0	492	1	US-08-462-859A-7	Sequence 7, Appl1
41	54	100.0	492	1	US-08-123-659A-7	Sequence 7, Appl1
42	54	100.0	492	1	US-08-464-247A-7	Sequence 7, Appl1
43	54	100.0	492	1	US-08-464-248A-7	Sequence 7, Appl1
44	54	100.0	537	1	US-08-453-552-4	Sequence 4, Appl1
45	54	100.0	537	2	US-08-710-637-4	Sequence 4, Appl1

## ALIGNMENTS

RESULT 1  
US-08-149-975A-3  
Sequence 3, Application US/08149975A  
Patent No. 5849600  
GENERAL INFORMATION:  
APPLICANT: Nixon, Ralph  
TITLE OF INVENTION: DIAGNOSTIC ASSAYS FOR ALZHEIMER'S  
TITLE OF INVENTION: DISEASE  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/149,975A  
FILING DATE: 11-NOV-1993  
CLASSIFICATION: 436  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 04843/016001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-149-975A-3

Query Match 100.0%; Score 54; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 0.00015;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KMDAEFRHDS 10  
DB 2 KMDAEFRHDS 11

RESULT 2  
US-08-141-324-11  
; Sequence 11, Application US/08141324  
; Patent No. 5475097  
; GENERAL INFORMATION:  
; APPLICANT: Travels, James  
; APPLICANT: Potempa, Jan S.  
; APPLICANT: Barr, Philip J.  
; APPLICANT: Pavloff, Nadine  
; APPLICANT: Pike, Robert N.  
; TITLE OF INVENTION: Lysine-specific Porphyromonas gingivalis  
; TITLE OF INVENTION: Protease  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Greenlee and Winner, P.C.  
; STREET: 5370 Manhattan Circle, Suite 201  
; CITY: Boulder  
; STATE: CO  
; COUNTRY: US  
; ZIP: 80303  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/141,324  
; FILING DATE: 21-OCT-1993  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ferber, Donna M.  
; REGISTRATION NUMBER: 33,878  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 303-499-8080  
; TELEFAX: 303-499-8089  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 27 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
US-08-141-324-11  
Query Match 100.0%; Score 54; DB 1; Length 27;  
Best Local Similarity 100.0%; Pred. No. 0.00022;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KMDAEFRHDS 10  
DB 7 KMDAEFRHDS 16  
RESULT 3  
US-08-541-902-11  
; Sequence 11, Application US/08541902  
; Patent No. 5707620  
; GENERAL INFORMATION:  
; APPLICANT: Travels, James  
; APPLICANT: Potempa, Jan S.  
; APPLICANT: Barr, Philip J.  
; APPLICANT: Pavloff, Nadine  
; APPLICANT: Pike, Robert N.  
; TITLE OF INVENTION: Lysine-specific Porphyromonas gingivalis  
; TITLE OF INVENTION: Protease  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Greenlee and Winner, P.C.

STREET: 5370 Manhattan Circle, Suite 201  
CITY: Boulder  
STATE: CO  
COUNTRY: US  
ZIP: 80303  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/541,902  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/141,324  
FILING DATE: 21-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Ferber, Donna M.  
REGISTRATION NUMBER: 33,878  
REFERENCE/DOCKET NUMBER: 44-93  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 303-499-8080  
TELEFAX: 303-499-8089  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-541-902-11  
Query Match 100.0%; Score 54; DB 1; Length 27;  
Best Local Similarity 100.0%; Pred. No. 0.00022;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KMDAEFRHDS 10  
DB 7 KMDAEFRHDS 16  
RESULT 4  
US-08-462-859A-5  
; Sequence 5, Application US/08462859A  
; Patent No. 5652092  
; GENERAL INFORMATION:  
; APPLICANT: Jacobsen, J. S.  
; APPLICANT: Vittek, M. P.  
; TITLE OF INVENTION: No. 5652092e1 Amyloid Precursor and Method of  
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation  
; TITLE OF INVENTION: of B-Amyloid Peptide  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: American Cyanamid Company  
; STREET: One Cyanamid Plaza  
; CITY: Wayne  
; STATE: New Jersey  
; COUNTRY: United States  
; ZIP: 07470-8426  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/462,859A  
; FILING DATE: 05-JUN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Barnhard, Elizabeth M.

REGISTRATION NUMBER: 31,088  
REFERENCE/DOCKET NUMBER: 31,844-04  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (201)831-3246  
TELEFAX: (201)831-3305  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 45 amino acids  
TYPE: amino acid  
STRANDEDNESS: linear  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-462-859A-5

Query Match 100.0%; Score 54; DB 1; Length 45;  
Best Local Similarity 100.0%; Pred. NO. 0.00038;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KMDAEPFRHDS 10  
Db 8 KMDAEPFRHDS 17

RESULT 5  
US-08-123-659A-5  
Sequence 5, Application US/08123659A  
Patent No. 5656477  
GENERAL INFORMATION:  
APPLICANT: Jacobsen, J. S.  
TITLE OF INVENTION: No. 5656477el Amyloid Precursor and Method of  
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation  
TITLE OF INVENTION: of B-Amyloid Peptide  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Anne Rosenblum  
STREET: 163 Delaware Avenue, Suite 212  
CITY: Delmar  
STATE: Delaware  
COUNTRY: U.S.A.  
ZIP: 12054  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/123,659A  
FILING DATE: 20-SEP-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Rosenblum, Anne M.  
REGISTRATION NUMBER: 30,419  
REFERENCE/DOCKET NUMBER: 31,844-01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (518)475-0611  
TELEFAX: (518)475-0619  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 45 amino acids  
TYPE: amino acid  
STRANDEDNESS: linear  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-123-659A-5

Query Match 100.0%; Score 54; DB 1; Length 45;  
Best Local Similarity 100.0%; Pred. NO. 0.00038;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KMDAEPFRHDS 10  
Db 8 KMDAEPFRHDS 17

RESULT 6  
US-08-464-247A-5  
Sequence 5, Application US/08464247A  
Patent No. 5693478  
GENERAL INFORMATION:  
APPLICANT: Jacobsen, J. S.  
TITLE OF INVENTION: No. 5693478el Amyloid Precursor and Method of  
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation  
TITLE OF INVENTION: of B-Amyloid Peptide  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: American Cyanamid Company  
STREET: One Campus Drive  
CITY: Parsippany  
STATE: New Jersey  
COUNTRY: United States  
ZIP: 07054  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/464,247A  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Barnhard, Elizabeth M.  
REGISTRATION NUMBER: 31,088  
REFERENCE/DOCKET NUMBER: 31,844-03  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-683-2158  
TELEFAX: 201-683-4117  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 45 amino acids  
TYPE: amino acid  
STRANDEDNESS: linear  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-464-247A-5

Query Match 100.0%; Score 54; DB 1; Length 45;  
Best Local Similarity 100.0%; Pred. NO. 0.00038;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KMDAEPFRHDS 10  
Db 8 KMDAEPFRHDS 17

RESULT 7  
US-08-464-248A-5  
Sequence 5, Application US/08464248A  
Patent No. 5703209  
GENERAL INFORMATION:  
APPLICANT: Jacobsen, J. S.  
TITLE OF INVENTION: No. 5703209el Amyloid Precursor and Method of  
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation  
TITLE OF INVENTION: of B-Amyloid Peptide  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: American Cyanamid Company  
STREET: One Cyanamid Plaza  
CITY: Wayne  
STATE: New Jersey  
COUNTRY: United States  
ZIP: 07470-8426  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/464,248A  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Barnhard, Elizabeth M.  
REGISTRATION NUMBER: 31,088  
REFERENCE/DOCKET NUMBER: 31,844-02  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (201)831-3246  
TELEFAX: (201)831-3305  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 45 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-464-248A-5

Query Match  
Best Local Similarity 100.0%; Score 54; DB 1; Length 45;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KMDAERRHDS 10  
DB 8 KMDAERRHDS 17  
|||||

RESULT 8  
US-09-173-887-5  
Sequence 5, Application US/09173887  
Patent No. 6245884  
GENERAL INFORMATION:  
APPLICANT: Hook, Vivian Y.H.  
TITLE OF INVENTION: SECRETASES RELATED TO ALZHEIMER'S DEMENTIA  
FILE REFERENCE: P-RAS 3337  
CURRENT APPLICATION NUMBER: US/09/173,887  
CURRENT FILING DATE: 1998-10-16  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 5  
LENGTH: 53  
TYPE: PRT  
ORGANISM: mammalian  
US-09-173-887-5

Query Match  
Best Local Similarity 100.0%; Score 54; DB 4; Length 53;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KMDAERRHDS 10  
DB 2 KMDAERRHDS 11  
|||||

RESULT 9  
US-08-371-930-25  
Sequence 25, Application US/08371930  
Patent No. 5578451  
GENERAL INFORMATION:  
APPLICANT: Nishimoto, Ikuo  
TITLE OF INVENTION: ALZHEIMER'S DISEASE THERAPEUTICS  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.

ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM PS/2 Model 502 or 555X  
OPERATING SYSTEM: MS-DOS (Version 5.0)  
SOFTWARE: Wordperfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/371,930  
FILING DATE:  
CLASSIFICATION: 436  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/019,208  
FILING DATE: February 18, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 00786/154001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 25:  
US-08-371-930-25

Query Match  
Best Local Similarity 100.0%; Score 54; DB 1; Length 58;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KMDAERRHDS 10  
DB 45 KMDAERRHDS 54  
|||||

RESULT 10  
PCT-US94-01712-25  
Sequence 25, Application PC/TUS9401712  
GENERAL INFORMATION:  
APPLICANT: Nishimoto, Ikuo  
TITLE OF INVENTION: ALZHEIMER'S DISEASE THERAPEUTICS  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM PS/2 Model 502 or 555X  
OPERATING SYSTEM: MS-DOS (Version 5.0)  
SOFTWARE: Wordperfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/01712  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/019,208  
FILING DATE: February 18, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 00786/154001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 25:



## SEQUENCE CHARACTERISTICS:

LENGTH: 58  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
PCR-US94-01712-25

Query Match 100.0%; Score 54; DB 5; Length 58;  
Best Local Similarity 100.0%; Pred. No. 0.0005;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KMDAEFRHDS 10  
DB 45 KMDAEFRHDS 54

## RESULT 11

US-08-484-969-3  
Sequence 3, Application US/08484969  
Patent No. 5679531

## GENERAL INFORMATION:

APPLICANT: Konig, Gerhard  
TITLE OF INVENTION: Monoclonal Antibody Specific for BA4  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Allegretti & Witcoff, Ltd.  
STREET: 10 South Wacker Drive Suite 3000  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,969  
FILING DATE:

## CLASSIFICATION: 424

## ATTORNEY/AGENT INFORMATION:

NAME: McDonnell, John J  
REGISTRATION NUMBER: 26,949  
REFERENCE/DOCKET NUMBER: 95,216  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-715-1000  
TELEFAX: 312-715-1234

## INFORMATION FOR SEQ ID NO: 3:

## SEQUENCE CHARACTERISTICS:

LENGTH: 59 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

## FEATURE:

NAME/KEY: Cleavage-site

LOCATION: 4..5

OTHER INFORMATION: /label= beta

OTHER INFORMATION: /note= "Beta cleavage site in App"

## FEATURE:

NAME/KEY: Cleavage-site

LOCATION: 20..21

OTHER INFORMATION: /label= Alpha

OTHER INFORMATION: /note= "Alpha cleavage site in App, residues 16/17

## FEATURE:

NAME/KEY: Cleavage-site

LOCATION: 46..47

OTHER INFORMATION: /label= Gamma

OTHER INFORMATION: /note= "Gamma cleavage site in App"

## NAME/KEY: Peptide

LOCATION: 5..47

OTHER INFORMATION: /label= BA4

OTHER INFORMATION: /note= "BA4 peptide"

## FEATURE:

NAME/KEY: Region

LOCATION: 33..56

OTHER INFORMATION: /label= Tm

OTHER INFORMATION: /note= "Transmembrane region of App"

## FEATURE:

NAME/KEY: Region

LOCATION: 1..32

OTHER INFORMATION: /label= Ex

OTHER INFORMATION: /note= "N-terminal extracellular part of App"

## Query Match

100.0%; Score 54; DB 1; Length 59;  
Best Local Similarity 100.0%; Pred. No. 0.00051;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KMDAEFRHDS 10  
DB 3 KMDAEFRHDS 12

## RESULT 12

US-08-472-627-3  
Sequence 3, Application US/08472627  
Patent No. 5693753

## GENERAL INFORMATION:

APPLICANT: Konig, Gerhard  
TITLE OF INVENTION: Monoclonal Antibody Specific for BA4  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Allegretti & Witcoff, Ltd.  
STREET: 10 South Wacker Drive Suite 3000  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/472,627  
FILING DATE:

## CLASSIFICATION: 424

## ATTORNEY/AGENT INFORMATION:

NAME: McDonnell, John J  
REGISTRATION NUMBER: 26,949  
REFERENCE/DOCKET NUMBER: 95,216  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-715-1000  
TELEFAX: 312-715-1234

## INFORMATION FOR SEQ ID NO: 3:

## SEQUENCE CHARACTERISTICS:

LENGTH: 59 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

## FEATURE:

NAME/KEY: Cleavage-site

LOCATION: 4..5

OTHER INFORMATION: /label= Beta

OTHER INFORMATION: /note= "Beta cleavage site in App"

## FEATURE:

NAME/KEY: Cleavage-site

LOCATION: 20..21

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? OTHER INFORMATION: /label= Alpha
? OTHER INFORMATION: /note= "Alpha cleavage site in App, residues 16/17
? OTHER INFORMATION: of BA4."
? FEATURE:
? NAME/KEY: Cleavage-site
? LOCATION: 46..47
? OTHER INFORMATION: /label= Gamma
? OTHER INFORMATION: /note= "Gamma cleavage site in App"
? FEATURE:
? NAME/KEY: Peptide
? LOCATION: 5..47
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? OTHER INFORMATION: /note= "BA4 peptide"
? FEATURE:
? NAME/KEY: Region
? LOCATION: 33..56
? OTHER INFORMATION: /label= Tm
? OTHER INFORMATION: /note= "Transmembrane region of App"
? FEATURE:
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? OTHER INFORMATION: /label= Ex
? OTHER INFORMATION: /note= "N-terminal extracellular part of App"
US-08-472-627-3

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Best Local Similarity 100.0%; Pred. No. 0.00051;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KMDAFFFFHDS 10
DB 3 KMDAFFFFHDS 12

RESULT 13
US-08-388-463-3
? Sequence 3, Application US/08388463
? Patent No. 5786180
? GENERAL INFORMATION:
? APPLICANT: Konig, Gerhard
? APPLICANT: Graham, Paul
? TITLE OF INVENTION: Monoclonal Antibody Specific for BA4
? TITLE OF INVENTION: Peptide
? NUMBER OF SEQUENCES: 3
? CORRESPONDENCE ADDRESS:
? ADDRESSER: Allegretti & Witcoff, Ltd.
? STREET: 10 South Wacker Drive Suite 3000
? CITY: Chicago
? STATE: Illinois
? COUNTRY: USA
? ZIP: 60606
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patent In Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/388,463
? FILING DATE:
? CLASSIFICATION: 435
? ATTORNEY/AGENT INFORMATION:
? NAME: McDonnell, John J
? REGISTRATION NUMBER: 26,949
? REFERENCE/DOCKET NUMBER: 95,216
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 312-715-1000
? TELEFAX: 312-715-1234
? INFORMATION FOR SEQ ID NO: 3:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 59 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
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? MOLECULE TYPE: peptide
? FEATURE:
? NAME/KEY: Cleavage-site
? LOCATION: 4..5
? OTHER INFORMATION: /label= Beta
? OTHER INFORMATION: /note= "Beta cleavage site in App"
? FEATURE:
? NAME/KEY: Cleavage-site
? LOCATION: 20..21
? OTHER INFORMATION: /label= Alpha
? OTHER INFORMATION: /note= "Alpha cleavage site in App, residues 16/17
? OTHER INFORMATION: of BA4."
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? OTHER INFORMATION: /label= Tm
? OTHER INFORMATION: /note= "Transmembrane region of App"
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? OTHER INFORMATION: /label= Ex
? OTHER INFORMATION: /note= "N-terminal extracellular part of App"
US-08-388-463-3

Query Match 100.0%; Score 54; DB 1; Length 59;
Best Local Similarity 100.0%; Pred. No. 0.00051;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KMDAFFFFHDS 10
DB 3 KMDAFFFFHDS 12

RESULT 14
US-08-462-859A-3
? Sequence 3, Application US/08462859A
? Patent No. 5652092
? GENERAL INFORMATION:
? APPLICANT: Jacobsen, J. S.
? APPLICANT: Vittek, M. P.
? TITLE OF INVENTION: No. 5652092el Amyloid Precursor and Method of
? TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate formation
? TITLE OF INVENTION: of B-Amyloid Peptide
? NUMBER OF SEQUENCES: 19
? CORRESPONDENCE ADDRESS:
? ADDRESSER: American Cyanamid Company
? STREET: One Cyanamid Plaza
? CITY: Wayne
? STATE: New Jersey
? COUNTRY: United States
? ZIP: 07470-8426
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patent In Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/462,859A
? FILING DATE: 05-JUN-1995
? CLASSIFICATION: 435
? ATTORNEY/AGENT INFORMATION:
? NAME: Barnhard, Elizabeth M.
? REGISTRATION NUMBER: 31,088
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Search completed: October 29, 2002, 10:32:08  
Job time : 9 secs

REFERENCE/DOCKET NUMBER: 31,844-04  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (201)831-3246  
TELEFAX: (201)831-3505  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 63 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-462-859A-3

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Best Local Similarity 100.0%; Pred. No. 0.00054;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KMDAERRHDS 10  
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Db 8 KMDAERRHDS 17

## RESULT 15

US-08-462-859A-4  
Sequence 4, Application US/08462859A  
Patent No. 5652092  
GENERAL INFORMATION:  
APPLICANT: Jacobsen, J. S.  
TITLE OF INVENTION: NO. 5652092el Amyloid Precursor and Method of  
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: American Cyanamid Company  
STREET: One Cyanamid Plaza  
CITY: Wayne  
STATE: New Jersey  
COUNTRY: United States  
ZIP: 07470-8426  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/462,859A  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Barnhard, Elizabeth M.  
REGISTRATION NUMBER: 31,088  
REFERENCE/DOCKET NUMBER: 31,844-04  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (201)831-3246  
TELEFAX: (201)831-3305  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 63 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-462-859A-4

Query Match 100.0%; Score 54; DB 1; Length 63;  
Best Local Similarity 100.0%; Pred. No. 0.00054;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KMDAERRHDS 10  
|||||  
Db 8 KMDAERRHDS 17



Tue Oct 29 11:23:24 2002

us-09-580-018-1.rag

Page 1

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OK protein - protein search, using sw model

Run on: October 29, 2002, 10:22:21 : Search time 23.1429 Seconds  
(without alignments)  
47.935 Million cell updates/sec

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Perfect score: 47  
Sequence: 1 EELSEYKMDA 10

Scoring table: BLOSUM62  
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Searched: 747574 seqs, 11073796 residues

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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	47	100.0	10	22	AA046205
2	47	100.0	16	22	AA066315
3	47	100.0	18	22	AA060608
4	47	100.0	20	22	AA069713
5	47	100.0	33	20	AA080002
6	47	100.0	39	21	AA069717
7	47	100.0	45	14	AA065172
8	47	100.0	45	18	AA063392
9	47	100.0	45	19	AA044778
10	47	100.0	45	19	AA042977
11	47	100.0	53	16	AA04169

12	47	100.0	57	21	AA010910	Human amyloid prec
13	47	100.0	58	15	AA089937	Amyloid precursor
14	47	100.0	63	16	AA06511	Amyloid precursor
15	47	100.0	63	16	AA06391	Amyloid precursor
16	47	100.0	63	16	AA04747	APP-REP 751 APP
17	47	100.0	63	16	AA04746	APP-REP 751 [BAP
18	47	100.0	63	16	AA042315	Beta-amyloid pep1
19	47	100.0	63	16	AA042316	Beta-amyloid pep1
20	47	100.0	67	15	AA01377	Peptide derived fr
21	47	100.0	67	15	AA01376	Peptide derived fr
22	47	100.0	112	17	AA033953	Novel human diago
23	47	100.0	112	20	AA032536	En113 Alzheimer
24	47	100.0	115	20	AA032535	London RAD APP pol
25	47	100.0	102	12	AA031013	Deduced sequence 1
26	47	100.0	102	12	AA031013	Beta-amyloid relat
27	47	100.0	102	14	AA032963	Beta-amyloid relat
28	47	100.0	264	10	AA030497	Protein sequence 1
29	47	100.0	264	10	AA030497	Sequence of amy 37
30	47	100.0	487	16	AA030912	Amyloid precursor
31	47	100.0	487	16	AA030912	Amyloid precursor
32	47	100.0	487	16	AA030912	APP-REP 751 precu
33	47	100.0	487	16	AA030912	APP-REP 751 precu
34	47	100.0	492	14	AA045228	Amyloid precursor
35	47	100.0	492	14	AA045228	Amyloid precursor
36	47	100.0	492	14	AA045228	Amyloid precursor
37	47	100.0	492	14	AA045228	Amyloid precursor
38	47	100.0	492	14	AA045228	Amyloid precursor
39	47	100.0	492	14	AA045228	Amyloid precursor
40	47	100.0	595	15	AA042978	Beta-amyloid precu
41	47	100.0	627	21	AA045797	Beta-amyloid precu
42	47	100.0	627	21	AA045797	Beta-amyloid precu
43	47	100.0	651	15	AA05796	Beta-amyloid precu
44	47	100.0	651	15	AA05796	Beta-amyloid precu
45	47	100.0	676	15	AA05795	APP751 beta-amyloi
			676	15	AA05795	Amyloid precursor
			695	9	AA081692	Sequence of human

#### ALIGNMENTS

RESULT 1	
ID	AA046205
XX	AA046205 standard; peptide; 10 AA.
AC	AA046205;
DT	04-APR-2001 (first entry)
XX	
XX	Human APP derived immunogenic peptide #1.
XX	
XX	Amyloid deposit; APP; A-beta; brain; human; clearing response; neurotropic;
XX	PC receptor mediated phagocytosis; immunogenic response; neuroprotective;
XX	amyloid precursor protein; Alzheimer's disease.
XX	
XX	Homo sapiens.
XX	
XX	MO200072880-A2.
XX	
XX	07-DEC-2000.
XX	
XX	26-MAY-2000; 2000MO-US14810.
XX	
XX	28-MAY-1999; 99US-0322289.
XX	
XX	(NEUR-) NEURALAB LTD.
XX	
XX	Schenk DB, Bard F, Vasquez NJ, Yednock T;
XX	
XX	WPI; 2001-032104/04.
XX	
XX	preventing or treating a disease associated with amyloid deposits,
XX	especially Alzheimer's disease, comprises administering amyloid
XX	specific antibody -
XX	
XX	

PS Disclosure; Figure 19; 143pp; English.

XX This invention describes a novel method of preventing or treating a  
 CC disease associated with amyloid deposits of amyloid precursor protein  
 CC (APP) Abeta fragments in the brain of a patient which comprises  
 CC administering to the patient: (a) an antibody that binds to Abeta, the  
 CC antibody binds to an amyloid deposit and induces a clearing response (PC  
 CC receptor mediated phagocytosis) against it (b) a polypeptide containing  
 CC an N-terminal segment of at least residues 1-5 of Abeta or (c) an agent  
 CC that induces an immunogenic response against residues 1-3 to 7,11  
 CC Abeta. The products of the invention have neurotropic and neuroprotective  
 CC activity. The method is also useful for monitoring a course of treatment  
 CC being administered to a patient e.g. active and passive immunization. The  
 CC methods are useful for prophylactic and therapeutic treatment of  
 CC Alzheimer's disease.

SO Sequence 10 AA;

Query Match 100.0%; Score 47; DB 22; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.0053;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EISEVVKMDA 10  
 |||||  
 DB 1 EISEVVKMDA 10

RESULT 2  
 ID AAB06315 standard; peptide; 16 AA.  
 XX AAB06315;  
 AC AAB06315;  
 XX  
 DT 03-OCT-2000 (first entry)  
 XX  
 DE Human beta-amyloid precursor protein beta-secretase cleavage site.  
 XX  
 KW Human; beta-amyloid precursor protein; beta-APP; beta-secretase;  
 KW subtilisin-kexin isoenzyme 1; SKI-1;  
 KW pro-brain-derived neurotrophic factor; proBDNF; anti-lipemic;  
 KW cytoskeletal; vasotropic; SKI-1 inhibitor; hypercholesterolemia;  
 KW liver steatosis; Ras-dependent cancer; restenosis;  
 KW amyloid protein formation.  
 XX  
 OS Homo sapiens.  
 XX  
 PH Key Location/Qualifiers  
 PH Cleavage-site 8..9  
 PN WO200026348-A2.  
 PD 11-MAY-2000.  
 XX  
 PP 04-NOV-1999; 99WO-CA01058.  
 PT  
 PR 04-NOV-1998; 98CA-2249648.  
 XX  
 PA (RECL-) INST RECH CLINIQUES MONTREAL.  
 XX  
 PI Seidah N, Chretien M, Marcinkiewicz M, Laaksonen R, Davignon J;  
 DR WPI: 2000-365601/31.  
 XX  
 PT Novel soluble proteic fragment of subtilisin-kexin isoenzyme for  
 PT producing a polypeptide useful for treating hypercholesterolemia, liver  
 PT steatosis and amyloidosis, comprises a specific amino acid sequence -  
 XX  
 PS Example 4; Page 51; 119pp; English.

XX The present sequence is the beta-secretase site of human beta-amyloid  
 CC precursor protein (beta-APP). The sequence may be cleaved  
 CC by a mammalian subtilase, specifically subtilisin-kexin isoenzyme 1  
 CC (SKI-1), a type-I membrane-bound proteinase. Peptides which bind to and

CC are cleaved by SKI-1 may be used for monitoring SKI-1 activity, for  
 CC screening inhibitors of SKI-1 activity, or for screening enhancers of  
 CC SKI-1 activity. Proteic fragments of SKI-1 which bind to the SKI-1  
 CC catalytic site may be used as inhibitors of SKI-1 activity. They may be  
 CC used to treat diseases involving overexpression of SKI-1 or SKI-1  
 CC substrate. Such diseases include hypercholesterolemia, high levels of  
 CC fatty acids, lipids or larnesyl pyrophosphate, liver steatosis,  
 CC Ras-dependent cancer, restenosis and amyloid protein formation.

SO Sequence 16 AA;

Query Match 100.0%; Score 47; DB 21; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 0.0089;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EISEVVKMDA 10  
 |||||  
 DB 1 EISEVVKMDA 10

RESULT 3  
 ID AAE00608 standard; peptide; 18 AA.  
 XX AAE00608;  
 AC AAE00608;  
 XX  
 DN 02-JUL-2001 (first entry)  
 XX  
 DE Beta-amyloid precursor protein beta-secretase cleavage site.  
 XX  
 KW Beta-amyloid precursor protein; beta-APP; caspase; beta-secretase;  
 KW cysteine protease; apoptosis; caspase expression cassette; metastasis;  
 KW tumour; cathepsin B; urokinase; proliferation; gene therapy;  
 KW interdomain linker; cleavage site; Alzheimer's disease.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200129232-A2.  
 PD 26-APR-2001.  
 XX  
 PP 19-OCT-2000; 2000WO-US28941.  
 XX  
 PR 20-OCT-1999; 99US-0160559.  
 PT  
 PR 14-AUG-2000; 2000US-0225564.  
 XX  
 PA (SCIO-) SCIOS INC.  
 XX  
 PI Cordell B, Li Y;  
 DR WPI: 2001-290920/30.  
 XX  
 PT Novel fusion polypeptide comprising first and second caspase subunit  
 PT separated by cleavage site not associated in nature with caspase  
 PT subunit, useful for cloning gene encoding enzymes involved in  
 PT proteolytic cleavage -  
 XX  
 PS Example 2; Page 26; 116pp; English.

XX The present sequence is a beta-secretase cleavage site of beta-amyloid  
 CC precursor protein (beta-APP). This sequence is used to construct  
 CC an artificially engineered chimeric cassette comprising human caspase-3  
 CC with interdomain linker replaced by swedish mutant beta-secretase  
 CC cleavage site. This modified caspase-3 plays a pivotal role in  
 CC Alzheimer's disease. Caspases are a family of cysteine proteases, that  
 CC participate in the initiation and execution of apoptosis.  
 CC The present invention relates to a method for functional cloning of genes  
 CC encoding proteins or enzymes involved in proteolytic cleavage. The  
 CC invention is based on the use of caspase expression cassettes comprising  
 CC the coding sequence of a proteolytic cleavage site flanked by sequences  
 CC encoding two caspase subunits. A fusion polypeptide comprising a first  
 CC and a second caspase subunit, separated by a cleavage site not associated  
 CC in nature, is useful for cloning gene encoding enzymes involved in

CC proteolytic cleavage. An expression cassette containing fusion  
 CC polypeptide is used to identify a mutant cell line deficient in an  
 CC enzyme of interest and is also useful for diagnosis and suppression of  
 CC proliferation or metastases of a tumour cell characterised by  
 CC overexpression of a polypeptide (e.g. Cathepsin B or tyrosinase,  
 CC selectively expressed in the tumour cells). DNA encoding fusion  
 CC polypeptide is used in gene therapy.

XX Sequence 18 AA;

Query Match

Best Local Similarity 100.0%; Score 47; DB 22; Length 18;  
 Pred. No. 0.01;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EEISEVKMDA 10  
 |||||  
 DB 3 EEISEVKMDA 12

RESULT 4

ID AAY69713 standard; peptide: 20 AA.

XX AAY69713;

DT 11-APR-2000 (first entry)

DE Beta-APP alpha-secretase substrate [KM]-APP(-10,+10).

XX Neurotropic; neuroprotective; beta-amyloid precursor protein; metabolism;  
 KM cleavage site; beta-secretase; neurodegenerative disease;

XX Alzheimer's disease.

XX Homo sapiens.

XX W09964587-A1.

XX 16-DEC-1999.

XX 04-JUN-1999; 99MO-FR01326.

XX 05-JUN-1998; 98FR-0007068.

XX 31-MAR-1999; 99US-0122599.

XX (RHON ) RHONE-POULENC ROHER SA.

XX (UYPA-) UNIV CURIE PARIS VI P & M.

XX Rholam M, Munoz-Gimenez N, Mouraouakil M, Cohen P, Bertrand P;

XX WPI: 2000-097537/08.

XX Polypeptide with beta-secretase activity, specific for wild-type  
 PT amyloid precursor protein, useful in treating Alzheimer's disease -

XX Example 3; Page 24; 44pp; French.

XX Peptides AAY69702-Y69718 represent synthetic peptide substrates for a  
 CC novel polypeptide with beta-secretase activity that can cleave  
 CC specifically the natural beta-amyloid precursor protein (bAPP). Normal  
 CC cleavage of the protein occurs between amino acids Met156-Asp597 and  
 CC Val636-Ile637 (positions 4-5 and 44-45 of AAY69701). The novel  
 CC polypeptide is used to identify agents that interact specifically with  
 CC it. These agents regulate metabolism of APP, particularly they slow down  
 CC or reduce production of beta-amyloid, so can be used to treat  
 CC neurodegenerative diseases, particularly Alzheimer's disease.

XX Sequence 20 AA;

Query Match

Best Local Similarity 100.0%; Score 47; DB 21; Length 20;  
 Pred. No. 0.011;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EEISEVKMDA 10

DB 3 EEISEVKMDA 12  
 |||||

RESULT 5

ID AAM98002 standard; Protein: 33 AA.

XX AAM98002;

DT 21-JUN-1999 (first entry)

DE Amyloid precursor protein (aa656-678) with Swedish mutation.

XX Amyloid precursor protein; APP; human; gene targeting;  
 KM homologous recombination; transgenic mouse; transgenic animal;  
 KM animal model; Alzheimer's disease.

XX Mus musculus.

XX W09909150-A1.

XX 25-FEB-1999.

XX 18-AUG-1997; 97MO-US14507.

XX 18-AUG-1997; 97MO-US14507.

XX (FARB ) BAYER CORP.

XX WIRAK DO;

XX WPI: 1999-181029/15.

XX Modification of target nucleic acids - by homologous recombination,  
 PT used particularly for introducing a humanised amyloid precursor  
 PT protein gene into rodents for producing models of Alzheimer's  
 PT disease

XX Disclosure: Page 145; 209pp; English.

XX This polypeptide comprises residues 656-678 of a murine amyloid  
 CC precursor protein (APP). The invention provides a novel gene  
 CC targeting strategy that facilitates the introduction of one or  
 CC more specific mutations into any gene in a single double reciprocal  
 CC homologous recombination step. The method has been used  
 CC particularly for introducing a humanised APP gene into rodents for  
 CC producing animal models of Alzheimer's disease (AD). 4 independent  
 CC lines of transgenic mice (lines ES5007, ES5103, ES5401 and ES5403)  
 CC have been created using the gene targeting technique applied to  
 CC embryonic stem cells. In each line, the mouse APP gene was modified  
 CC to encode a mouse/human hybrid (m/hAPP) where amino acid residues  
 CC 666-770 of APP770 were encoded by human cDNA sequences instead of  
 CC mouse genomic exons (exons 16-18). Within these residues, only 3  
 CC amino acid differences exist between the mouse and human proteins,  
 CC i.e. Gly-676 to Arg, Phe-681 to Thr and Arg-684 to His. The  
 CC exon-cDNA fusion gene therefore encodes an APP containing a APP  
 CC humanised beta-amyloid domain. Swedish- and/or London-PAD APP  
 CC mutations have also been introduced (see also AAM97997-W98001).

XX Sequence 33 AA;

Query Match

Best Local Similarity 100.0%; Score 47; DB 20; Length 33;  
 Pred. No. 0.02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EEISEVKMDA 10  
 |||||

DB 9 EEISEVKMDA 18

RESULT 6

AAY69717

```

ID AAY69717 standard; peptide: 39 AA.
XX
AC AAY69717;
XX
XX
DT 11-APR-2000 (first entry)
XX
DE Beta-APP alpha-secretase substrate [KM]-APP(-20,+20).
XX
KW Neotropic; neuroprotective; beta-amyloid precursor protein; metabolism;
KW cleavage site; beta-secretase; neurodegenerative disease;
KW Alzheimer's disease.
XX
OS Homo sapiens.
XX
PN MO9964587-A1.
XX
PD 16-DEC-1999.
XX
PP 04-JUN-1999; 99MO-FR01326.
XX
PR 05-JUN-1998; 98PR-0007068.
PR 31-MAR-1999; 99US-0122599.
XX
PA (RHON ) RHONE-POULENC ROHER SA.
PA (DIPA-) UNIV CURIE PARIS VI P & M.
PI Rhoïam M, Munoz-Gimenez N, Moutaouakil M, Cohen P, Bertrand P;
DR WPI: 2000-097537/08.
XX
XX Polypeptide with beta-secretase activity, specific for wild-type
PT amyloid precursor protein, useful in treating Alzheimer's disease
XX
XX Example 3, Page 24; 44pp; French.
XX
CC Peptides AAY69702-Y69718 represent synthetic peptide substrates for a
CC novel polypeptide with beta-secretase activity that can cleave
CC specifically the natural beta-amyloid precursor protein (BAP). Normal
CC cleavage of the protein occurs between amino acids Met596-Asp597 and
CC Val636-Ile637 (positions 4-5 and 44-45 of AAY69701). The novel
CC polypeptide is used to identify agents that interact specifically with
CC it. These agents regulate metabolism of APP, particularly they slow down
CC or reduce production of beta-amyloid, so can be used to treat
CC neurodegenerative diseases, particularly Alzheimer's disease.
XX
SQ Sequence 39 AA;
Query Match 100.0%; Score 47; DB 21; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EEISEVKMDA 10
Db 12 EEISEVKMDA 21
IIIIIIIIII

RESULT 7
ID AAM26512 standard; Peptide: 45 AA.
XX
AC AAM26512;
XX
XX
DT 06-JAN-1998 (first entry)
XX
DE Amyloid precursor protein fragment APP-REP 751 (BAP del11-28).
XX
KW Amyloid precursor protein; APP; beta-amyloid protein; BAP;
KW substrate; mutelin; secretase; Alzheimer's disease; human.
XX
XX Chimeric Homo sapiens.
OS Chimeric synthetic.
XX
PH Key Location/Qualifiers

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```

FT Cleavage-site 7..8
FT /note= "secretase cleavage site"
FT Peptide 10..33
FT /label= BAP(del11-28)
FT /note= "truncated beta-amyloid protein"
FT Domain 20..42
FT /label= Transmembrane
XX
PN US5656477-A.
XX
PD 12-AUG-1997.
XX
PP 01-MAY-1992; 92US-0877675.
XX
PR 20-SEP-1993; 93US-0123659.
PR 01-MAY-1992; 92US-0877675.
XX
PA (AMCY ) AMERICAN CYANAMID CO.
PI Jacobsen JS, Vitek MP;
DR WPI: 1997-414594/38.
XX
XX Nucleic acid encoding amyloid precursor mutelin(s) - comprising
PT reporter gene and coding sequence, for identifying compounds which
PT modify the activity of proteolytic enzymes which cleave APP
XX
XX Disclosure; Fig 5A; 84pp; English.
XX
CC This peptide sequence shows the region of amyloid precursor protein
CC (APP) that includes a truncated beta-amyloid protein (BAP) lacking
CC the native secretase cleavage/recognition site. In an attempt to
CC engineer an APP non-cleavable substrate for secretase, an
CC APP-reporter (APP-RBP) protein that carries the BAP deletion has
CC been expressed in recombinant host cells. Deletion of these 18
CC amino acids, however, still resulted in the secretion of APP.
CC N-terminal APP-reporter fragment into the cytoplasm. Non-
CC cleavable APP substrates can be used to detect other putative
CC abnormal APP processing events. They can also be used to
CC investigate cellular post-translational modifications to APP in
CC order to determine the potential influence on normal secretase and
CC abnormal BAP 'clipping' activities.
XX
SQ Sequence 45 AA;
Query Match 100.0%; Score 47; DB 18; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EEISEVKMDA 10
Db 2 EEISEVKMDA 11
IIIIIIIIII

RESULT 8
ID AAM26392 standard; Peptide: 45 AA.
XX
AC AAM26392;
XX
XX
DT 15-DEC-1997 (first entry)
XX
DE Amyloid precursor protein fragment APP-REP 751 (BAP del11-28).
XX
KW Amyloid precursor protein; APP; beta-amyloid protein; BAP;
KW substrate; mutelin; secretase; Alzheimer's disease; human.
XX
XX Chimeric Homo sapiens.
OS Chimeric synthetic.
XX
PH Key Location/Qualifiers
FT Cleavage-site 7..8
FT /note= "secretase cleavage site"

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```

FT Peptide 10..33
FT /label= BAP(delta11-28)
FT /note= "truncated beta-amyloid protein"
FT Domain 20..42
FT /label= Transmembrane
XX US5652092-A.
XX
XX 29-JUL-1997.
XX
XX 01-MAY-1992: 92US-0877675.
XX
XX 20-SEP-1993: 93US-0123659.
XX 01-MAY-1992: 92US-0877675.
XX 05-JUN-1995: 95US-0462859.
XX
XX (AMCY ) AMERICAN CYANAMID CO.
XX
XX Jacobson JS, Vittek MP;
XX
XX WPI: 1997-392937/36.
XX
XX Screening for compounds which reduce beta-amyloid protein formation
XX - using cells which express a construct encoding a marker and an
XX amyloid precursor muttein derived from APP isoforms
XX
XX PS Disclosure: Fig 5A; 84pp; English.
XX
XX CC This peptide sequence shows the region of amyloid precursor protein
XX (APP) that includes a truncated beta-amyloid protein (BAP) lacking
XX the native secretase cleavage/recognition site. In an attempt to
XX engineer an APP non-cleavable substrate for secretase, an
XX APP-reporter (APP-REP) protein that carries the BAP deletion has
XX been expressed in recombinant host cells. Deletion of these 18
XX amino acids, however, still resulted in the secretion of an
XX N-terminal APP-reporter fragment into the cytoplasm. Non-
XX cleavable APP substrates can be used to detect other putative
XX abnormal APP processing events. They can also be used to
XX investigate cellular post-translational modifications to APP in
XX order to determine the potential influence on normal secretase and
XX abnormal BAP 'clipping' activities.
XX
XX SO Sequence 45 AA:
XX
XX Query Match 100.0%; Score 47; DB 18; Length 45;
XX Best Local Similarity 100.0%; Pred. No. 0.028;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 EISEYKMDA 10
XX |||||
XX 2 EISEYKMDA 11
XX
XX RESULT 9
XX ID AAM44748 standard; protein: 45 AA.
XX
XX AC AAM44748;
XX
XX DT 01-JUN-1998 (first entry)
XX
XX DE APP-REP 751 [BAP delta(11-28)] peptide.
XX
XX KW Amyloid precursor protein; APP; APP 751 isoform; deletion; substrate P;
XX KW epsilon; Met-enkephalin; detection; secretase; beta-amyloid protein; BAP;
XX KW Alzheimer's disease; cleavage.
XX
XX OS Homo sapiens.
XX
XX OS Synthetic.
XX
XX Key Location/Qualifiers
XX FH Cleavage-site 7..8
XX FT /note= "putative secretase cleavage site"

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FT Misc-difference 19..20
FT /note= "residues 11-28 of the wild type BAP sequence
FT are deleted from between these positions"
XX
XX US5693478-A.
XX
XX 02-DEC-1997.
XX
XX 05-JUN-1995: 95US-0464247.
XX
XX 20-SEP-1993: 93US-0123659.
XX 01-MAY-1992: 92US-0877675.
XX 05-JUN-1995: 95US-0464247.
XX
XX (AMCY ) AMERICAN CYANAMID CO.
XX
XX Jacobson JS, Vittek MP;
XX
XX WPI: 1998-031744/03.
XX
XX Amyloid precursor muttein reporter molecule assay containing antibody
XX recognised marker - used to study pathways associated with
XX Alzheimer's disease
XX
XX PS Disclosure: Fig 5A; 84pp; English.
XX
XX CC This sequence represent the beta-amyloid protein sequence from the
XX construct APP-REP751 [BAP delta(11-28)]. The mutant sequence contains
XX a deletion of the wild type BAP residues 11-28. This causes a
XX shortening of the BAP sequence. This may affect cleavage of the BAP by
XX the "secretase" dependent on whether the "secretase" recognises the
XX cleavage site by a positional effect or by sequence. The mutant sequence
XX can be used in a method to study secretase and beta-amyloid protein
XX (BAP) generating pathways associated with Alzheimer's disease by
XX studying proteolytic cleavage of the reporter polypeptides (e.g.
XX AAM44744 and AAM44745).
XX
XX SO Sequence 45 AA:
XX
XX Query Match 100.0%; Score 47; DB 19; Length 45;
XX Best Local Similarity 100.0%; Pred. No. 0.028;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 EISEYKMDA 10
XX |||||
XX 2 EISEYKMDA 11
XX
XX RESULT 10
XX ID AAM42977 standard; peptide: 45 AA.
XX
XX AC AAM42977;
XX
XX DT 01-MAY-1998 (first entry)
XX
XX DE Deletion beta-amyloid peptide (BAP) derived from APP-REP 751.
XX
XX KW Beta-amyloid peptide; BAP; extracellular BAP plaque;
XX KW cerebrovascular deposit; Alzheimer's disease; Downs syndrome;
XX KW amyloid precursor protein; APP; secretase; BAP aggregation;
XX KW abnormal proteolytic cleavage.
XX
XX OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX FH Domain 20..43
XX FT /note= "putative transmembrane domain"
XX
XX US5703209-A.
XX
XX 30-DEC-1997.

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PF 05-JUN-1995; 95US-0464248.
XX
XX 20-SEP-1993; 93US-0123659.
PR 01-MAY-1992; 92US-0877675.
XX
XX (AMCY ) AMERICAN CYANAMID CO.
XX
XX Jacobson JS, Vitek MP;
XX WPI: 1998-076482/07.
XX
XX Amyloid precursor protein fusion polypeptides - comprising APP
XX fragment and marker, useful for research and drug screening
XX
XX Disclosure; Fig 5A; BAPP; English.
XX
XX The present sequence represents a beta-amyloid peptide (BAP), with
XX a deletion amino acids 11-28 (numbered according to AAM42976). Abnormal
XX accumulation of extracellular BAP in plaques and cerebrovascular
XX deposits is characteristic in brains of individuals suffering from
XX Alzheimer's disease and Down's syndrome. BAP is a poorly soluble,
XX self-aggregating protein which is derived from a larger amyloid precursor
XX protein (APP). APP is expressed as an integral membrane protein, and is
XX cleaved by secretase, between BAP 16lys and 17leu. Cleavage at this site
XX precludes amyloidogenesis and results in the release of the
XX amino-terminal APP fragment. Three major isoforms of APP exist: APP-695,
XX APP-751 and APP-770. These isoforms are derived by alternative splicing.
XX APP-APP 751 is a deletion construct of APP-751, which has a deletion of
XX 276 amino acids to within 15 amino acids of the BAP domain. APP can be
XX used as a substrate for studying abnormal proteolytic cleavage which
XX results in the release of BAP, and also to screen for drugs that will
XX inhibit such cleavage.
XX
XX Sequence 45 AA:
XX
XX Query Match 100.0%; Score 47; DB 19; Length 45;
XX Best Local Similarity 100.0%; Pred. No. 0.028; Indels 0; Gaps 0;
XX Matches 10; Conservative 0; Mismatches 0;
XX
XX QY 1 EELSEVKMDA 10
XX Db 2 EELSEVKMDA 11
XX
XX RESULT 11
XX AAR64168
XX ID AAR64168 standard; peptide: 53 AA.
XX
XX AAR64168;
XX
XX 02-AUG-1995 (first entry)
XX
XX Variant beta amyloid protein with 10 preceeding amino acids of APP.
XX
XX beta amyloid protein; mutant; variant; detection: amyloid deposition;
XX diagnosis: amyloidosis associated disease; Alzheimer's disease;
XX Down's syndrome; APP; amyloid precursor protein.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Peptide 1..10
XX /note= "the preceeding 10 amino acids of APP"
XX Peptide 11..53
XX /note= "beta amyloid protein variant"
XX
XX W09428412-A.
XX
XX 08-DEC-1994.
XX
XX 27-MAY-1994; 94WO-US05809.
XX
XX 28-MAY-1993; 93US-0069010.

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XX
XX (MIRI-) MIRIAM HOSPITAL.
XX
XX MaJocha RE, Marotta CA;
XX
XX WPI: 1995-023013/03.
XX
XX Amyloid binding composition comprising labelled amyloid protein
XX and carrier useful for in vivo imaging of amyloid deposits, for
XX diagnosing Alzheimer's disease and Down's Syndrome.
XX
XX Claim 5; Page 43; 58pp; English.
XX
XX AAR64168 shows the amino acid sequence of the beta amyloid protein
XX plus the 10 amino acids preceeding the amyloid precursor protein. The
XX protein binds amyloid and is useful for in vivo imaging of amyloid
XX deposits and hence diagnosis of an amyloidosis-associated disease, such
XX as Alzheimer's disease or Down's syndrome. AAR64165 shows the generic
XX sequence of the amyloid protein for generation of variants.
XX
XX Sequence 53 AA:
XX
XX Query Match 100.0%; Score 47; DB 16; Length 53;
XX Best Local Similarity 100.0%; Pred. No. 0.033;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 EELSEVKMDA 10
XX Db 3 EELSEVKMDA 12
XX
XX RESULT 12
XX AAB10910
XX ID AAB10910 standard; peptide: 57 AA.
XX
XX AAB10910;
XX
XX 30-JAN-2001 (first entry)
XX
XX Human amyloid precursor APP770 A-beta1-40/42 protein fragment.
XX
XX APP; amyloid precursor protein; APP770; human; copper agonist; treatment;
XX amyloid-Abeta-peptide; neurotropic; neuroprotective; Alzheimer's disease.
XX
XX Homo sapiens.
XX
XX DE1909357-A1.
XX
XX 07-SEP-2000.
XX
XX 03-MAR-1999; 99DE-1009357.
XX
XX 03-MAR-1999; 99DE-1009357.
XX
XX (MUL/T) MUTHAUP G.
XX (BEYR/) BEYREUTHER K.
XX
XX Beyreuther K, Muthaup G, Masters CL;
XX WPI: 2000-595035/57.
XX
XX Copper agonist binds to the copper binding site of amyloid precursor
XX protein, useful for treating Alzheimer's disease -
XX
XX Example 1; Fig 1; 14pp; German.
XX
XX This invention describes a novel copper agonist (1) capable of binding to
XX the copper binding site of an amyloid precursor protein (APP) and/or
XX preventing or reducing the release of amyloid-Abeta-peptides. The
XX invention also describes (1) a medicament comprising (1) in combination
XX with a carrier; (2) identifying (1), comprising: (a) contacting potential
XX (1) with APP; and (b) detecting a reduction of Abeta-proteins; and (3)
XX identifying (1) comprising: (a) contacting APP or the copper-binding

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CC site-carrying fragment with a solution of, immobilized substance  
 CC libraries of, or low molecular weight substances from microorganisms or  
 CC plants; (b) performing a competitive assay by adding copper ions to form  
 CC complexes with the ligands; (c) identifying the ligands; and (d)  
 CC selecting ligands, which bind the APP copper binding site or which reduce  
 CC the Abeta peptide release. The products of the invention have neurotropic  
 CC and neuroprotective activity. (I) and the resulting medicament are used  
 CC for preventing or treating Alzheimer's disease.

XX Sequence 57 AA;

Query Match 100.0%; Score 47; DB 21; Length 57;  
 Best Local Similarity 100.0%; Pred. No. 0.036;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EISEVKMDA 10  
 |||||||||  
 Db 6 EISEVKMDA 15

RESULT 13

AAR58937 standard; peptide; 58 AA.

AC AAR58937;

DT 15-APR-1995 (first entry)

XX Amyloid precursor protein residues 551-608.

XX Amyloid precursor protein; beta amyloid; monoclonal antibody;

KW Anti-Alz 90; Alzheimer's disease.

XX Homo sapiens.

PN WO9419692-A.

PD 01-SEP-1994.

PF 17-FEB-1994; 94WO-US01712.

PR 18-FEB-1993; 93US-0019208.

PA (GENO ) GEN HOSPITAL CORP.

PI Nishimoto I;

DR WPI; 1994-294486/36.

XX Identifying cpds. useful for treating or preventing Alzheimer's  
 PT disease - by determining whether it interferes with the  
 PT association of the couplone portion of amyloid precursor protein  
 PT to G polypeptide

PS Disclosure; Page 40-41; 71pp; English.

XX Beta amyloid is synthesized as part of a larger protein referred to  
 CC as amyloid precursor protein (APP) which has a number of isoforms  
 CC in humans, including APP695 and APP770. APP forms a complex with Go,  
 CC a GTP-binding protein (or "G protein") in brain. It is suggested  
 CC that abnormal APP-GO signalling is involved in the Alzheimer's  
 CC disease process. Anti-Alz 90 is a mouse monoclonal antibody  
 CC specific for an epitope corresp. to residues 551-608 of APP,  
 CC a section of APP that is within the extracellular domain.

XX Sequence 58 AA;

Query Match 100.0%; Score 47; DB 15; Length 58;  
 Best Local Similarity 100.0%; Pred. No. 0.037;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EISEVKMDA 10  
 |||||||||

Db 39 EISEVKMDA 48

RESULT 14

AAW26511 standard; Peptide; 63 AA.

XX AAW26511;

DT 06-JAN-1998 (first entry)

XX Amyloid precursor protein fragment APP-REP 751 (BAP E220).

XX Amyloid precursor protein; APP; beta-amyloid protein; BAP;

XX substrate; secretase; Alzheimer's disease;

XX hereditary cerebral haemorrhage with amyloidosis; human.

OS Homo sapiens.

PH Key Location/Qualifiers

FT Peptide 10..51  
 FT /label= BAP(E220)  
 FT /note= "beta-amyloid protein E220 mutant"

FT Cleavage-site 25..26  
 FT /note= "secretase cleavage site"  
 FT Domain 38..61  
 FT /label= Transmembrane

XX US5656477-A.

XX 12-AUG-1997.

XX 01-MAY-1992; 92US-0877675.

XX 20-SEP-1993; 93US-0123659.

XX 01-MAY-1992; 92US-0877675.

XX (AMCY ) AMERICAN CYANAMID CO.

PI Jacobsen JS, Vitek MP;

DR WPI; 1997-414594/38.

XX Nucleic acid encoding amyloid precursor muten(s) - comprising  
 PT reporter gene and coding sequence, for identifying compounds which  
 PT modify the activity of proteolytic enzymes which cleave APP  
 XX Disclosure; Fig 5A; 84pp; English.

XX This peptide sequence shows the region of amyloid precursor protein  
 CC (APP) that includes a beta-amyloid protein (BAP) carrying a point  
 CC mutation (BAP E220) found in patients with hereditary cerebral  
 CC haemorrhage with amyloidosis of Dutch origin (HCHWA-D). In an  
 CC attempt to engineer an APP non-cleavable substrate for secretase,  
 CC an APP-reporter (APP-REP) protein that carries the E22Q mutation  
 CC has been expressed in recombinant host cells. This resulted in the  
 CC secretion of an N-terminal fragment indistinguishable from that of  
 CC APP-REP 751 (see AAW26393-94). Non-cleavable APP substrates can be  
 CC used to detect other putative abnormal APP processing events. They  
 CC can also be used to investigate cellular post-translational  
 CC modifications to APP in order to determine the potential influence  
 CC on normal secretase and abnormal BAP 'clipping' activities.

XX Sequence 63 AA;

Query Match 100.0%; Score 47; DB 18; Length 63;  
 Best Local Similarity 100.0%; Pred. No. 0.04;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EISEVKMDA 10  
 |||||||||  
 Db 2 EISEVKMDA 11

RESULT 15  
AAW26391

ID AAW26391 standard; Peptide: 63 AA.

XX AAW26391;

DT 15-DEC-1997 (first entry)

XX Amyloid precursor protein fragment APP-REP 751 (BAP E22Q).

KW Amyloid precursor protein; APP; beta-amyloid protein; BAP;  
KW substrate; muten; secretase; Alzheimer's disease;  
KW hereditary cerebral haemorrhage with amyloidosis; human.

OS Homo sapiens.

PH Key Location/Qualifiers  
FT Peptide 10..51  
FT /label= BAP(E22Q)

FT Cleavage-site /note= "beta-amyloid protein E22Q mutant"  
FT 25..26  
FT /note= "secretase cleavage site"

FT Domain 38..61  
FT /label= Transmembrane

PN US5652092-A.

PD 29-JUL-1997.

PF 01-MAY-1992; 92US-0877675.

PR 20-SEP-1993; 93US-0123659.

PR 01-MAY-1992; 92US-0877675.

PR 05-JUN-1995; 95US-0462859.

PA (AMCY ) AMERICAN CYANAMID CO.

PI Jacobsen JS, Vitek MP;

DR MPI; 1997-392937/36.

PT Screening for compounds which reduce beta-amyloid protein formation  
PT - using cells which express a construct encoding a marker and an  
PT amyloid precursor muten derived from APP isoforms

PS Disclosure: Fig 5A: 8app; English.

CC This peptide sequence shows the region of amyloid precursor protein  
CC (APP) that includes a beta-amyloid protein (BAP) carrying a point  
CC mutation (BAP E22Q) found in patients with hereditary cerebral  
CC haemorrhage with amyloidosis of Dutch origin (HCHWA-D). In an  
CC attempt to engineer an APP non-cleavable substrate for secretase,  
CC an APP-reporter (APP-REP) protein that carries the E22Q mutation,  
CC has been expressed in recombinant host cells. This resulted in the  
CC secretion of an N-terminal fragment indistinguishable from that of  
CC APP-REP 751 (see AAW26393-94). Non-cleavable APP substrates can be  
CC used to detect other putative abnormal APP processing events. They  
CC can also be used to investigate cellular post-translational  
CC modifications to APP in order to determine the potential influence  
CC on normal secretase and abnormal BAP 'clipping' activities.

CC Sequence 63 AA:

Query Match 100.0%; Score 47; DB 18; Length 63;

Best Local Similarity 100.0%; Pred. No. 0.04; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEISEVKMDA 10  
Db 2 EEISEVKMDA 11

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 29, 2002, 10:23:36 : Search time 10.4286 Seconds  
(without alignments)  
92.140 Million cell updates/sec

Title: US-09-580-018-1  
Perfect score: 47  
Sequence: 1 EISEVWKMDA 10

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	100.0	82	2 P00438	Alzheimer's disease
2	47	100.0	695	1 A49795	Alzheimer's disease
3	47	100.0	695	2 A27485	Alzheimer's disease
4	47	100.0	695	2 S00550	Alzheimer's disease
5	47	100.0	770	1 QH0044	Alzheimer's disease
6	44	93.6	747	1 JH0773	Alzheimer's disease
7	37	78.7	146	2 C69136	hypothetical prote
8	34	72.3	62	2 T12832	hypothetical prote
9	33	70.2	33	2 S23094	beta-amyloid prote
10	33	70.2	57	2 E60045	Alzheimer's disease
11	33	70.2	57	2 E60045	Alzheimer's disease
12	33	70.2	57	2 G60045	Alzheimer's disease
13	33	70.2	57	2 D60045	Alzheimer's disease
14	33	70.2	57	2 A60045	Alzheimer's disease
15	33	70.2	57	2 B60045	Alzheimer's disease
16	33	70.2	64	2 T29313	hypothetical prote
17	33	70.2	95	2 A75133	hypothetical prote
18	33	70.2	96	2 D71075	hypothetical prote
19	33	70.2	370	2 T48633	hypothetical prote
20	33	70.2	389	2 G84245	NADH dehydrogenase
21	33	70.2	743	2 D84854	hypothetical prote
22	32	68.1	84	2 T27174	hypothetical prote
23	32	68.1	151	2 H90256	hypothetical prote
24	32	68.1	244	2 G96507	hypothetical prote
25	32	68.1	427	2 R5436	hypothetical prote
26	32	68.1	488	2 JH0359	gamma-aminobutyric
27	32	68.1	489	2 S68280	protein disulfide-
28	32	68.1	576	2 S27790	SWI protein homol
29	32	68.1	941	2 B96533	hypothetical prote

30	32	68.1	1121	2 G64103	exodeoxyribonuclea
31	32	68.1	1286	2 T02187	probable ABC trans
32	32	68.1	1637	2 T46438	hypothetical prote
33	31	66.0	105	2 PH1526	gamma-aminobutyric
34	31	66.0	140	2 T47308	hypothetical prote
35	31	66.0	143	2 T19218	hypothetical prote
36	31	66.0	178	2 C69206	hypothetical prote
37	31	66.0	195	2 A85070	hypothetical prote
38	31	66.0	244	2 E86471	unknown protein li
39	31	66.0	252	2 T05813	hypothetical prote
40	31	66.0	253	2 B84408	hypothetical prote
41	31	66.0	261	1 C64572	conserved hypotet
42	31	66.0	261	2 F71867	hypothetical prote
43	31	66.0	281	2 AH3629	taurine transport
44	31	66.0	288	2 T48268	DP-2 transcription
45	31	66.0	304	2 150721	syemnin - chicken

## ALIGNMENTS

## RESULT 1

P00438 Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C>Date: 30-Sep-1993 #sequence\_revision 19-Oct-1995 #text\_change 19-Oct-1995  
C:Accession: P00438; C60045  
R:Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.E.  
Biochem. Biophys. Res. Commun. 188, 905-911, 1992  
A:Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precurs  
A:Reference number: P00438; MUID:93075180  
A:Accession: P00438  
A:Molecule type: DNA  
A:Residues: 1-82 <DNA>  
A:Cross-references: GB:M83558; GB:M83657  
R:Johnstone, E.M.; Chaney, M.O.; Morris, F.H.; Pascual, R.; Little, S.P.  
Brain Res. Mol. Brain Res. 10, 299-305, 1991  
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d  
A:Reference number: A60045; MUID:92017079  
A:Accession: C60045  
A:Molecule type: mRNA  
A:Residues: 12-68 <JON>  
A:Cross-references: EMBL:X56129  
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas  
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match 100.0%; Score 47; DB 2; Length 82;  
Best Local Similarity 100.0%; Pred. No. 0.017;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EISEVWKMDA 10  
Db 9 EISEVWKMDA 18

## RESULT 2

A49795 Alzheimer's disease amyloid beta protein precursor - crab-eating macaque  
C:Species: Macaca fascicularis (crab-eating macaque)  
C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C:Accession: A49795  
R:Podlasky, M.B.; Tolan, D.R.; Seikoe, D.J.  
Am. J. Pathol. 138, 1423-1435, 1991  
A:Title: Homology of the amyloid beta protein precursor in monkey and human supports  
A:Reference number: A49795; MUID:91273117  
A:Accession: A49795  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-695 <POD>  
A:Cross-references: GB:M58727; P1DN:AAA36829.1; P1D:9342063  
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas  
C:Keywords: alternative splicing

Query Match 100.0%; Score 47; DB 1; Length 695;  
 Best Local Similarity 100.0%; Pred. No. 0.19;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EETSEVKMDA 10  
 |||||||||  
 Db 589 EETSEVKMDA 598

## RESULT 3

A27485  
 Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse  
 N:Alternate names: proteinase nexin II  
 C:Species: Mus musculus (house mouse)  
 C>Date: 31-Mar-1989 #sequence,revision 31-Mar-1989 #text\_change 13-Aug-1999  
 C:Accession: A27485; S19727; I49485  
 R:Yamada, T.; Sasaki, H.; Furuya, H.; Miyata, T.; Goto, I.; Sakaki, Y.  
 Biochem. Biophys. Res. Commun. 149, 665-671, 1987  
 A:Title: Complementary DNA for the mouse homolog of the human amyloid beta protein precu  
 A:Reference number: A27485; MUID:88106489  
 A:Accession: A27485  
 A:Molecule type: mRNA  
 A:Residues: 1-695 <TA>  
 A:Cross-references: GB:M18373; NID:q191568; PIDN:AAA37139.1; PID:q309085  
 A:Experimental source: Brain  
 R:de Strooper, B.; van Leuven, F.; van den Berghe, H.  
 Biochim. Biophys. Acta 1129, 141-143, 1991  
 A:Title: The amyloid beta protein precursor or proteinase nexin II from mouse is closer  
 A:Reference number: S19727; MUID:92096458  
 A:Accession: S19727  
 A:Molecule type: mRNA  
 A:Residues: 1-210, 'G', 212-220, 'S', 222-396, 'A', 398-402, 'T', 404-448, 'A', 450-695 <STR>  
 A:Cross-references: EMBL:X59379  
 R:Izumi, R.; Yamada, T.; Yoshikata, S.; Sasaki, H.; Hattori, M.; Sakaki, Y.  
 Gene 112, 189-195, 1992  
 A:Title: Positive and negative regulatory elements for the expression of the Alzheimer's  
 A:Reference number: I49485; MUID:92209398  
 A:Accession: I49485  
 A>Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-19 <RES>  
 A:Cross-references: GB:D10603; NID:q220328; PIDN:BA01456.1; PID:q220329  
 C:Genetics:  
 A:Map position: 16c3  
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinase  
 C:Keywords: alternative splicing; amyloid; transmembrane protein

Query Match 100.0%; Score 47; DB 2; Length 695;  
 Best Local Similarity 100.0%; Pred. No. 0.19;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EETSEVKMDA 10  
 |||||||||  
 Db 589 EETSEVKMDA 598

## RESULT 4

S00550  
 Alzheimer's disease amyloid beta protein precursor - rat  
 N:Alternate names: beta-A4 amyloid protein  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 30-Jun-1989 #sequence,revision 30-Jun-1989 #text\_change 13-Aug-1999  
 C:Accession: S00550; A41245; A39820; S46251  
 R:Shivers, B.D.; Hlilich, C.; Multhaupt, G.; Salbaum, M.; Beyreuther, K.; Seeburg, P.H.  
 EMBO J. 7, 1363-1370, 1988  
 A:Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brain  
 A:Reference number: S00550; MUID:88312583  
 A:Accession: S00550  
 A:Molecule type: mRNA  
 A:Residues: 1-695 <SH>  
 A:Cross-references: EMBL:X07648; NID:q55616; PIDN:CAA30488.1; PID:q55617  
 R:Schubert, D.; Schroeder, R.; Iacorbriere, M.; Saitoh, T.; Cole, G.  
 Science 241, 223-226, 1988

A:Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan co  
 A:Reference number: A41245; MUID:88264430  
 A:Accession: A41245  
 A:Molecule type: Protein  
 A:Residues: 18-37, 'X', 39-40, 'X', 42-44 <SCH>  
 A>Note: evidence for heparan sulfate attachment  
 R:Hesse, L.; Beher, D.; Masters, C.L.; Multhaupt, G.  
 FEBS Lett. 349, 109-116, 1994  
 A:Title: The beta-A4 amyloid precursor protein binding to copper.  
 A:Reference number: S46251; MUID:94320627  
 A:Contents: annotation; copper binding sites  
 A>Note: rat peptides were isolated but not sequenced  
 R:Potempska, A.; Styles, J.; Mehta, P.; Kim, K.S.; Miller, D.L.  
 J. Biol. Chem. 266, 8464-8469, 1991  
 A:Title: Purification and tissue level of the beta-amyloid peptide precursor of rat b  
 A:Reference number: A39820; MUID:91217087  
 A:Accession: A39820  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 18-32 <POT>  
 A:Experimental source: brain  
 C:Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques is  
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinas  
 C:Keywords: alternative splicing; amyloid; glycoprotein; transmembrane protein  
 F:625-648/Domain: transmembrane #status predicted <TM>

Query Match 100.0%; Score 47; DB 2; Length 695;  
 Best Local Similarity 100.0%; Pred. No. 0.19;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EETSEVKMDA 10  
 |||||||||  
 Db 589 EETSEVKMDA 598

## RESULT 5

ORMDA4  
 Alzheimer's disease amyloid beta protein precursor (validated) - human  
 N:Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor XIIa inh  
 N:Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vascu  
 protein precursor splice form APP(770)  
 C:Species: Homo sapiens (man)  
 C>Date: 30-Jun-1987 #sequence,revision 28-Jul-1995 #text\_change 15-Sep-2000  
 C:Accession: S02260; S05194; A32277; A3260; A3486; I39451; I39453; I59562;  
 4668; A28583; A29302; A60805; J00038; S06121; A60355; A50111; A38384; S29076; S38252;  
 R:Lemstra, H.G.; Salbaum, J.M.; Multhaupt, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.;  
 Nucleic Acids Res 17, 517-522, 1989  
 A:Title: The PreA4(655) precursor protein of Alzheimer's disease A4 amyloid is encode  
 A:Reference number: S02260; MUID:89128427  
 A:Accession: S02260  
 A:Molecule type: DNA  
 A:Residues: 1-288, 'V', 365-770 <LEM1>  
 A:Cross-references: EMBL:X13466  
 A>Note: alternative splice form APP(695)  
 R:Lemstra, H.G.  
 submitted to the EMBL Data Library, November 1988  
 A:Reference number: S05194  
 A:Accession: S05194  
 A:Molecule type: DNA  
 A:Residues: 1-14, 'W', 17-288, 'V', 365-770 <LEM2>  
 A:Cross-references: EMBL:X13466; NID:q35398; PIDN:CAA31830.1; PID:q871360  
 A>Note: alternative splice form APP(695)  
 R:Paul, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.  
 Biochem. Biophys. Res. Commun. 159, 297-304, 1989  
 A:Title: Characterization of the 5'-end region and the first two exons of the beta-pr  
 A:Reference number: A32277; MUID:89165870  
 A:Accession: A32277  
 A:Molecule type: DNA  
 A:Residues: 1-75 <LAF>  
 A:Cross-references: GB:M24546; GB:M24547; NID:q341202; PIDN:AA013654.1; PID:q516074  
 R:Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.  
 Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989  
 A:Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows simila

A:Reference number: A33260; MUID:89392030  
A:Accession: A33260  
A:Molecule type: DNA  
A:Residues: 656-737 <J06H>  
A:Cross-references: GB:M29270; NID:g178663; PIDN:AAA1768.1; PID:g178665  
R:Prell, F.; Levy, E.; Van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B.  
Biochem. Biophys. Res. Commun. 170, 301-307, 1990  
A:Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid of  
A:Reference number: A35486; MUID:90321244  
A:Accession: A35486  
A:Molecule type: DNA  
A:Residues: 672-710 <PRE1>  
A:Note: 693-Gln was found in DNA isolated from HCMA-D patients  
R:Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sasaki, Y.  
Gene 87, 257-263, 1990  
A:Title: Genomic organization of the human amyloid beta-protein precursor gene.  
A:Reference number: I39451; MUID:90236318  
A:Accession: I39452  
A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMF  
A:Molecule type: DNA  
A:Residues: 1-770 <YOS1>  
A:Cross-references: GB:M33112; NID:g178613; PIDN:AAB59502.1; PID:g178616  
A:Accession: I39451  
A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMF  
A:Molecule type: DNA  
A:Residues: 1-530, 'QMLMPVIPAFWEAKVGR' <YOS2>  
A:Cross-references: GB:M34875; NID:g178608; PIDN:AAB59501.1; PID:g178615  
R:Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sasaki, Y.  
Gene 102, 291-292, 1991  
A:Reference number: A59020; MUID:91340168  
A:Accession: A59020  
A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMF  
A:Contents: annotation: erratum  
A:Note: revised physical map for reference I39451  
R:Levy, E.; German, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van Duine  
Science 248, 1122-1126, 1990  
A:Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemorrh  
A:Reference number: I39453; MUID:90260663  
A:Accession: I39453  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 656-737 <LEV>  
A:Cross-references: GB:M37896; NID:g178618; PIDN:AAA51727.1; PID:g178620  
A:Note: a mutation with 693-Gln is presented  
R:Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.  
Science 254, 97-99, 1991  
A:Title: A mutation in the amyloid precursor protein associated with hereditary Alzheimer  
A:Reference number: I59562; MUID:92022553  
A:Accession: I59562  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 686-716, 'F', 718-737 <MR>  
A:Cross-references: GB:S57665; NID:g236720; PIDN:AAB19991.1; PID:g236721  
R:Kamino, K.; Ort, R.T.; Payami, H.; Wlismann, E.M.; Alonso, M.E.; Pulst, S.M.; Anderson,  
araksis, S.E.; Korenberg, J.R.; Sharma, V.; Kukul, W.; Larson, E.; Heston, L.L.; Martin,  
Am. J. Hum. Genet. 51, 998-1014, 1992  
A:Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for the  
A:Reference number: A44017; MUID:93035397  
A:Accession: A44017  
A:Molecule type: DNA  
A:Residues: 687-692, 'G', 694-718 <KAM1>  
A:Cross-references: GB:S45135; NID:g257377; PIDN:AAB23645.1; PID:g257378  
A:Experimental source: familial Alzheimer disease family SR  
A:Note: sequence extracted from NCBI backbone (NCBI:P.115374)  
A:Accession: B44017  
A:Molecule type: DNA  
A:Residues: 687-718 <KAM2>  
A:Cross-references: GB:S45136; NID:g257379; PIDN:AAB23646.1; PID:g257380  
A:Experimental source: familial Alzheimer disease family LT  
A:Note: sequence extracted from NCBI backbone (NCBI:P.115376)  
A:Note: this sequence has a silent mutation  
R:Kang, J.; Lemaitre, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.H.;  
Nature 335, 733-736, 1987  
A:Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surface  
A:Reference number: A03134; MUID:87144572

A:Accession: A03134  
A:Molecule type: mRNA  
A:Residues: 1-288, 'V', 365-770 <KAN>  
A:Cross-references: GB:Y00264; NID:g28525; PIDN:CAA68374.1; PID:g28526  
A:Note: alternative splice form APP(695)  
R:Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.  
Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987  
A:Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascula  
A:Reference number: A29030; MUID:87231971  
A:Accession: A29030  
A:Molecule type: mRNA  
A:Residues: 284-288, 'V', 365-646, 'E', 648-770 <ROB>  
A:Cross-references: GB:M6765; NID:g178539; PIDN:AAA51722.1; PID:g178540  
A:Note: the authors translated the codon GAG for residue 647 as Asp  
R:Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Safitoff, U.; Gajdusek, D.C.  
Science 235, 877-880, 1987  
A:Title: Characterization and chromosomal localization of a cDNA encoding brain amylo  
A:Reference number: A47584; MUID:87120328  
A:Accession: A47584  
A:Molecule type: mRNA  
A:Residues: 674-756, 'S', 758-770 <GOL>  
A:Cross-references: GB:M15533; NID:g178706; PIDN:AAA35540.1; PID:g178707  
A:Experimental source: brain  
R:Tanzil, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van  
Science 235, 880-884, 1987  
A:Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near  
A:Reference number: A47585; MUID:87120329  
A:Accession: A47585  
A:Molecule type: mRNA  
A:Residues: 674-703 <TAN1>  
R:Dyck, T.; Weldmann, A.; Multhaup, G.; Salbaum, J.M.; Lemaitre, H.G.; Kang, J.; Mue  
EMBO J. 7, 949-957, 1988  
A:Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 p  
A:Reference number: S02638; MUID:88296437  
A:Accession: S02638  
A:Molecule type: mRNA  
A:Residues: 672-678 <DR>  
R:Tanzil, R.E.; McClatchey, A.I.; Lamperti, E.D.; Villa-Komaroff, L.; Gusella, J.F.; N  
Nature 331, 528-530, 1988  
A:Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA assoc  
A:Reference number: S00707; MUID:88122640  
A:Accession: S00707  
A:Molecule type: mRNA  
A:Residues: 286-344, 'I', 365-366 <TAN2>  
A:Cross-references: EMBL:X06982; NID:g28817; PIDN:CAA30042.1; PID:g28812  
A:Experimental source: promyelocytic leukemia cell line HL60  
A:Note: alternative splice form APP(751)  
R:Ponte, P.; Gonzalez-Denit, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.;  
Nature 331, 525-527, 1988  
A:Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inh  
A:Reference number: S00925; MUID:88122639  
A:Accession: S00925  
A:Molecule type: mRNA  
A:Residues: 1-344, 'V', 365-770 <PO2>  
A:Cross-references: GB:X06989; EMBL:Y00297; NID:g28720; PIDN:CAA30050.1; PID:g28721  
A:Note: alternative splice form APP(770)  
R:Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.  
Nature 331, 530-532, 1988  
A:Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibi  
A:Reference number: A38949; MUID:88122642  
A:Accession: A38949  
A:Molecule type: mRNA  
A:Residues: 287-367 <KIT>  
A:Cross-references: GB:X06981; NID:g28816; PIDN:CAA30041.1; PID:g28811  
A:Experimental source: glioblastoma cell line  
A:Note: alternative splice form APP(770)  
R:Vittek, M.P.; Rasool, C.G.; de Sauvage, F.; Vittek, S.M.; Bartus, R.T.; Beer, B.; Ash  
Brain Res. Mol. Brain Res. 4, 121-131, 1988  
A:Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of thre  
A:Reference number: A30320  
A:Accession: A30320  
A:Status: not compared with conceptual translation

A:Molecule type: mRNA  
 A:Residues: 284-288 'V', 365-770 <VIT1>  
 A:Accession: B30320  
 A>Status: not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 122-288 'V', 365-770 <VIT2>  
 A:Accession: C30320  
 A>Status: not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 606-770 <VIT3>  
 R:Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta, C.A.  
 Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988  
 A:Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease by  
 A:Reference number: A31087; MUID:88124954  
 A:Accession: A31087  
 A:Molecule type: mRNA  
 A:Residues: 507-770 <VIT>  
 A:Cross-references: GB:M18734; NID:q178572; PIDN:AA51726.1; PID:q178573  
 A:Note: the authors translated the codon GAA for residue 599 as Gly, ACC for residue 603  
 8 as Val, GTG for residue 609 as Asn, AAT for residue 610 as Gly, and GGT for residue 65  
 A:Note: The cited Genbank accession number, J03594, is not in release 10.1.0  
 R:Maisters, C.L.; Multhaup, G.; Simms, G.; Potgiesser, J.; Martins, R.N.; Beyreuther, K.  
 Query Match 100.0%; Score 47; DB 1; Length 770;  
 Best Local Similarity 100.0%; Pred. No. 0.21;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 EISEVXMDA 10  
 DB 664 EISEVXMDA 673  
 RESULT 6  
 JH0773  
 Alzheimer's disease amyloid beta protein precursor - African clawed frog  
 A:Species: Xenopus laevis (African clawed frog)  
 C>Date: 10-Jun-1993 #sequence\_revision 10-Jun-1993 #text\_change 13-Aug-1999  
 C:Accession: JH0773  
 R:Okado, H.; Okamoto, H.  
 Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992  
 A:Title: A Xenopus homologue of the human beta-amyloid precursor protein: developmental  
 A:Reference number: JH0773; MUID:93129227  
 A:Accession: JH0773  
 A:Molecule type: mRNA  
 A:Residues: 1-747 COKA  
 A:Cross-references: GB:S52417; NID:g263150; PIDN:AA824853.1; PID:g263151  
 A:Experimental source: larva  
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinase  
 C:Keywords: alternative splicing; amyloid  
 F:287-337/Domain: animal kunitz-type proteinase inhibitor homology <BPI>  
 Query Match 93.6%; Score 44; DB 2; Length 747;  
 Best Local Similarity 90.0%; Pred. No. 0.83;  
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 EISEVXMDA 10  
 DB 641 EISEVXMDA 650  
 RESULT 7  
 C69136  
 hypothetical protein MTH286 - Methanobacterium thermoautotrophicum (strain Delta H)  
 C:Species: Methanobacterium thermoautotrophicum  
 C>Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 22-Oct-1999  
 C:Accession: C69136  
 R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;  
 Qiu, D.; Spadafora, R.; Vitale, R.; Wang, Y.; Wlaczowski, J.; Gibson, R.; Jiwani, N.  
 K.; Church, G.M.; Daniels, C.D.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.  
 J. Bacteriol. 179, 7135-7155, 1997  
 A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct  
 A:Reference number: A69000; MUID:98037514  
 A:Accession: C69136

A>Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-146 <MTH>  
 A:Cross-references: GB:AE000814; GB:AE000666; NID:g2621334; PIDN:AA84792.1; PID:g262  
 A:Experimental source: strain Delta H  
 C:Genetics:  
 A:Gene: MTH286  
 A:Start codon: GTG  
 C:Superfamily: Methanobacterium thermoautotrophicum hypothetical protein MTH286  
 Query Match 78.7%; Score 37; DB 2; Length 146;  
 Best Local Similarity 77.8%; Pred. No. 3.6;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 OY 1 EISEVXMD 9  
 DB 125 EELKVKMD 133  
 RESULT 8  
 T12832  
 hypothetical protein yonU - Bacillus subtilis phage SPBc2  
 C:Species: Bacillus subtilis phage SPBc2  
 C>Date: 13-Aug-1999 #sequence\_revision 13-Aug-1999 #text\_change 15-Oct-1999  
 C:Accession: T12832; D69915  
 R:Lazarevic, V.; Duesterhoeft, A.; Soldo, B.; Hilbert, H.; Mauel, C.; Karamata, D.  
 submitted to the EMBL Data Library, August 1997  
 A:Description: The complete nucleotide sequence of the Bacillus subtilis spBc2 pro  
 A:Reference number: 217583  
 A:Accession: T12832  
 A>Status: preliminary; translated from GB/EMBL/DDA3  
 A:Molecule type: DNA  
 A:Residues: 1-62 <LAT>  
 A:Cross-references: EMBL:AF020713; NID:g3025478; PID:g3025546; PIDN:AA13041.1  
 R:Kunet, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Aevedo, V.; Ber  
 C:Bron, S.; Brouillet, S.; Brusch, C.V.; Calowell, B.; Capuano, V.; Carter, N.M.;  
 A.: Ehrlich, S.D.; Emmertson, P.T.; Ehtian, K.D.; Errington, J.; Fabre, C.; Ferrari,  
 Nature 390, 249-256, 1997  
 A:Authors: Foulger, D.; Filtz, C.; Fujita, M.; Fujita, Y.; Funo, S.; Galizzi, A.; Gal  
 lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holstappel, S.; Hosono, S.; Hullo, M  
 Koeltter, P.; Konigstein, G.; Krogh, V.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino  
 A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau  
 Y., M.; Ogawa, K.; Ogihara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete  
 Rieger, M.; Rivolta, C.; Roeha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanl  
 A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se  
 Akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchida  
 T.; Winters, P.; Wippl, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida  
 A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.  
 A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtili  
 A:Reference number: A69580; MUID:98044033  
 A:Accession: D69915  
 A>Status: nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-62 <KND>  
 A:Cross-references: GB:g99115; GB:AL009126; NID:g26344478; PIDN:CA14017.1; PID:el1835  
 A:Experimental source: strain 168  
 C:Genetics:  
 A:Gene: yonU  
 Query Match 72.3%; Score 34; DB 2; Length 62;  
 Best Local Similarity 77.8%; Pred. No. 5.6;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 OY 1 EISEVXMD 9  
 DB 42 EELKVKMD 50  
 RESULT 9  
 S23094  
 beta-amyloid protein precursor - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 03-May-1996



C:Accession: S23094  
 R:Kojima, S.; Omori, M.  
 FEBS Lett. 304, 57-60, 1992  
 A:Title: Two-way cleavage of beta-amyloid protein precursor by multicatalytic proteinase  
 A:Reference number: S23094; MUID:92316198  
 A:Accession: S23094  
 A:Molecule type: protein  
 A:Residues: 1-33 <JO>  
 A:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase

Query Match  
 Best Local Similarity 70.2%; Score 33; DB 2; Length 33;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 SEVKMDA 10  
 Db 1 SEVKMDA 7

# RESULT 10

E60045  
 Alzheimer's disease amyloid beta/A4 protein precursor - sheep (fragment)  
 C:Species: Ovis sp. (sheep)  
 C:Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 28-Jul-1995  
 C:Accession: E60045  
 R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
 Brain Res. Mol. Brain Res. 10, 299-305, 1991  
 A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,  
 A:Reference number: A60045; MUID:92017079  
 A:Accession: E60045  
 A:Molecule type: mRNA  
 A:Residues: 1-57 <JOH>  
 A:Cross-references: EMBL:X56130  
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase  
 C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match  
 Best Local Similarity 70.2%; Score 33; DB 2; Length 57;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 SEVKMDA 10  
 Db 1 SEVKMDA 7

# RESULT 11

F60045  
 Alzheimer's disease amyloid beta/A4 protein precursor - pig (fragment)  
 C:Species: Sus scrofa domestica (domestic pig)  
 C:Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 13-Aug-1999  
 C:Accession: F60045  
 R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
 Brain Res. Mol. Brain Res. 10, 299-305, 1991  
 A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,  
 A:Reference number: A60045; MUID:92017079  
 A:Accession: F60045  
 A:Molecule type: mRNA  
 A:Residues: 1-57 <JOH>  
 A:Cross-references: EMBL:X56127; NID:g1895; PIDN:CAA39592.1; PID:g1896  
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase  
 C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match  
 Best Local Similarity 70.2%; Score 33; DB 2; Length 57;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 SEVKMDA 10  
 Db 1 SEVKMDA 7

# RESULT 12

G60045

Alzheimer's disease amyloid beta/A4 protein precursor - guinea pig (fragment)  
 C:Species: Cavia porcellus (guinea pig)  
 C:Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 28-Jul-1995  
 C:Accession: G60045  
 R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
 Brain Res. Mol. Brain Res. 10, 299-305, 1991  
 A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d  
 A:Reference number: A60045; MUID:92017079  
 A:Accession: G60045  
 A:Molecule type: mRNA  
 A:Residues: 1-57 <JOH>  
 A:Cross-references: EMBL:X56126  
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase  
 C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match  
 Best Local Similarity 70.2%; Score 33; DB 2; Length 57;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 SEVKMDA 10  
 Db 1 SEVKMDA 7

# RESULT 13

D60045  
 Alzheimer's disease amyloid beta/A4 protein precursor - bovine (fragment)  
 C:Species: Bos primigenius taurus (cattle)  
 C:Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 28-Jul-1995  
 C:Accession: D60045  
 R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
 Brain Res. Mol. Brain Res. 10, 299-305, 1991  
 A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d  
 A:Reference number: A60045; MUID:92017079  
 A:Accession: D60045  
 A:Molecule type: mRNA  
 A:Residues: 1-57 <JOH>  
 A:Cross-references: EMBL:X56124  
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase  
 C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match  
 Best Local Similarity 70.2%; Score 33; DB 2; Length 57;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 SEVKMDA 10  
 Db 1 SEVKMDA 7

# RESULT 14

A60045  
 Alzheimer's disease amyloid beta/A4 protein precursor - dog (fragment)  
 C:Species: Canis lupus familiaris (dog)  
 C:Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 28-Jul-1995  
 C:Accession: A60045  
 R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
 Brain Res. Mol. Brain Res. 10, 299-305, 1991  
 A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d  
 A:Reference number: A60045; MUID:92017079  
 A:Accession: A60045  
 A:Molecule type: mRNA  
 A:Residues: 1-57 <JOH>  
 A:Cross-references: EMBL:X56125  
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase  
 C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match  
 Best Local Similarity 70.2%; Score 33; DB 2; Length 57;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 SEVKMDA 10  
 Db 1 SEVKMDA 7

Db 1 SEVKMDA 7

## RESULT 15

B60045

Alzheimer's disease amyloid beta/A4 protein precursor - polar bear (fragment)

C:Species: ursus maritimus (polar bear)

C:Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 13-Aug-1999

C:Accession: B60045

R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,

A:Reference number: A60045; MUID:92017079

A:Accession: B60045

A:Molecule type: mRNA

A:Residues: 1-57 &lt;IOH&gt;

A:Cross-references: EMBL:X56128; NID:92165; PIDN:CA39593.1; PID:92166

C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinase

C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

## Query Match

70.2%; Score 33; DB 2; Length 57;

Best Local Similarity 100.0%; Pred. No. 8.1;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SEVKMDA 10

Db 1 SEVKMDA 7

Search completed: October 29, 2002, 10:30:57  
Job time : 12.4286 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 29, 2002, 10:22:36 ; Search time 5 Seconds  
(77,439 Million cell updates/sec)

Title: US-09-580-018-1  
Perfect score: 47  
Sequence: 1 EISEVKKMDA 10

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	47	100.0	751 1 A4_SAIISC	Q95241 salmirl sci
2	47	100.0	770 1 A4_HUMAN	P05067 homo sapien
3	47	100.0	770 1 A4_MOUSE	P12023 mus musculu
4	47	100.0	770 1 A4_RAT	P08592 rattus norv
5	37	78.7	58 1 A4_CANFA	Q28280 canis fami
6	37	78.7	59 1 A4_BOVIN	Q28053 bos taurus
7	34	72.3	638 1 A4_MOUSE	Q31151 mus musculu
8	33	70.2	57 1 A4_PIG	Q29149 sus scrofa
9	33	70.2	57 1 A4_GRSMA	Q29149 ursus marit
10	33	70.2	58 1 A4_RABIT	Q28748 oryctolagu
11	33	70.2	58 1 A4_SHEEP	Q28757 ovis arie
12	32	68.1	230 1 T2E7_ECOLI	P50134 escherichia
13	32	68.1	332 1 MDHC_BETUV	Q9SM18 beta vulgar
14	32	68.1	488 1 GABA_CHICK	P14205 gallus gall
15	32	68.1	575 1 SLP1_CAMEL	P14260 camorhadi
16	32	68.1	632 1 GAT_HUMAN	Q4968 homo sapien
17	32	68.1	1121 1 EXSC_HAEN	Q92550 haemophilu
18	31	65.0	227 1 G786_HUMAN	Q51676 paracoccu
19	31	65.0	451 1 HEMN_PANDE	Q14790 h caspase-8
20	31	65.0	479 1 ICEG_HUMAN	Q46083 lactobacilli
21	31	65.0	500 1 STEL_HABDE	P43007 homo sapien
22	31	65.0	532 1 SART_HUMAN	P20616 bos tauru
23	31	65.0	613 1 SG2_BOVIN	Q9X149 bos tauru
24	31	65.0	630 1 S6A4_BOVIN	Q53859 cavia porce
25	31	65.0	630 1 S6A4_CAVPO	P11645 macaca mula
26	31	65.0	630 1 S6A4_HUMAN	Q9MYX0 macaca mula
27	31	65.0	630 1 S6A4_MACMU	Q60857 mus musculu
28	31	65.0	630 1 S6A4_MOUSE	P11652 rattus norv
29	31	65.0	630 1 S6A4_RAT	P36842 leptosphaer
30	31	65.0	630 1 NIA_LEPMC	P19331 clostridium
31	31	65.0	630 1 BMD_CLOBO	O51339 borrelia bu
32	31	65.0	1276 1 RPOC_BOBBU	P19598 plasmodium
33	31	65.0	1682 1 MSP1_PLAF3	

34	30	63.8	61 1 RL29_CAMJE	Q9P199 campylobact
35	30	63.8	94 1 RL23_MYCCA	P10140 mycoplasma
36	30	63.8	104 1 YB04_MYCPN	P75565 mycoplasma
37	30	63.8	141 1 RL11_HELPY	P56037 helicobacte
38	30	63.8	257 1 YAI3_MYCPN	P75100 mycoplasma
39	30	63.8	263 1 AF11_THFTE	P58315 thermoprote
40	30	63.8	297 1 PHE7_MYCTU	O59566 mycobacteri
41	30	63.8	305 1 YOB8_BACSU	P45918 bacillus su
42	30	63.8	336 1 KCB1_BOVIN	P35507 bos tauru
43	30	63.8	432 1 OV71_ONCYO	P31732 onchocerca
44	30	63.8	442 1 SR54_METH	O27376 methanobact
45	30	63.8	464 1 GAR3_RAT	P50373 rattus norv

## ALIGNMENTS

RESULT 1	ID	A4_SAIISC	STANDARD:	PRT:	751 AA.
AC	Q95241:				
DT	15-DEC-1998 (Rel. 37, Created)				
DT	15-DEC-1998 (Rel. 37, Last sequence update)				
DT	15-OCT-2001 (Rel. 40, Last annotation update)				
DE	Alzheimer's disease amyloid A4 protein precursor [contains: Beta-amyloid protein (Beta-Ap4) (A-beta)].				
CN	APP.				
OS	Saimiri sciureus (Common squirrel monkey).				
CC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
CC	Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Saimiri.				
OX	NCBI_Taxid=9521;				
NP	SEQUENCE FROM N.A.				
RC	HLSDU-1487, and Kidney,				
RA	MEHLIN-96108492; PubMed-8532114;				
RA	Levy E., Amorim A., Frangione B., Walker L.C.;				
RT	"beta-amyloid precursor protein gene in squirrel monkeys with cerebral amyloid angiopathy."				
RL	Neurobiol. Aging 16:805-808(1995).				
CC	-1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN G(O).				
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.				
CC	-1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF PHOSPHORYLATION (BY SIMILARITY).				
CC	-1- SIMILARITY: BELONGS TO THE APP FAMILY.				
CC	-1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> )				
CC	EMBL: S81024; A014347.1; -				
DR	HSPD: P05067; IAPP				
DR	InterPro: IPR001866; A4_APP.				
DR	InterPro: IPR002223; Kunitz_BPTI.				
DR	Pfam: PF02177; A4_EXTRA; 1.				
DR	Pfam: PF00014; Kunitz_BPTI; 1.				
DR	PRINTS: PR00203; AMYLOID4.				
DR	PRINTS: PR00759; BASICPEASE.				
DR	SMART: SM00006; A4_EXTRA; 1.				
DR	SMART: SM00131; KU; 1.				
DR	PROSITE: PS00319; A4_EXTRA; 1.				
DR	PROSITE: PS00320; A4_INTRA; 1.				
DR	PROSITE: PS00280; BPTI_KUNITZ_1; 1.				
DR	PROSITE: PS00279; BPTI_KUNITZ_2; 1.				

KM Glycoprotein; Amyloid; Neurone; Transmembrane; Alternative splicing;  
 KW Signal: Serine protease inhibitor.  
 FT CHAIN 1 17 BY SIMILARITY.  
 FT CHAIN 18 751 A4 PROTEIN.  
 FT CHAIN 653 695 BETA-AMYLOID PROTEIN (POTENTIAL).  
 FT DOMAIN 18 680 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 681 704 POTENTIAL.  
 FT DOMAIN 705 751 CYTOSOLIC (POTENTIAL).  
 FT DOMAIN 287 345 BPT/UNIT-1 INHIBITOR.  
 FT SITE 740 745 CATHRIN-BINDING (BY SIMILARITY).  
 FT ACT\_SITE 301 302 REACTIVE BOND.  
 FT DISULFID 341 341 BY SIMILARITY.  
 FT DISULFID 300 324 BY SIMILARITY.  
 FT DISULFID 316 337 BY SIMILARITY.  
 FT CARBOHYD 523 523 N-LINKED (GLCNAC. . .) (PROBABLE).  
 FT CARBOHYD 552 552 N-LINKED (GLCNAC. . .) (PROBABLE).  
 SQ SEQUENCE 751 AA; 84893 MM; 6C3E431089569049 CRC64;  
 Query Match Score 47; DB 1; Length 751;  
 Best Local Similarity 100.0%; Pred. No. 0.13;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EISEVAKMDA 10  
 Db 645 EISEVAKMDA 654  
 RESULT 2  
 A4\_HUMAN STANDARD; PRT: 770 AA.  
 ID A4\_HUMAN  
 AC P05067; P05000; Q16011;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 01-NOV-1991 (Rel. 20, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Alzheimer's disease amyloid A4 protein precursor (Protease nexin-II) (PN-II) (APP) [contains: Beta-amyloid protein (beta-APP) (A-beta)].  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Brain:  
 RX MEDLINE-87144572; PubMed-2881207;  
 RA Kang U., Lemaitre H.-G., Unterbeck A., Salbaum J.M., Masters C.L.,  
 RA Grieschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.;  
 RT "The precursor of Alzheimer's disease amyloid A4 protein resembles a  
 cell-surface receptor.";  
 RL Nature 325:733-736(1987).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-8812639; PubMed-2893289;  
 RA Ponte P., Gonzalez-Dewhilt P., Schilling J., Miller J., Hsu D.,  
 RA Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F.,  
 RA Cordell B.;  
 RT "A new A4 amyloid mRNA contains a domain homologous to serine  
 proteinase inhibitors.";  
 RL Nature 331:525-527(1988).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-89128427; PubMed-2783775;  
 RA Lemaitre H.-G., Salbaum J.M., Multhaup G., Kang J., Bayney R.M.,  
 RA Unterbeck A., Beyreuther K., Mueller-Hill B.;  
 RT "The P36A1(695) precursor protein of Alzheimer's disease A4 amyloid  
 is encoded by 16 exons.";  
 RL Nucleic Acids Res. 17:517-522(1989).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-97263807; PubMed-9108154;  
 RA Hattori M., Tsukahara F., Furukawa Y., Tanenashi H., Hirose M.,  
 RA Saito M., Tsukuni S., Sakaki Y.;  
 RT "A novel method for making nested deletions and its application for

RT sequencing of a 300 kb region of human APP locus.";  
 RL Nucleic Acids Res. 25:1802-1808(1997).  
 RN [5]  
 RP SEQUENCE OF 286-345 AND 365-366 FROM N.A.  
 RX MEDLINE-88122640; PubMed-2893290;  
 RA Tanzi R.E., McClatchey A.I., Lamperti E.D., Villa-Komaroff L.,  
 RA Guevelia J.F., Neve R.L.;  
 RT "Protease inhibitor domain encoded by an amyloid protein precursor  
 mRNA associated with Alzheimer's disease.";  
 RL Nature 331:528-530(1988).  
 RN [6]  
 RP SEQUENCE OF 287-367 FROM N.A.  
 RX MEDLINE-88122641; PubMed-2893291;  
 RA Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.;  
 RT "Novel precursor of Alzheimer's disease amyloid protein shows  
 protease inhibitory activity.";  
 RL Nature 331:530-532(1988).  
 RN [7]  
 RP SEQUENCE OF 284-289 AND 365-770 FROM N.A.  
 RX MEDLINE-87231971; PubMed-3035574;  
 RA Robakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;  
 RT "Molecular cloning and characterization of a cDNA encoding the  
 cerebrovascular and the neuritic plaque amyloid peptides.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).  
 RN [8]  
 RP SEQUENCE OF 507-770 FROM N.A.  
 RX MEDLINE-88124954; PubMed-2893379;  
 RA Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,  
 RA Marotta C.A.;  
 RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer  
 disease brain: coding and noncoding regions of the fetal precursor  
 mRNA are expressed in the cortex.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).  
 RN [9]  
 RP SEQUENCE OF 672-681.  
 RX MEDLINE-88035004; PubMed-3312495;  
 RA Farridge W.M., Vinters H.V., Tang J., Eisenberg J., Choi T.B.,  
 RA Tourtelotte W.W., Huebner V., Shively J.E.;  
 RT "Amyloid angiopathy of Alzheimer's disease: amino acid composition  
 and partial sequence of a 4,200-dalton peptide isolated from cortical  
 microvessels.";  
 RL J. Neurochem. 49:1394-1401(1987).  
 RN [10]  
 RP SEQUENCE OF 739-770 FROM N.A.  
 RX MEDLINE-90236318; PubMed-2110105;  
 RA Yoshikai S.-I., Sasaki H., Doh-ura K., Furuya H., Sakaki Y.;  
 RT "Genomic organization of the human amyloid beta-protein precursor  
 gene.";  
 RL Gene 87:257-263(1990).  
 RN [11]  
 RP SEQUENCE OF 1-10 FROM N.A.  
 RC TISSUE-Liver:  
 RX MEDLINE-89016647; PubMed-3140222;  
 RA Schon E.A., Mita S., Sadlock J., Herbert J.;  
 RT "A cDNA specifying the human amyloid beta precursor protein (ABPP).  
 RT encodes a 95-kDa polypeptide.";  
 RL Nucleic Acids Res. 16:9351-9351(1988).  
 RN [12]  
 RP SEQUENCE OF 18-50.  
 RX MEDLINE-87250462; PubMed-3597385;  
 RA van Nostrand W.E., Cunningham D.D.;  
 RT "Purification of protease nexin II from human fibroblasts.";  
 RL J Biol. Chem. 262:8508-8514(1987).  
 RN [13]  
 RP IDENTITY OF APP WITH NEXIN-II.  
 RX MEDLINE-89384866; PubMed-2506449;  
 RA Oltersdorf T., Fritz L.C., Schenk D.B., Lieberburg I.,  
 RA Johnson-Wood K.L., Beattie E.C., Ward P.J., Blacher R.W., Dovey H.F.,  
 RA Sinha S.;  
 RT "The secreted form of the Alzheimer's amyloid precursor protein with  
 the Kunitz domain is protease nexin-II.";  
 RL Nature 341:144-147(1989).  
 RN [14]

RP PROTEASE-SPECIFICITY OF INHIBITOR DOMAIN.  
 RX MEDLINE=90211252; PubMed=1969731;  
 RA Kido H., Fukutomi A., Schilling J., Wang Y., Cordell B., Katunuma N.;  
 RT "Protease-specificity of Kunitz inhibitor domain of Alzheimer's  
 RT disease amyloid protein precursor.";  
 RL Biochem. Biophys. Res. Commun. 167:716-721(1990).  
 RN [15]  
 RP COMPLEX WITH G(O).  
 RX MEDLINE=93188965; PubMed=8446172;  
 RA Nishimoto I., Okamoto T., Matsura Y., Takahashi S., Okamoto T.,  
 RA Murayama Y., Ogata E.;  
 RT "Alzheimer amyloid protein precursor complexes with brain GTP-binding  
 RT protein G(O).";  
 RL Nature 362:75-79(1993).  
 RN [16]  
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 28-133.  
 RX MEDLINE=99215582; PubMed=10201399;  
 RA Rossjohn J., Cappai R., Fell S.C., Henry A., Mckinstrey W.J.,  
 RA Galatis D., Hesse L., Multhaup G., Beyreuther K., Masters C.L.,  
 RA Parker M.W.;  
 RT "Crystal structure of the N-terminal, growth factor-like domain of  
 RT Alzheimer amyloid precursor protein.";  
 RL Nat. Struct. Biol. 6:327-331(1999).  
 RN [17]  
 RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF 287-344.  
 RX MEDLINE=91104913; PubMed=2125487;  
 RA Hyres T.R., Randal M., Kennedy L.A., Eigenbrodt C., Kosiakof A.A.;  
 RT "X-ray crystal structure of the protease inhibitor domain of  
 RT Alzheimer's amyloid beta-protein precursor.";  
 RL Biochemistry 29:10018-10022(1990).  
 RN [18]  
 RP STRUCTURE BY NMR OF 289-344.  
 RX MEDLINE=92031488; PubMed=1718421;  
 RA Heald S.L., Tilton R.F. Jr., Hammond L.S., Lee A., Bayney R.M.,  
 RA Kambeck M.E., Ramabhadran T.V., Dreyer R.N., Davis G., Unterbeck A.,  
 RA Tamburini P.P.;  
 RT "Sequential NMR resonance assignment and structure determination of  
 RT the Kunitz-type inhibitor domain of the Alzheimer's beta-amyloid  
 RT precursor protein.";  
 RL Biochemistry 30:10467-10478(1991).  
 RN [19]  
 RP STRUCTURE BY NMR OF 672-699.  
 RX MEDLINE=94281210; PubMed=7516706;  
 RA Talatous J., Marciniowski K.J., Klopman G., Zagorski M.G.;  
 RT "Solution structure of residues 1-28 of the amyloid beta-peptide.";  
 RL Biochemistry 33:7788-7796(1994).  
 RN [20]  
 RP STRUCTURE BY NMR OF 696-706.  
 RX MEDLINE=97128622; PubMed=8973180;  
 RA Kohno T., Kobayashi K., Maeda T., Sato K., Takashima A.;  
 RT "Three-dimensional structures of the amyloid beta peptide (25-35) in  
 RT membrane-mimicking environment.";  
 RL Biochemistry 35:16094-16104(1996).  
 RN [21]  
 RP STRUCTURE BY NMR OF 672-711.  
 RX MEDLINE=98359783; PubMed=9693002;  
 RA Coles M., Bicknell W., Watson A.A., Fairlie D.P., Craik D.J.;  
 RT "Solution structure of amyloid beta-peptide(1-40) in a water-miscelle  
 RT environment. Is the membrane-spanning domain where we think it is?";  
 RL Biochemistry 37:11064-11077(1998).  
 RN [22]  
 RP STRUCTURE BY NMR OF 672-699.  
 RX MEDLINE=20400066; PubMed=10940222;  
 RA Poulsen S.-A., Watson A.A., Craik D.J.;  
 RT "Solution structures in aqueous SDS micelles of two amyloid beta  
 RT peptides of Abeta(1-28) mutated at the alpha-secretase cleavage  
 RT site.";  
 RL J. Struct. Biol. 130:142-152(2000).  
 RN [23]  
 RP STRUCTURE BY NMR OF 681-706.  
 RX MEDLINE=20400065; PubMed=10940221;  
 RA Zhang S., Iwata K., Lachemann M.J., Peng J.W., Li S., Stinson E.R.,  
 RA Lu Y., Felix A.M., Maggio J.E., Lee J.P.;

RT "The Alzheimer's peptide a beta adopts a collapsed coil structure in  
 RT water.";  
 RL J. Struct. Biol. 130:130-141(2000).  
 RN [24]  
 RP SIGNAL SEQUENCE CLEAVAGE SITE, AND TOPOLOGY.  
 RX MEDLINE=88296437; PubMed=2900137;  
 RA Dykx T., Weidemann A., Multhaup G., Salbaum J.M., Lemaire H.-G.,  
 RA Kang J., Mueller-Hill B., Masters C.L., Beyreuther K.;  
 RT "Identification, transmembrane orientation and biogenesis of the  
 RT amyloid A4 precursor of Alzheimer's disease.";  
 QY Query Match 100.0%; Score 47; DB 1; Length 770;  
 Best Local Similarity 100.0%; Pred. No. 0.13;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DB 664 EISEVAKMDA 673  
 QY 1 EISEVAKMDA 10  
 DB 664 EISEVAKMDA 673  
 RESULT 3  
 A4\_MOUSE STANDARD: PRT; 770 AA.  
 ID A4\_MOUSE  
 AC P12023;  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Alzheimer's disease amyloid A4 protein homolog precursor  
 DE (Amyloidogenic glycoprotein) (AG).  
 GN APP  
 OS Mus musculus (Mouse)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.  
 KC STRAIN-BALB/C; TISSUE-Brain;  
 RX MEDLINE=92096458; PubMed=1756177;  
 RA de Strooper B., van Leuven F., van den Bergh H.;  
 RT "The amyloid beta protein precursor or proteinase nexin II from mouse  
 RT is closer related to its human homolog than previously reported.";  
 RL Biochim. Biophys. Acta 1129:141-143(1991).  
 RN [2]  
 RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.  
 KC TISSUE-Brain;  
 RX MEDLINE=88106489; PubMed=3322280;  
 RA Yamada T., Sasaki H., Furuya H., Miyata T., Goto I., Sasaki Y.;  
 RT "Complementary DNA for the mouse homolog of the human amyloid beta  
 RT protein precursor.";  
 RL Biochem. Biophys. Res. Commun. 149:665-671(1987).  
 RN [3]  
 RP REVISIONS.  
 RA Yamada T.;  
 RL Submitted (MAR-1988) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE OF 289-364 FROM N.A.  
 KC STRAIN-CD-1; TISSUE-Placenta;  
 RX MEDLINE=89345111; PubMed=2569710;  
 RA Fukuchi K., Martin G.M., Deeb S.S.;  
 RT "Sequence of the protease inhibitor domain of the A4 amyloid protein  
 RT precursor of Mus domestica.";  
 RL Nucleic Acids Res. 17:5396-5396(1989).  
 RN [5]  
 RP SEQUENCE OF 1-19 FROM N.A.  
 RX MEDLINE=92209998; PubMed=1555768;  
 RA Izumi R., Yamada T., Yoshikai S.I., Sasaki H., Hattori M.,  
 RA Sakai Y.;  
 RT "Positive and negative regulatory elements for the expression of the  
 RT Alzheimer's disease amyloid precursor-encoding gene in mouse.";  
 RL Gene 112:189-195(1992).  
 RN [6]  
 RP SEQUENCE OF 281-380 FROM N.A., AND ALTERNATIVE SPLICING.  
 RE TISSUE-Brain, and Kidney;

```

RX MEDLINE-89149813; PubMed-2493250;
RA Yamada T., Sasaki H., Dohura K., Ooto I., Sakaki Y.;
RT "Structure and expression of the alternatively-spliced forms of mRNA
RT for the mouse homolog of Alzheimer's disease amyloid beta protein
RT precursor.";
RL Biochem. Biophys. Res. Commun. 158:906-912(1989).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS: APP(395), APP(563), APP(695),
CC APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE
CC SPLICING.
CC -1- TISSUE SPECIFICITY: AAA(770) IS EXPRESSED IN KIDNEY. AAA(751) IS
CC WIDELY EXPRESSED. AAA(695) IS EXPRESSED IN BRAIN, KIDNEY AND
CC LIVER.
CC -1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
CC WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
CC NXYX MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
CC PHOSPHORYLATION (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
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CC -----
DR EMBL: X59379; -; NOT ANNOTATED_CDS.
DR EMBL: M18373; AAA3739.1; -
DR EMBL: X15210; CAA33280.1; -
DR EMBL: D10603; BAA01456.1; -
DR EMBL: M24387; AAA39929.1; -
DR PIR: A27485; A27485.
DR PIR: S04855; S04855.
DR PIR: S19727; S19727.
DR HSSP: P05067; IQCM.
DR MGD: MGI:88059; APP.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam: PF02177; A4_EXTRA.1.
DR Pfam: PF00014; Kunitz_BPTI.1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PRINTS: PR00759; BASICPTASE.
DR SMART: SM00006; A4_EXTRA.1.
DR SMART: SM00131; KU.1.
DR PROSITE: PS00319; A4_EXTRA.1.
DR PROSITE: PS00320; A4_INTRA.1.
DR PROSITE: PS00280; BPTI_KUNITZ.1.
DR PROSITE: PS0279; BPTI_KUNITZ.2.1.
KW Glycoprotein; Amyloid; Neurope; Transmembrane; Signal;
KW Alternative splicing; Serine protease inhibitor.
FT SIGNAL 18 770
FT CHAIN 18 770
FT TRANSHEM 18 599
FT TRANSHEM 700 723
FT DOMAIN 724 770
FT DOMAIN 673 715
FT DOMAIN 287 345
FT SITE 759 762
FT DISULFID 291 341
FT DISULFID 300 324
FT DISULFID 316 337
FT CARBOHYD 542 542
FT CARBOHYD 571 571
FT CARBOHYD 289 289
FT VARSPLIC 290 364
FT VARSPLIC 346 380
FT SEQUENCE 770 AA: 86752 MW: 26C5D0E890CA7A CAC64;
Query Match 100.0%; Score 47; DB 1; Length 770;

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Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
QY 1 EISEVXMDA 10
Db 664 EISEVXMDA 673
RESULT 4
ID A4_RAT STANDARD; PRT; 770 AA.
AC P08592;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog precursor
DE (Amyloidogenic glycoprotein) (Ag).
GN App.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE-98312583; PubMed=2900758;
RA Shivers B.D., Hilbich C., Multhaup G., Salbaum J.M., Beyreuther K.,
RA Seeburg P.H.;
RT "Alzheimer's disease amyloidogenic glycoprotein: expression pattern
RT in rat brain suggests a role in cell contact.";
RL EMBO J. 7:1365-1370(1988).
RP SEQUENCE OF 289-364 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE-89183625; PubMed=2648331;
RA Kang J., Moellier Hill B.;
RT "The sequence of the two extra exons in rat preA4.";
RL Nucleic Acids Res. 17:2130-2130(1989).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS: APP(395), APP(563), APP(695),
CC APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE
CC SPLICING.
CC -1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
CC WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
CC NXYX MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
CC PHOSPHORYLATION (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
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CC -----
DR EMBL: X07648; CAA30488.1; -
DR EMBL: X14066; CAA32229.1; -
DR PIR: S00550; S00550.
DR PIR: S03607; S03607.
DR HSSP: P05067; IAAP.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam: PF02177; A4_EXTRA.1.
DR Pfam: PF00014; Kunitz_BPTI.1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PRINTS: PR00759; BASICPTASE.
DR SMART: SM00006; A4_EXTRA.1.
DR SMART: SM00131; KU.1.
DR PROSITE: PS00319; A4_EXTRA.1.
DR PROSITE: PS00320; A4_INTRA.1.

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DR PROSITE; PS00280; BPTL_KUNITZ_1;
DR PROSITE; PS00279; BPTL_KUNITZ_2; 1.
KM Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;
KW Alternative splicing; Serine protease inhibitor.
FT SIGNAL 1 17
FT CHAIN 18 770
FT DOMAIN 18 699
FT TRANSSEM 700 723
FT DOMAIN 724 770
FT DOMAIN 673 715
FT DOMAIN 287 345
FT SITE 759 762
FT DISULFID 291 341
FT DISULFID 300 324
FT DISULFID 316 337
FT CARBOHYD 542 542
FT CARBOHYD 571 571
FT VARSPIC 289 289
FT VARSPIC 290 364
SQ SEQUENCE 770 AA; 86704 MW; C26C9D6BBD292A7 CRC64;

Query Match
Best Local Similarity 100.0%; Score 47; DB 1; Length 770;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 EISEVKMDA 10
Db 664 EISEVKMDA 673

RESULT 5
A4 CANFA STANDARD; PRT; 58 AA.
AC Q28280;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-Ap) (A-beta)] (Fragment).
GN App.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC GAO (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
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CC -----
DR EMBL; X56125; CAA39590.1; -
DR HSSP; P05067; 1BA4.
DR InterPro; IPR001868; A4_APP.
DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR PROSITE; PS00320; A4_INTRA; PARTIAL.
DR PROSITE; PS00320; A4_INTRA; PARTIAL.

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KM Glycoprotein; Amyloid; Neurone; Transmembrane.
FT NON_TER 1 1
FT CHAIN 7 49
FT DOMAIN <1 34
FT TRANSSEM 35 58
FT NON_TER 58 58
SQ SEQUENCE 58 AA; 6285 MW; 8469DA8BA2E12DFA CRC64;

Query Match
Best Local Similarity 78.7%; Score 37; DB 1; Length 58;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 ISEVKMDA 10
Db 1 ISEVKMDA 8

RESULT 6
A4 BOVIN STANDARD; PRT; 59 AA.
ID A4_BOVIN
AC Q28053;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-Ap) (A-beta)] (Fragment).
GN App.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC GAO (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
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CC -----
DR EMBL; X56124; CAA39589.1; -
DR EMBL; X56126; CAA39591.1; -
DR HSSP; P05067; 1BA4.
DR InterPro; IPR001868; A4_APP.
DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR PROSITE; PS00320; A4_INTRA; PARTIAL.
KM Glycoprotein; Amyloid; Neurone; Transmembrane.
FT NON_TER 1 1
FT CHAIN 7 49
FT DOMAIN <1 34
FT TRANSSEM 35 58
FT DOMAIN >59 59
FT NON_TER 59 59
SQ SEQUENCE 59 AA; 6414 MW; F43469D488A2E12D CRC64;

Query Match
Best Local Similarity 78.7%; Score 37; DB 1; Length 59;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY      3 ISEYKMDA 10
DB      1 ISEYKMDA 8

RESULT 7
GAAT_MOUSE STANDARD: PRT: 638 AA.
ID GAAT_MOUSE STANDARD: PRT: 638 AA.
AC Q9JLF1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Gamma-aminobutyric-acid receptor theta subunit precursor (GABA(A)
DE receptor).
GN GABRO.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-2026167; PubMed=10804200;
RA Salkkonen S.T., Hanna M.C., Kirkness E.F., Korpi E.R.;
RA "GABAA receptor epsilon and theta subunits display unusual structural
RT variation between species and are enriched in the rat locus
RT ceruleus."
RL J. Neurosci. 20:3588-3595(2000).
CC -1- FUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN THE
CC VERTEBRATE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING TO THE
CC GABA/BENZODIAZEPINE RECEPTOR AND OPENING AN INTEGRAL CHLORIDE
CC CHANNEL.
CC -1- SUBUNIT: GENERALLY PENTAMERIC. THIS SUBUNIT COASSEMBLES WITH
CC ALPHA-2, BETA-1, AND GAMMA-1.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC
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CC
CC EMBL: AF189260; AAF70381.1; -.
CC MCD: MGI:1888498; Gabrg.
DR InterPro: IPR001175; Neur_chan.
DR Pfam: PF02931; Neur_chan_LBD; 1.
DR PRINTS: PR02932; NRIONCHANNEL.
DR PROSITE: PS00236; NEURORF_ION_CHANNEL; 1.
KW Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW Multigene family; Transmembrane.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 638 GAMMA-AMINOBUTYRIC-ACID RECEPTOR THETA
FT SUBUNIT.
FT DOMAIN 22 267 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 266 288 POTENTIAL.
FT TRANSMEM 326 346 POTENTIAL.
FT TRANSMEM 618 638 POTENTIAL.
FT DISULFID 183 197 BY SIMILARITY.
FT CARBOHYD 127 127 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 638 AA: 72799 MW: 452440295BFA3 CRC64.

Query Match 72.3%; Score 34; DB 1; Length 638;
Best Local Similarity 66.7%; Pred. No. 39;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
OY      1 EISEVKMD 9
DB      95 EISEVKMD 103

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RESULT 8
A4_PIG STANDARD: PRT: 57 AA.
ID A4_PIG STANDARD: PRT: 57 AA.
AC Q29023;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-ApP) (A-beta)] (Fragment).
GN APP.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Morris F.H., Pascual R., Little S.P.;
RA "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis."
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC
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CC
CC EMBL: X56127; CAA39592.1; -.
CC HSSP: P05067; 1BA4.
DR InterPro: IPR001868; A4_APP.
DR PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR PROSITE: PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.
FT NON_TER 1 1
FT CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 34 57 POTENTIAL.
FT NON_TER 57 57
SQ SEQUENCE 57 AA: 6172 MW: 84209D88EBA82DFA CRC64.

Query Match 70.2%; Score 33; DB 1; Length 57;
Best Local Similarity 100.0%; Pred. No. 4; 9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      4 SEYKMDA 10
DB      1 SEYKMDA 7

RESULT 9
A4_URSMA STANDARD: PRT: 57 AA.
ID A4_URSMA STANDARD: PRT: 57 AA.
AC Q29149;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (beta-ApP) (A-beta)] (Fragment).
GN APP.
OS Ursus maritimus (Polar bear) (Thalarcos maritimus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.

```



```
OX NCB1_TaxID=29073;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
  peptide in dog, polar bear and five other mammals by cross-species
  polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
  INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
  G(O) (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
-----
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  or send an email to license@isb-sib.ch).
-----
DR EMBL: X56128; CAA39593.1; -.
DR HSSP: P05067; IAML.
DR InterPro: IPR001868; A4_APP.
DR PROSITE: PS00319; A4_EXTRA: PARTIAL.
DR PROSITE: PS00320; A4_INTRA: PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.
FT NON_TER 1
FT CHAIN 1
FT DOMAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).
FT TRANSMEM 34 57 EXTRACELLULAR (POTENTIAL).
FT NON_TER 57 57 POTENTIAL.
SQ SEQUENCE 57 AA; 6172 MW; 84209D88EBA82D CRC64;

Query Match 70.2%; Score 33; DB 1; Length 57;
Best Local Similarity 100.0%; Pred. No. 4.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SEVKMDA 10
Db 1 SEVKMDA 7
|||||
A4_RABIT STANDARD; PRT; 58 AA.
AC Q28748;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
  protein (Beta-Ap4) (A-beta)] (Fragment).
GN APP.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCB1_TaxID=9986;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
  peptide in dog, polar bear and five other mammals by cross-species
  polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
  INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
  G(O) (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
-----
-!- SUBCELLULAR LOCATION: Type I membrane protein.
```

```
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
-----
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-----
DR EMBL: X56129; CAA39594.1; -.
DR HSSP: P05067; IBA4.
DR InterPro: IPR001868; A4_APP.
DR PROSITE: PS00319; A4_EXTRA: PARTIAL.
DR PROSITE: PS00320; A4_INTRA: PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.
FT NON_TER 1
FT CHAIN 1
FT DOMAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).
FT TRANSMEM 34 57 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 58 57 POTENTIAL.
FT NON_TER 58 58 CYTOPLASMIC (POTENTIAL).
SQ SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;

Query Match 70.2%; Score 33; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SEVKMDA 10
Db 1 SEVKMDA 7
|||||
A4_SHEEP STANDARD; PRT; 58 AA.
AC Q28757;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
  protein (Beta-Ap4) (A-beta)] (Fragment).
GN APP.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
  Bovidae; Caprinae; Ovis.
OX NCB1_TaxID=9940;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
  peptide in dog, polar bear and five other mammals by cross-species
  polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
  INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
  G(O) (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
-----
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-----
DR EMBL: X56130; CAA39595.1; -.
DR HSSP: P05067; IAML.
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DR InterPro: IPR001868; A4_APP.
DR PROSITE: PS00319; A4_EXTRA: PARTIAL.
DR PROSITE: PS00320; A4_INTRA: PARTIAL.
KM Glycoprotein; Amyloid; Neutrone; Transmembrane.
FT NON_TER 1 1
FT CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 34 57 POTENTIAL.
FT DOMAIN 58 >58 CYTOSOLASMIC (POTENTIAL).
FT NON_TER 58 58
SQ SEQUENCE 58 AA: 6300 MW: F43420988BBA82D CRC64:

Query Match 70.2%; Score 33; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SEVKMDA 10
   1111111
DB 1 SEVKMDA 7

RESULT 12
T2E7_ECOLI STANDARD; PRT; 230 AA.
AC P50194;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Type II restriction enzyme Eco47I (EC 3.1.21.4) (Endonuclease Eco47I)
DE (R.Eco47I).
GN Eco47IR.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=REL47;
RX MEDLINE=95331599; PubMed=7607524;
RA Stakkevicius K., Povilionis P., Lubys A., Menkevicius S.,
RA Janulaitis A.;
RT "Cloning and characterization of the unusual restriction-modification
RT system comprising two restriction endonucleases and one
RT methyltransferase."
RL Gene 157:49-53(1995).
CC -1- FUNCTION: RECOGNIZES THE DOUBLE-STRANDED SEQUENCE GGMCC AND
CC CLEAVES AFTER G-1.
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage of DNA to give
CC specific double-stranded fragments with terminal 5'-phosphates.
CC -1- SIMILARITY: 70 R.SIM1.
-----
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-----
CC
CC EMBL: X62105; CAA57630.1; -.
DR REBASE: 930; Eco47I.
KM Hydrolyase; Endonuclease; Nuclease; Restriction system.
SQ SEQUENCE 230 AA: 26864 MW: AA3621FF506DFB11 CRC64:

Query Match 68.1%; Score 32; DB 1; Length 230;
Best Local Similarity 60.0%; Pred. No. 33;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EISEVKMDA 10
   1111111
DB 12 EELAKOKMDA 21

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RESULT 13
MDHC_BEYU STANDARD; PRT; 332 AA.
ID MDHC_BEYU
AC Q9SMD8;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Malate dehydrogenase, cytoplasmic (EC 1.1.1.37).
GN NRI.
OS Beta vulgaris (Sugar beet).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Beta.
OX NCBI_TaxID=3555;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RA Juergensen K., Buck F., Lange S., Kleine M., Grundler F.M.W.;
RT "A Beta vulgaris cDNA coding for a putative cytoplasmatic malate
RT dehydrogenase."
RL (In) Plant Gene Register PGR00-023.
CC -1- CATALYTIC ACTIVITY: (S)-malate + NAD(+) = oxaloacetate + NADH.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE LDH FAMILY. MDH SUBFAMILY.
-----
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-----
CC
CC EMBL: AJ251083; CAB61618.1; -.
DR HSSP; P11708; 4MDH.
DR InterPro: IPR001252; MDH_actsite.
DR InterPro: IPR001236; Idh.
DR Pfam; PFC00056; Idh; 1.
DR Pfam; PFC02866; Idh_C; 1.
DR ProDom; PD003052; MDH_actsite; 1.
DR PROSITE; PS00066; MDH; 1.
RW Oxidoreductase; Tricarboxylic acid cycle; NAD.
FT ACT_SITE 160 160 PROTON-RELAY (BY SIMILARITY).
FT BINDING 163 163 SUBSTRATE CARBOXYL GROUP (BY SIMILARITY).
FT ACT_SITE 188 188 PROTON-RELAY (BY SIMILARITY).
SQ SEQUENCE 332 AA: 35434 MW: 2B9E6495EFCDD12A CRC64:

Query Match 68.1%; Score 32; DB 1; Length 332;
Best Local Similarity 60.0%; Pred. No. 49;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 EISEVKMDA 10
   1111111
DB 306 DEVSRQKMDA 315

RESULT 14
GAB4_CHICK STANDARD; PRT; 488 AA.
ID GAB4_CHICK
AC P24045;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Gamma-aminobutyric-acid receptor beta-4 subunit precursor (GABA(A)
DE receptor).
GN GABRA4.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.

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RC TISSUE=Brain;
RX MEDLINE=91162222; PubMed=1848280;
RA Bateson A.N., Lasham A., Darlison M.G.;
RT "Gamma-aminobutyric acid A receptor heterogeneity is increased by
RL alternative splicing of a novel beta-subunit gene transcript.";
RJ J. Neurochem. 56:1437-1440(1991).
CC -1- FUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN THE
CC VERTEBRATE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING TO THE
CC GABA/BENZODIAZEPINE RECEPTOR AND OPENING AN INTEGRAL CHLORIDE
CC CHANNEL.
CC -1- SUBUNIT: GENERALLY PENTAMERIC. THERE ARE FIVE TYPES OF GABA(A)
CC RECEPTOR CHAINS: ALPHA, BETA, GAMMA, DELTA, AND RHO.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: BETA-4 AND BETA-4' (SHOWN HERE);
CC ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC -----
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CC -----
DR EMBL: X56647; CA39969.1; -.
DR EMBL: X56648; CA39970.1; ALT_SEQ.
DR PIR: JH0360; JH0360.
DR PIR: JH0359; JH0359.
DR InterPro: IPR000188; GABA_A_receptor.
DR InterPro: IPR001175; Neur_channel.
DR Pfam: PF02931; Neur_chan_LBD.1.
DR Pfam: PF02932; Neur_chan_memb.1.
DR PRINTS: PR00252; NRIONCHANNEL.
DR PROSITE: PS00236; NEUROTR_ION_CHANNEL.1.
DR Postsyaptic membrane; Ionic channel; Glycoprotein; Signal;
KM Multigene family; Transmembrane; Alternative splicing.
FT SIGNAL 1 25
FT CHAIN 26 488
FT DOMAIN 26 244 GAMMA-AMINOBUTYRIC-ACID RECEPTOR BETA-4
FT TRANSMEM 245 266 SUBUNIT.
FT TRANSMEM 271 292 EXTRACELLULAR (PROBABLE).
FT TRANSMEM 304 326 PROBABLE.
FT DOMAIN 327 465 PROBABLE.
FT TRANSMEM 466 487 CYTOPLASMIC (PROBABLE).
FT CARBOHYD 32 32 PROBABLE.
FT CARBOHYD 104 104 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 173 173 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 160 174 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPIC 361 364 BY SIMILARITY.
SQ SEQUENCE 488 AA; 56068 MW; 164A75314BDB2C12 CRC64;

Query Match 68.1%; Score 32; DB 1; Length 488;
Best Local Similarity 66.7%; Pred. No. 73;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EISEVKMD 9
DB 72 DQISEVND 80

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RESULT 15
SLIP1_CAEEL STANDARD; PRT; 575 AA.
AC P34260;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein slip-1.
GN SLP-1 OR B0303.9.
OS Caenorhabditis elegans.

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OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=92168156; PubMed=1538779;
RA Sulston J., Du Z., Thomas K., Wilson R., Hillier L., Staden R.,
RA Halloran N., Green P., Thierry-Mieg J., Qin L., Dear S., Coulson A.,
RA Craxton M., Durbin R.K., Berks M., Metzstein M., Hawkins T.,
RA Alnouch R., Waterston R.;
RT "The C. elegans genome sequencing project: a beginning.";
RL Nature 356:37-41(1992).
CC -1- SIMILARITY: TO YEAST SLP1.
CC -----
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CC -----
DR EMBL: M77697; AAA27901.1; -.
DR PIR: S27790; S27790.
DR WormPep: B0303.9; CE00539.
DR InterPro: IPR001619; Sec1.
DR Pfam: PF00995; Sec1.1.
KM Protein transport.
SQ SEQUENCE 575 AA; 64814 MW; 7FC4A06D896C9AAB CRC64;

Query Match 68.1%; Score 32; DB 1; Length 575;
Best Local Similarity 66.7%; Pred. No. 86;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EISEVKMD 9
DB 476 EFSEAKLD 484

```

Search completed: October 29, 2002, 10:27:24  
Job time : 7 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 29, 2002, 10:23:11 : Search time 18 seconds  
(without alignments)  
96.108 Million cell updates/sec

Title: US-09-580-018-1

Perfect score: 47

Sequence: 1 EISEVKMDA 10

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL.19:\*  
1: sp.archaea:\*  
2: sp.bacteria:\*  
3: sp.fungi:\*  
4: sp.human:\*  
5: sp.invertebrate:\*  
6: sp.mammal:\*  
7: sp.mhc:\*  
8: sp.organelle:\*  
9: sp.phage:\*  
10: sp.plant:\*  
11: sp rodent:\*  
12: sp.virus:\*  
13: sp.vertebrate:\*  
14: sp.unclassified:\*  
15: sp.virus:\*  
16: sp.bacteriap:\*  
17: sp.archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	100.0	79	11	035463
2	47	100.0	82	4	P78438
3	47	100.0	82	4	016014
4	47	100.0	82	4	016019
5	47	100.0	82	4	016020
6	47	100.0	607	11	099K32
7	47	100.0	695	6	095KN7
8	47	100.0	695	11	P97487
9	47	100.0	695	11	060496
10	47	100.0	770	6	09TUI0
11	46	97.9	534	13	093296
12	46	97.9	569	13	09PVL1
13	46	97.9	695	13	09DGJ7
14	46	97.9	751	13	09DCJ7
15	44	93.6	693	13	098SG0
16	44	93.6	695	13	098SF9

17	44	93.6	747	13	091963	091963 xenopus. ap
18	37	78.7	146	17	026386	026386 methanother
19	37	78.7	857	15	066956	066956 feline immu
20	35	74.5	1103	10	09LYJ3	091YJ3 arabidopsis
21	34	72.3	62	9	064081	064081 bacterioph
22	34	72.3	62	16	031940	031940 bacillus su
23	34	72.3	141	2	044749	044749 borrelia bu
24	34	72.3	141	2	044784	044784 borrelia bu
25	34	72.3	141	2	09R3H3	09R3H3 borrelia bu
26	34	72.3	141	2	09R9B8	09R9B8 borrelia bu
27	34	72.3	141	2	09S0J3	09S0J3 borrelia bu
28	34	72.3	141	2	09S0A9	09S0A9 borrelia bu
29	34	72.3	141	2	09S037	09S037 borrelia bu
30	34	72.3	141	2	09RZY5	09RZY5 borrelia bu
31	34	72.3	141	2	086117	086117 borrelia bu
32	34	72.3	141	2	007496	007496 borrelia bu
33	34	72.3	141	2	044779	044779 borrelia bu
34	34	72.3	141	2	044788	044788 borrelia bu
35	34	72.3	545	10	09FF41	09FF41 arabidopsis
36	34	72.3	635	11	0912M7	0912M7 rattus norv
37	34	72.3	869	5	09V6T0	09V6T0 drosophila
38	33	70.2	64	5	P91000	P91000 caenorhabdi
39	33	70.2	95	17	09V0C6	09V0C6 pyrococcus
40	33	70.2	96	17	074008	074008 pyrococcus
41	33	70.2	233	4	095999	095999 homo sapien
42	33	70.2	233	11	0920H7	0920H7 mus musculu
43	33	70.2	233	11	09QYN5	09QYN5 rattus norv
44	33	70.2	370	10	09LYK0	09LYK0 arabidopsis
45	33	70.2	389	17	09HR27	09hr27 halobacteri

## ALIGNMENTS

RESULT 1						
ID	035463	PRELIMINARY;	PRT;	79	AA.	
AC	035463:					
DT	01-JAN-1998 (TREMBLrel. 05, Created)					
DT	01-JAN-1998 (TREMBLrel. 05, Last sequence update)					
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)					
DE	ALZHEIMER'S AMYLOID BETA PROTEIN (FRAGMENT).					
GN	BETA APP.					
OS	Cricetulus griseus (Chinese hamster).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;					
OC	Cricetulus.					
OX	NCBI_TaxID=10029;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RA	Sambamurti K., Pinnix I., Gandhi S.;					
RL	Submitted (OCT-1997) to the EMBL/Genbank/DBJ databases.					
DR	EMBL; AF030413; AAB86608.1; .					
DR	HSSP; P05067; IBA4.					
FT	NON_TER	1				
FT	NON_TER	79	79			
SEQ	SEQUENCE	79	AA;	8538	MM;	37F2C6C3BF3F597 CRC64;
Query Match				100.0%;	Score 47;	DB 11;
Best Local Similarity				100.0%;	Pred. No. 0.057;	Length 79;
Matches	10;	Conservative	0;	Mismatches	0;	Indels
						Gaps 0;
QY	1 EISEVKMDA 10					
DB	13 EISEVKMDA 22					
RESULT 2						
ID	P78438	PRELIMINARY;	PRT;	82	AA.	
AC	P78438:					
DT	01-MAY-1997 (TREMBLrel. 03, Created)					
DT	01-MAY-1997 (TREMBLrel. 03, Last sequence update)					

```
DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
DE AMYLOID PROTEIN (BETA-AMYLOID PROTEIN) (FRAGMENT).
GN APP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89392030; PubMed=2675837;
RA Johnstone E.M., Chaney M.O., Moore R.E., Ward K.E., Norris F.H.,
RA Little S.P.;
RT "Alzheimer's disease amyloid peptide is encoded by two exons and shows
RT similarity to soybean trypsin inhibitor.";
RL Biochem. Biophys. Res. Commun. 163:1248-1255(1989).
RN [2]
RP SEQUENCE OF 19-48 FROM N.A.
RX MEDLINE=87120329; PubMed=2949367;
RA Tanzi R.E., Gusella J.F., Watkins P.C., Bruns G.A., George-Hyslop P.,
RA Van Keuren M.L., Patterson D., Pagan S., Kurnit D.M., Neve R.L.;
RT "Amyloid beta protein gene: cDNA, mRNA distribution, and genetic
RT linkage near the Alzheimer locus.";
RL Science 235:880-884(1987).
RN [3]
RP SEQUENCE OF 32-63 FROM N.A.
RX MEDLINE=93035397; PubMed=1415269;
RA Kamino K., Orr H.T., Payami H., Wajsbman E.M., Alonso M.E., Pulst S.M.,
RA Anderson L., O'dahl S., Nemens E., White J.A.;
RT "Linkage and mutational analysis of familial Alzheimer disease
RT kindreds for the APP gene region.";
RL Am. J. Hum. Genet. 51:998-1014(1992).
DR EMBL: M29270; AA51768.1; -.
DR EMBL: M29269; AA51768.1; JOINED.
DR EMBL: M15532; AA51564.1; -.
DR EMBL: S45136; AAB23646.1; -.
DR HSSP: P05067; IBA4.
FT NON_TER 1
SQ SEQUENCE 82 AA; 8994 MW; 8DA9E42B813A070E CRC64;

Query Match
Best Local Similarity 100.0%; Score 47; DB 4; Length 82;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EISEVKKMDA 10
Db 9 EISEVKKMDA 18

RESULT 3
Q16014 PRELIMINARY; PRT; 82 AA.
AC Q16014;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE BETA-AMYLOID PEPTIDE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93236601; PubMed=8476439;
RA Denman R.B., Rosenzwaig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
RT mutations on the processing of the beta-amyloid peptide precursor.";
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR EMBL: S60721; AAB26263.2; -.
DR HSSP: P05067; IBA4.
FT NON_TER 1
SQ SEQUENCE 82 AA; 8972 MW; F534AA5B3EA9230A CRC64;
```

```
Query Match
Best Local Similarity 100.0%; Score 47; DB 4; Length 82;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EISEVKKMDA 10
Db 10 EISEVKKMDA 19

RESULT 4
Q16019 PRELIMINARY; PRT; 82 AA.
AC Q16019;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE BETA-AMYLOID PEPTIDE (FRAGMENT).
GN BETA APP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93236601; PubMed=8476439;
RA Denman R.B., Rosenzwaig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
RT mutations on the processing of the beta-amyloid peptide precursor.";
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR EMBL: S61380; AAB26264.2; -.
DR HSSP: P05067; IBA4.
FT NON_TER 1
SQ SEQUENCE 82 AA; 8938 MW; F534AA5DE579230A CRC64;

Query Match
Best Local Similarity 100.0%; Score 47; DB 4; Length 82;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EISEVKKMDA 10
Db 10 EISEVKKMDA 19

RESULT 5
Q16020 PRELIMINARY; PRT; 82 AA.
AC Q16020;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE BETA-AMYLOID PEPTIDE (FRAGMENT).
GN BETA APP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93236601; PubMed=8476439;
RA Denman R.B., Rosenzwaig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
RT mutations on the processing of the beta-amyloid peptide precursor.";
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR EMBL: S61383; AAB26265.2; -.
DR HSSP: P05067; IBA4.
FT NON_TER 1
SQ SEQUENCE 82 AA; 8882 MW; F534AA5DE59230A CRC64;
```

QY 1 EISEVXKMDA 10  
 |||||||  
 Db 10 EISEVXKMDA 19

RESULT 6  
 099K32 PRELIMINARY; PRT; 607 AA.

AC 099K32: 01-JUN-2001 (TREMBlrel. 17, Created)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE HYPOTHETICAL 68.4 KDA PROTEIN (FRAGMENT).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=MAMMARY TUMOR. MAP-TGF ALPHA MODEL. 7 MONTHS OLD. GROSS  
 RC TISSUE;  
 RA Strauberg R.;  
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; EC005490; AA05490.1; -.  
 DR HSSP; P05067; 1AAP.  
 DR InterPro; IPR001868; A4\_APP.  
 DR InterPro; IPR002223; Kunitz\_BPTI.  
 DR Pfam; PF00014; Kunitz\_BPTI. 1.  
 DR PRINTS; PR00203; AMYLOIDA4.  
 DR PRINTS; PR00759; BASICPTASE.  
 DR SMART; SM00131; KU; 1.  
 DR PROSITE; PS00319; A4\_EXTRA; 1.  
 DR PROSITE; PS00320; A4\_INTRA; 1.  
 DR PROSITE; PS00280; BPTI\_KUNITZ\_1; 1.  
 DR PROSITE; PS50279; BPTI\_KUNITZ\_2; 1.  
 KM Hypothetical protein; Serine protease inhibitor.  
 FT NON\_TER  
 FT SEQUENCE 607 AA; 68391 MW; BFR02214CBA7D172 CRC64;  
 SO Query Match  
 Best Local Similarity 100.0%; Score 47; DB 11; Length 607;  
 Pred. No. 0.46;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EISEVXKMDA 10  
 |||||||  
 Db 501 EISEVXKMDA 510

RESULT 7  
 095KN7 PRELIMINARY; PRT; 695 AA.

AC 095KN7: 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE AMYLOID B-PROTEIN PRECURSOR.  
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecinae; Macaca.  
 OX NCBI\_TaxID=9541;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=CEREBELLUM;  
 RX MEDLINE=91273117; PubMed=1905108;  
 RA Podlasky M.B., Tolan D.R., Selkoe D.J.;  
 RT "Homology of the amyloid beta protein precursor in monkey and human  
 RT supports a primate model for beta amyloidosis in Alzheimer's  
 RT disease".  
 RL Am. J. Pathol. 138:1423-1435(1991).  
 DR EMBL; M58727; AAA36829.1; -.  
 FT SIGNAL 17 POTENTIAL.

FT CHAIN 597 636 POTENTIAL.  
 SO SEQUENCE 695 AA; 78663 MW; 4F6EA0139F969D56 CRC64;

Query Match  
 Best Local Similarity 100.0%; Score 47; DB 6; Length 695;  
 Pred. No. 0.53;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EISEVXKMDA 10  
 |||||||  
 Db 589 EISEVXKMDA 598

RESULT 8  
 P97487 PRELIMINARY; PRT; 695 AA.

AC P97487: 01-MAY-1997 (TREMBlrel. 03, Created)  
 DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE HIPPOCAMPAL AMYLOID PROTEIN.  
 GN APP.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SAMP8; TISSUE=HIPPOCAMPUS;  
 RA Flood J.F., Kumar V.B., Sasser T., Word I., Morley J.E.;  
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE OF 581-662 FROM N.A.  
 RC STRAIN=129SV;  
 RA Wraag M.A., Busfield F., Duff K., Korenblat K., Capech M.,  
 RA Loring J.F., Goate A.M.;  
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U84012; AAB41502.1; -.  
 DR EMBL; U82624; AAB40919.1; -.  
 DR HSSP; P05067; 1MMP.  
 DR MCD; MGI:88059; APP.  
 DR InterPro; IPR001868; A4\_APP.  
 DR Pfam; PF02177; A4\_EXTRA; 1.  
 DR PRINTS; PR00203; AMYLOIDA4.  
 DR SMART; SM00006; A4\_EXTRA; 1.  
 DR PROSITE; PS00319; A4\_EXTRA; 1.  
 DR PROSITE; PS00320; A4\_INTRA; 1.  
 SO SEQUENCE 695 AA; 78414 MW; 9A5FBEE2ED261236E CRC64;

Query Match  
 Best Local Similarity 100.0%; Score 47; DB 11; Length 695;  
 Pred. No. 0.53;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EISEVXKMDA 10  
 |||||||  
 Db 589 EISEVXKMDA 598

RESULT 9  
 060496 PRELIMINARY; PRT; 695 AA.

AC 060496: 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE PUTATIVE AMYLOID PRECURSOR PROTEIN.  
 OS Cavia sp. Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.  
 OX NCBI\_TaxID=10143;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=BRAIN;  
 RX MEDLINE=97236426; PubMed=9116031;

RA Beck M., Mueller D., Bigl V.;  
 "Amyloid precursor protein in Guinea pigs - complete cDNA sequence and  
 RT alternative splicing";  
 RT Biochim Biophys Acta 1351:17-21(1997).  
 DR EMBL: X97631; CA66230.1; -.  
 DR HSSP: P05067; 1BA4.  
 DR InterPro: IPR001868; A4\_APP.  
 DR Pfam: PF02177; A4\_EXTRA; 1.  
 DR PRINTS: PR00203; AMYLOIDA.  
 DR SMART: SM00006; A4\_EXTRA; 1.  
 DR PROSITE: PS00319; A4\_EXTRA; 1.  
 DR PROSITE: PS00320; A4\_INTRA; 1.  
 SQ SEQUENCE 695 AA; 78701 MW; 5196A0C4017F16AB CRC64;

Query Match 100.0%; Score 47; DB 11; Length 695;  
 Best Local Similarity 100.0%; Pred. No. 0.53;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEISEVKMDA 10  
 |||  
 DB 589 EEISEVKMDA 598

RESULT 10  
 Q9TUI0 PRELIMINARY; PRT; 770 AA.  
 ID Q9TUI0  
 AC Q9TUI0  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE AMYLOID PRECURSOR PROTEIN.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euteria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kimura A., Takahashi T.;  
 RT "Amyloid Precursor Protein 770.";  
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AB032550; BAA84580.1; -.  
 DR HSSP: P05067; 1AAP.  
 DR InterPro: IPR001868; A4\_APP.  
 DR InterPro: IPR002223; Kunitz\_BPTI.  
 DR Pfam: PF02177; A4\_EXTRA; 1.  
 DR Pfam: PF00014; Kunitz\_BPTI; 1.  
 DR PRINTS: PR00203; AMYLOIDA.  
 DR PRINTS: PR00759; BASICPTASE.  
 DR SMART: SM00006; A4\_EXTRA; 1.  
 DR SMART: SM00131; KU; 1.  
 DR PROSITE: PS00319; A4\_EXTRA; 1.  
 DR PROSITE: PS00320; A4\_INTRA; 1.  
 DR PROSITE: PS00280; BPTI\_KUNITZ\_1; 1.  
 DR PROSITE: PS50279; BPTI\_KUNITZ\_2; 1.  
 KW Serine protease inhibitor.  
 SQ SEQUENCE 770 AA; 86961 MW; 5F7A1DCB2BCC583E CRC64;

Query Match 100.0%; Score 47; DB 6; Length 770;  
 Best Local Similarity 100.0%; Pred. No. 0.59;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEISEVKMDA 10  
 |||  
 DB 664 EEISEVKMDA 673

RESULT 11  
 ID 093296 PRELIMINARY; PRT; 534 AA.  
 AC 093296  
 DT 01-NOV-1998 (TREMBlrel. 08, Created)  
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE AMYLOID PROTEIN (FRAGMENT).  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-98337885; PubMed-9671674;  
 RA Barnes N.Y., Li L., Yoshikawa K., Schwartz L.M., Oppenheim R.W.,  
 RA Milligan C.E.;  
 RT "Increased production of amyloid precursor protein provides a  
 RT substrate for caspase-3 in dying motoneurons";  
 RL J. Neurosci. 18:5869-5880(1998).  
 DR EMBL: AF042098; AAC25052.1; -.  
 DR HSSP: P05067; 1BA4.  
 DR InterPro: IPR001868; A4\_APP.  
 DR PRINTS: PR00203; AMYLOIDA.  
 DR PROSITE: PS00319; A4\_EXTRA; 1.  
 DR PROSITE: PS00320; A4\_INTRA; 1.  
 FT NON\_TER 1  
 SQ SEQUENCE 534 AA; 60597 MW; FB53EC2E66D4C92 CRC64;

Query Match 97.9%; Score 46; DB 13; Length 534;  
 Best Local Similarity 90.0%; Pred. No. 0.64;  
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEISEVKMDA 10  
 |||  
 DB 428 EEISEVKMDA 437

RESULT 12  
 Q9PVL1 PRELIMINARY; PRT; 569 AA.  
 ID Q9PVL1  
 AC Q9PVL1  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE AMYLOID PROTEIN (FRAGMENT).  
 GN APP.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-BRAIN;  
 RA Coulson E.J., Palla K., Beyreuther K., Masters C.L.;  
 RT "What the evolution of the amyloid protein precursor supergene family  
 RT tells us about its function.";  
 RL Neurochem. Int. 0:0-0(2000).  
 DR EMBL: AF030341; AAF12698.1; -.  
 DR HSSP: P05067; 1BA4.  
 DR InterPro: IPR001868; A4\_APP.  
 DR Pfam: PF02177; A4\_EXTRA; 1.  
 DR PRINTS: PR00203; AMYLOIDA.  
 DR SMART: SM00006; A4\_EXTRA; 1.  
 DR PROSITE: PS00319; A4\_EXTRA; 1.  
 DR PROSITE: PS00320; A4\_INTRA; 1.  
 FT NON\_TER 1  
 SQ SEQUENCE 569 AA; 64753 MW; 0AB8B851863A19D CRC64;

Query Match 97.9%; Score 46; DB 13; Length 569;  
 Best Local Similarity 90.0%; Pred. No. 0.68;  
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEISEVKMDA 10  
 |||  
 DB 464 EEISEVKMDA 473



RESULT 13

Q9DGJ8 PRELIMINARY; PRT; 695 AA.

AC Q9DGJ8; 01-MAR-2001 (TREMBLrel. 16, Created)

DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)

DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE BETA-AMYLOID PRECURSOR PROTEIN 695 ISOFORM.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauaria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

OC NCBI\_TaxID=9031;

OK [1]

RN [1]

RP SEQUENCE FROM N.A.

RA Sarasa M., Rodolose A., Sorribas V.;

RT "Cloning of full-length chicken beta-amyloid precursor protein isoforms.";

RT Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.

RL EMBL; AF289218; AAC00593.1; -.

DR HSSP; P05067; 1BA4.

DR InterPro; IPR001868; A4\_APP.

DR Pfam; PF02177; A4\_EXTRA; 1.

DR PRINTS; PR00203; AMYLOIDA4.

DR SMART; SM00006; A4\_EXTRA; 1.

DR PROSITE; PS00319; A4\_EXTRA; 1.

SQ SEQUENCE 695 AA; 78565 MW; F20LED02AEC86D95 CRC64;

Query Match 97.9%; Score 46; DB 13; Length 695;

Best Local Similarity 90.0%; Pred. NO. 0.84;

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EISEVVKMDA 10  
 ||:|||||||  
 Db 589 EEVSEVKMDA 598

RESULT 14

Q9DGJ7 PRELIMINARY; PRT; 751 AA.

AC Q9DGJ7; 01-MAR-2001 (TREMBLrel. 16, Created)

DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)

DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE BETA-AMYLOID PRECURSOR PROTEIN 751 ISOFORM.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauaria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

OC NCBI\_TaxID=9031;

OK [1]

RN [1]

RP SEQUENCE FROM N.A.

RA Sarasa M., Rodolose A., Sorribas V.;

RT "Cloning of full-length chicken beta-amyloid precursor protein isoforms.";

RT Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.

RL EMBL; AF289219; AAC00594.1; -.

DR HSSP; P05067; 1BA4.

DR InterPro; IPR001868; A4\_APP.

DR Pfam; PF02177; A4\_EXTRA; 1.

DR Pfam; PF02177; A4\_EXTRA; 1.

DR PRINTS; PR00203; AMYLOIDA4.

DR PRINTS; PR00759; BASICPTASE.

DR SMART; SM00006; A4\_EXTRA; 1.

DR SMART; SM00131; KU; 1.

DR PROSITE; PS00280; BPTI\_KUNITZ\_1; 1.

DR PROSITE; PS50279; BPTI\_KUNITZ\_2; 1.

KW Serine protease inhibitor.

SQ SEQUENCE 751 AA; 84705 MW; E78E9413A8033D84 CRC64;

Query Match 97.9%; Score 46; DB 13; Length 751;

Best Local Similarity 90.0%; Pred. NO. 0.91;

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EISEVVKMDA 10  
 ||:|||||||  
 Db 645 EEVSEVKMDA 654

RESULT 15

Q98SG0 PRELIMINARY; PRT; 693 AA.

AC Q98SG0; 01-JUN-2001 (TREMBLrel. 17, Created)

DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)

DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE BETA-AMYLOID PRECURSOR PROTEIN A.

GN APP.

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;

OC Xenopodinae; Xenopus.

OC NCBI\_TaxID=8355;

OK [1]

RN [1]

RP SEQUENCE FROM N.A.

RA Van den Hurk W.H.;

RL Thesis (2001), Department of Biological Sciences, University of Nijmegen, Nijmegen, Netherlands.

RL EMBL; AJ298150; CAC37193.1; -.

DR HSSP; P05067; 1HZ3.

DR InterPro; IPR001868; A4\_APP.

DR Pfam; PF02177; A4\_EXTRA; 1.

DR PRINTS; PR00203; AMYLOIDA4.

DR SMART; SM00006; A4\_EXTRA; 1.

DR PROSITE; PS00319; A4\_EXTRA; 1.

DR PROSITE; PS00320; A4\_INTRA; 1.

KW Signal.

FT SIGNAL.

SQ SEQUENCE 693 AA; 78568 MW; CAFIDF655C1AB653 CRC64;

Query Match 93.6%; Score 44; DB 13; Length 693;

Best Local Similarity 90.0%; Pred. NO. 2.1;

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EISEVVKMDA 10  
 |||||||||  
 Db 587 EEISEVVKMDS 596

Search completed: October 29, 2002, 10:29:37

Job time : 19.1429 secs



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OM protein - protein search, using sw model

Run on: October 29, 2002, 10:23:56 : Search time 9 seconds  
(without alignments)  
27.140 Million cell updates/sec

Title: US-09-580-018-1  
Perfect score: 47  
Sequence: 1 FEISEVKMDA 10

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database :

Issued Patents AA:\*  
1: /cgn2.6/ptodata/1/1aa/5A.COMB.pep:\*  
2: /cgn2.6/ptodata/1/1aa/5B.COMB.pep:\*  
3: /cgn2.6/ptodata/1/1aa/6A.COMB.pep:\*  
4: /cgn2.6/ptodata/1/1aa/6B.COMB.pep:\*  
5: /cgn2.6/ptodata/1/1aa/PCUS.COMB.pep:\*  
6: /cgn2.6/ptodata/1/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	47	100.0	27	1	US-08-541-902-11
3	47	100.0	45	1	US-08-462-859A-5
4	47	100.0	45	1	US-08-123-659A-5
5	47	100.0	45	1	US-08-464-247A-5
6	47	100.0	45	1	US-08-464-248A-5
7	47	100.0	58	1	US-08-371-930-25
8	47	100.0	58	5	PCT-US94-01712-25
9	47	100.0	63	1	US-08-462-859A-3
10	47	100.0	63	1	US-08-462-859A-4
11	47	100.0	63	1	US-08-123-659A-3
12	47	100.0	63	1	US-08-123-659A-4
13	47	100.0	63	1	US-08-464-247A-3
14	47	100.0	63	1	US-08-464-247A-4
15	47	100.0	63	1	US-08-464-248A-3
16	47	100.0	63	1	US-08-464-248A-4
17	47	100.0	152	6	5187153-4
18	47	100.0	162	6	5220013-4
19	47	100.0	162	6	5223482-4
20	47	100.0	264	1	US-07-990-893-5
21	47	100.0	487	1	US-08-462-859A-9
22	47	100.0	487	1	US-08-123-659A-9
23	47	100.0	487	1	US-08-464-247A-9
24	47	100.0	487	1	US-08-464-248A-9
25	47	100.0	492	1	US-08-462-859A-7
26	47	100.0	492	1	US-08-123-659A-7
27	47	100.0	492	1	US-08-464-247A-7

28	47	100.0	492	1	US-08-464-248A-7	Sequence 7, Appl1
29	47	100.0	656	1	US-08-371-930-23	Sequence 23, Appl1
30	47	100.0	656	5	PCT-US94-01712-23	Sequence 23, Appl1
31	47	100.0	676	1	US-08-371-930-24	Sequence 24, Appl1
32	47	100.0	676	5	PCT-US94-01712-24	Sequence 24, Appl1
33	47	100.0	694	1	US-08-339-152A-18	Sequence 18, Appl1
34	47	100.0	694	2	US-08-007-999B-5	Sequence 5, Appl1
35	47	100.0	694	2	US-08-689-276A-5	Sequence 5, Appl1
36	47	100.0	695	1	US-08-371-930-27	Sequence 27, Appl1
37	47	100.0	695	1	US-08-123-702-2	Sequence 2, Appl1
38	47	100.0	695	1	US-08-339-152A-30	Sequence 30, Appl1
39	47	100.0	695	2	US-08-104-165-1	Sequence 1, Appl1
40	47	100.0	695	3	US-08-464-250-1	Sequence 1, Appl1
41	47	100.0	695	4	US-08-464-250-1	Sequence 1, Appl1
42	47	100.0	695	4	US-09-458-481B-4	Sequence 4, Appl1
43	47	100.0	695	4	US-09-458-481B-6	Sequence 6, Appl1
44	47	100.0	695	4	US-09-458-481B-6	Sequence 6, Appl1
45	47	100.0	695	4	US-09-458-481B-7	Sequence 7, Appl1

## ALIGNMENTS

RESULT 1  
US-08-141-324-11  
Sequence 11, Application US/08141324  
Patent No. 5475097  
GENERAL INFORMATION:  
APPLICANT: Travisa, James  
APPLICANT: Potempa, Jan S.  
APPLICANT: Barr, Philip J.  
APPLICANT: Pavloff, Nadine  
APPLICANT: Pike, Robert N.  
TITLE OF INVENTION: Lysine-specific Porphyromonas gingivalis  
TITLE OF INVENTION: Protease  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Greenlee and Winner, P.C.  
STREET: 5370 Manhattan Circle, Suite 201  
CITY: Boulder  
STATE: CO  
COUNTRY: US  
ZIP: 80303  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/141,324  
FILING DATE: 21-OCT-1993  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Ferber, Donna M.  
REGISTRATION NUMBER: 33,878  
REFERENCE/DOCKET NUMBER: 44-93  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 303-499-8080  
TELEFAX: 303-499-8089  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-141-324-11  
Query Match 100.0%, Score 47, DB 1, Length 27;  
Best Local Similarity 100.0%, Pred. No. 0.0047;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 EISESEVKMDA 10  
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Db 1 EISESEVKMDA 10

## RESULT 2

US-08-541-902-11  
; Sequence 11, Application US/08541902  
; Patent No. 5707620  
; GENERAL INFORMATION:  
; APPLICANT: Travis, James  
; APPLICANT: Potempa, Jan S.  
; APPLICANT: Barr, Philip J.  
; APPLICANT: Pavloff, Nadine  
; APPLICANT: Pike, Robert N.  
; TITLE OF INVENTION: Lysine-specific Porphyromonas gingivalis  
; TITLE OF INVENTION: Protease  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Greenlee and Winner, P.C.  
; STREET: 5370 Manhattan Circle, Suite 201  
; CITY: Boulder  
; STATE: CO  
; COUNTRY: US  
; ZIP: 80303  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/541,902  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/141,324  
; FILING DATE: 21-OCT-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ferber, Donna M.  
; REGISTRATION NUMBER: 33,878  
; REFERENCE/DOCKET NUMBER: 44-93  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 303-499-8080  
; TELEFAX: 303-499-8089  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 27 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHEICAL: NO  
; ANTI-SENSE: NO  
; US-08-541-902-11  
Query Match 100.0%; Score 47; DB 1; Length 27;  
Best Local Similarity 100.0%; Pred. No. 0.0047;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 EISESEVKMDA 10  
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Db 1 EISESEVKMDA 10

## RESULT 3

US-08-462-859A-5  
; Sequence 5, Application US/08462859A  
; Patent No. 5652092  
; GENERAL INFORMATION:  
; APPLICANT: Jacobsen, J. S.  
; APPLICANT: Vittek, M. P.  
; TITLE OF INVENTION: No. 5652092el Amyloid Precursor and Method of

; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation  
; TITLE OF INVENTION: of B-Amyloid Peptide  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: American Cyanamid Company  
; STREET: One Cyanamid Plaza  
; CITY: Wayne  
; STATE: New Jersey  
; COUNTRY: United States  
; ZIP: 07470-8426  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/462,859A  
; FILING DATE: 05-JUN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Barnhard, Elizabeth M.  
; REGISTRATION NUMBER: 31,088  
; REFERENCE/DOCKET NUMBER: 31,844-04  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (201)831-3305  
; TELEFAX: (201)831-3246  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 45 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-462-859A-5  
Query Match 100.0%; Score 47; DB 1; Length 45;  
Best Local Similarity 100.0%; Pred. No. 0.0083;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 EISESEVKMDA 10  
| | | | |  
Db 2 EISESEVKMDA 11

## RESULT 4

US-08-123-659A-5  
; Sequence 5, Application US/08123659A  
; Patent No. 5656477  
; GENERAL INFORMATION:  
; APPLICANT: Jacobsen, J. S.  
; APPLICANT: Vittek, M. P.  
; TITLE OF INVENTION: No. 5656477el Amyloid Precursor and Method of  
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation  
; TITLE OF INVENTION: of B-Amyloid Peptide  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Anne Rosenblum  
; STREET: 163 Delaware Avenue, Suite 212  
; CITY: Delmar  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 12054  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/123,659A  
; FILING DATE: 20-SEP-1993  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Rosenblum, Anne M.

REGISTRATION NUMBER: 30,419  
REFERENCE/DOCKET NUMBER: 31,844-01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (518)475-0611  
TELEFAX: (518)475-0619  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 45 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-123-659A-5

Query Match 100.0%; Score 47; DB 1; Length 45;  
Best Local Similarity 100.0%; Pred. No. 0.0083;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 E1E1SEVKMDA 10  
Db 2 E1E1SEVKMDA 11

## RESULT 5

US-08-464-247A-5  
Sequence 5, Application US/08464247A  
Patent No. 5693478  
GENERAL INFORMATION:  
APPLICANT: Jacobsen, J. S.  
APPLICANT: Vittek, M. P.  
TITLE OF INVENTION: No. 5693478e1 Amyloid Precursor and Method of  
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation  
TITLE OF INVENTION: of B-Amyloid Peptide  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: American Cyanamid Company  
STREET: One Campus Drive  
CITY: Parsippany  
STATE: New Jersey  
COUNTRY: United States  
ZIP: 07054  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/464,247A  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Barnhard, Elizabeth M.  
REGISTRATION NUMBER: 31,088  
REFERENCE/DOCKET NUMBER: 31,844-03  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-683-4117  
TELEFAX: 201-683-2158  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 45 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-464-247A-5

Query Match 100.0%; Score 47; DB 1; Length 45;  
Best Local Similarity 100.0%; Pred. No. 0.0083;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 E1E1SEVKMDA 10  
Db 2 E1E1SEVKMDA 11

RESULT 6  
US-08-464-248A-5  
Sequence 5, Application US/08464248A  
Patent No. 5703209  
GENERAL INFORMATION:  
APPLICANT: Jacobsen, J. S.  
APPLICANT: Vittek, M. P.  
TITLE OF INVENTION: No. 5703209e1 Amyloid Precursor and Method of  
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation  
TITLE OF INVENTION: of B-Amyloid Peptide  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: American Cyanamid Company  
STREET: One Cyanamid Plaza  
CITY: Wayne  
STATE: New Jersey  
COUNTRY: United States  
ZIP: 07470-8426  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/464,248A  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Barnhard, Elizabeth M.  
REGISTRATION NUMBER: 31,088  
REFERENCE/DOCKET NUMBER: 31,844-02  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (201)831-3246  
TELEFAX: (201)831-3305  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 45 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-464-248A-5

Query Match 100.0%; Score 47; DB 1; Length 45;  
Best Local Similarity 100.0%; Pred. No. 0.0083;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 E1E1SEVKMDA 10  
Db 2 E1E1SEVKMDA 11

RESULT 7  
US-08-371-930-25  
Sequence 25, Application US/08371930  
Patent No. 5578451  
GENERAL INFORMATION:  
APPLICANT: Nishimoto, Ikuro  
TITLE OF INVENTION: ALZHEIMER'S DISEASE THERAPEUTICS  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Fish & Richardson  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM PS/2 Model 502 or 555X  
OPERATING SYSTEM: MS-DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/371,930
; FILING DATE:
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/019,208
; FILING DATE: February 18, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/154001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
;
US-08-371-930-25
;
Query Match 100.0%; Score 47; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEISEVKMDA 10
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Db 39 EEISEVKMDA 48

RESULT 8
PCT-US94-01712-25
; Sequence 25, Application PC/TUS9401712
; GENERAL INFORMATION:
; APPLICANT: Nishimoto, Ikuo
; TITLE OF INVENTION: ALZHEIMER'S DISEASE THERAPEUTICS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; ZIP: 02110-2804
; COUNTRY: U.S.A.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" diskette, 1.44 Mb
; OPERATING SYSTEM: MS-DOS (version 5.0)
; SOFTWARE: WordPerfect (version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/01712
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/019,208
; FILING DATE: February 18, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/154001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
;
PCT-US94-01712-25
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Query Match 100.0%; Score 47; DB 5; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEISEVKMDA 10
|
Db 39 EEISEVKMDA 48

RESULT 9
US-08-462-859A-3
; Sequence 3, Application US/08462859A
; Patent No. 5652092
; GENERAL INFORMATION:
; APPLICANT: Jacobsen, J. S.
; APPLICANT: Vittek, M. P.
; TITLE OF INVENTION: No. 5652092a1 Amyloid Precursor and Method of
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
; TITLE OF INVENTION: of B-Amyloid Peptide
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: United States
; ZIP: 07470-8426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,859A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 31,844-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201)831-3246
; TELEFAX: (201)831-3305
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 63 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-462-859A-3
;
Query Match 100.0%; Score 47; DB 1; Length 63;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEISEVKMDA 10
|
Db 2 EEISEVKMDA 11

RESULT 10
US-08-462-859A-4
; Sequence 4, Application US/08462859A
; Patent No. 5652092
; GENERAL INFORMATION:
; APPLICANT: Jacobsen, J. S.
; APPLICANT: Vittek, M. P.
; TITLE OF INVENTION: No. 5652092a1 Amyloid Precursor and Method of
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
; TITLE OF INVENTION: of B-Amyloid Peptide
; NUMBER OF SEQUENCES: 19
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CORRESPONDENCE ADDRESS:  
ADDRESSEE: American Cyanamid Company  
STREET: One Cyanamid Plaza  
CITY: Wayne  
STATE: New Jersey  
COUNTRY: United States  
ZIP: 07470-8426  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/462,859A  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Barnhard, Elizabeth M.  
REGISTRATION NUMBER: 31,088  
REFERENCE/DOCKET NUMBER: 31,844-04  
TELEPHONE: (201)831-3246  
TELEFAX: (201)831-3305  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 63 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-462-859A-4

Query Match 100.0%; Score 47; DB 1; Length 63;  
Best Local Similarity 100.0%; Pred. No. 0.012;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EISEVVKMDA 10  
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Db 2 EISEVVKMDA 11

RESULT 11  
US-08-123-659A-3  
Sequence 3, Application US/08123659A  
Patent No. 5656477  
GENERAL INFORMATION:  
APPLICANT: Jacobsen, J. S.  
TITLE OF INVENTION: No. 5656477e1 Amyloid Precursor and Method of  
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation  
TITLE OF INVENTION: of B-Amyloid Peptide  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Anne Rosenblum  
STREET: 163 Delaware Avenue, Suite 212  
CITY: Delmar  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 12054  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/123,659A  
FILING DATE: 20-SEP-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Rosenblum, Anne M.  
REGISTRATION NUMBER: 30,419  
REFERENCE/DOCKET NUMBER: 31,844-01  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (518)475-0611  
TELEFAX: (518)475-0619  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 63 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-123-659A-3

Query Match 100.0%; Score 47; DB 1; Length 63;  
Best Local Similarity 100.0%; Pred. No. 0.012;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EISEVVKMDA 10  
|||||  
Db 2 EISEVVKMDA 11

RESULT 12  
US-08-123-659A-4  
Sequence 4, Application US/08123659A  
Patent No. 5656477  
GENERAL INFORMATION:  
APPLICANT: Jacobsen, J. S.  
TITLE OF INVENTION: No. 5656477e1 Amyloid Precursor and Method of  
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation  
TITLE OF INVENTION: of B-Amyloid Peptide  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Anne Rosenblum  
STREET: 163 Delaware Avenue, Suite 212  
CITY: Delmar  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 12054  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/123,659A  
FILING DATE: 20-SEP-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Rosenblum, Anne M.  
REGISTRATION NUMBER: 30,419  
REFERENCE/DOCKET NUMBER: 31,844-01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (518)475-0611  
TELEFAX: (518)475-0619  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 63 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-123-659A-4

Query Match 100.0%; Score 47; DB 1; Length 63;  
Best Local Similarity 100.0%; Pred. No. 0.012;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EISEVVKMDA 10  
|||||  
Db 2 EISEVVKMDA 11

RESULT 13  
US-08-464-247A-3  
Sequence 3, Application US/08464247A

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; Patent No. 5693478
; GENERAL INFORMATION:
; APPLICANT: Jacobsen, J. S.
; APPLICANT: Vittek, M. P.
; TITLE OF INVENTION: No. 5693478e1 Amyloid Precursor and Method of
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
; TITLE OF INVENTION: of B-Amyloid Peptide
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Campus Drive
; CITY: Parsippany
; STATE: New Jersey
; COUNTRY: United States
; ZIP: 07054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,247A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 31,844-03
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-683-2158
; TELEFAX: 201-683-4117
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 63 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-464-247A-3

Query Match          100.0%; Score 47; DB 1; Length 63;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEISEVKMDA 10
    |||||||
Db 2 EEISEVKMDA 11

RESULT 14
US-08-464-247A-4
; Sequence 4, Application US/08464247A
; Patent No. 5693478
; GENERAL INFORMATION:
; APPLICANT: Jacobsen, J. S.
; APPLICANT: Vittek, M. P.
; TITLE OF INVENTION: No. 5693478e1 Amyloid Precursor and Method of
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
; TITLE OF INVENTION: of B-Amyloid Peptide
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Campus Drive
; CITY: Parsippany
; STATE: New Jersey
; COUNTRY: United States
; ZIP: 07054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/08/464,247A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 31,844-03
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-683-2158
; TELEFAX: 201-683-4117
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 63 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-464-247A-4

Query Match          100.0%; Score 47; DB 1; Length 63;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEISEVKMDA 10
    |||||||
Db 2 EEISEVKMDA 11

RESULT 15
US-08-464-248A-3
; Sequence 3, Application US/08464248A
; Patent No. 5703209
; GENERAL INFORMATION:
; APPLICANT: Jacobsen, J. S.
; APPLICANT: Vittek, M. P.
; TITLE OF INVENTION: No. 5703209e1 Amyloid Precursor and Method of
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
; TITLE OF INVENTION: of B-Amyloid Peptide
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne Jersey
; STATE: New Jersey
; COUNTRY: United States
; ZIP: 07470-8426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,248A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 31,844-02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201)831-3246
; TELEFAX: (201)831-3305
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 63 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-464-248A-3

Query Match          100.0%; Score 47; DB 1; Length 63;
Best Local Similarity 100.0%; Pred. No. 0.012;
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Matches	10;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
OY	1	EEISEVKMDA	10						
DB	2	EEISEVKMDA	11						

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Job time : 10 secs

1  
2  
3  
4

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 29, 2002, 10:22:21 ; Search time 23.1429 Seconds

(without alignments)  
47.995 Million cell updates/sec

Title: us-09-580-018-2  
Perfect score: 47  
Sequence: 1 EISEVKNDAE-10

Scoring table: BLOSUM62  
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Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	100.0	10	22	AA046206 Human APP derived
2	47	100.0	13	19	AA070869 Beta-amyloid pepit
3	47	100.0	16	21	AA060315 Human beta-amyloid
4	47	100.0	18	22	AA060608 Beta-amyloid precu
5	47	100.0	20	21	AA069713 Beta-APP alpha-sec
6	47	100.0	33	20	AA098002 Amyloid precursor
7	47	100.0	39	21	AA069717 Beta-APP alpha-sec
8	47	100.0	45	18	AA026512 Amyloid precursor
9	47	100.0	45	18	AA026392 Amyloid precursor
10	47	100.0	45	19	AA044748 APP-REP 751 [BAP d
11	47	100.0	45	19	AA042977 Deletion beta-amy1

12	47	100.0	53	16	AA064168 Variant beta amylo
13	47	100.0	57	21	AA010910 Human amyloid prec
14	47	100.0	58	15	AA058937 Amyloid precursor
15	47	100.0	63	18	AA026511 Amyloid precursor
16	47	100.0	63	18	AA026391 Amyloid precursor
17	47	100.0	63	19	AA044747 APP-REP 751 BAP pe
18	47	100.0	63	19	AA044746 APP-REP 751 [BAP E
19	47	100.0	63	19	AA042975 Beta-amyloid pepit
20	47	100.0	63	19	AA042976 Beta-amyloid pepit
21	47	100.0	67	19	AA071377 Peptide derived fr
22	47	100.0	93	22	AB019083 Novel human diagno
23	47	100.0	112	17	AA093556 Familial Alzheimer
24	47	100.0	115	20	AA097999 London-FAD APP pol
25	47	100.0	162	9	AA083151 Deduced sequence 1
26	47	100.0	162	12	AA010023 Beta-amyloid-relat
27	47	100.0	162	14	AA037863 Deduced from clone
28	47	100.0	249	15	AA065798 Beta-amyloid precu
29	47	100.0	264	10	AA090497 Protein sequence 1
30	47	100.0	264	10	AA090609 Sequence of amy 37
31	47	100.0	487	18	AA026510 Amyloid precursor
32	47	100.0	487	18	AA026394 Amyloid precursor
33	47	100.0	487	19	AA044745 APP-REP 751 protei
34	47	100.0	487	19	AA042979 Amyloid precursor
35	47	100.0	492	14	AA045229 APP-REP 751 amyloi
36	47	100.0	492	18	AA026509 Amyloid precursor
37	47	100.0	492	18	AA026393 Amyloid precursor
38	47	100.0	492	19	AA044744 APP-REP 751 protei
39	47	100.0	492	19	AA042978 Amyloid precursor
40	47	100.0	537	14	AA040114 APP-HCV-E2 fusion
41	47	100.0	596	15	AA065797 Beta-amyloid precu
42	47	100.0	627	21	AA010955 SEAP-human amyloid
43	47	100.0	651	15	AA065796 Beta-amyloid precu
44	47	100.0	656	15	AA058935 Amyloid precursor
45	47	100.0	670	15	AA065795 APP751 beta-amyloi

#### ALIGNMENTS

##### RESULT 1

AA046206 standard; peptide; 10 AA.

04-APR-2001 (first entry)

Human APP derived immunogenic peptide #2.

Amyloid deposit; APP; Abeta; brain; human; clearing response; neurotrophic;

KW Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;

amyloid precursor protein; Alzheimer's disease.

XX Homo sapiens.

XX OS Homo sapiens.

XX PN WO200072880-A2.

XX PD 07-DEC-2000.

XX PF 26-MAY-2000; 2000WO-US14810.

XX PR 28-MAY-1999; 99US-0322289.

XX PA (NEUR-) NEURALAB LTD.

XX PI Schenk DB, Bard F, Vasquez NJ, Yednock T;

XX DR WPI; 2001-032104/04.

XX PT Preventing or treating a disease associated with amyloid deposits, especially Alzheimer's disease, comprises administering amyloid specific antibody

PS Disclosure: Figure 19; 143pp: English.

CC This invention describes a novel method of preventing or treating a  
CC disease associated with amyloid deposits of amyloid precursor protein  
CC (APP) A-beta fragments in the brain of a patient, which comprises  
CC administering to the patient: (a) an antibody that binds to A-beta, the  
CC antibody binds to an amyloid deposit and induces a clearing response (Fc  
CC receptor mediated phagocytosis) against it (b) a polypeptide containing  
CC an N-terminal segment of at least residues 1-5 of A-beta; or (c) an agent  
CC that induces an immunogenic response against residues 1-3 to 7-11 of  
CC A-beta. The products of the invention have neurotropic and neuroprotective  
CC activity. The method is also useful for monitoring a course of treatment  
CC being administered to a patient, e.g. active and passive immunization. The  
CC methods are useful for prophylactic and therapeutic treatment of  
CC Alzheimer's disease.

SQ Sequence 10 AA:

Query Match 100.0%; Score 47; DB 22; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0024;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EISEVKMDAE 10  
Db 1 EISEVKMDAE 10

RESULT 2

ID AAM70869 standard; peptide; 13 AA.

AC AAM70869;

DT 04-FEB-1999 (first entry)

DE Beta-amyloid peptide to create a monoclonal antibody.

KW Beta-amyloid precursor protein; beta-APP; beta-amyloid peptide;  
KW antibody; amyloid deposit; Alzheimer's disease.

OS Synthetic.

OS Homo sapiens.

PN W03844955-A1.

PD 15-OCT-1998.

PF 09-APR-1998; 98WO-US06900.

PR 09-APR-1997; 97US-0041850.

PA (MCIN/) MCINNIS P. A.  
PA (MIND-) MINDSER LTD.

F1 Chain DG;

DR WPI; 1998-594476/50.

PT Preventing or inhibiting progression of Alzheimer's Disease -  
PT comprises use of recombinant DNA encoding an antibody specific for  
PT the N- or C-terminus of an amyloid-beta peptide

PS Example 1; Page 47; 58pp: English.

CC The present sequence represents a peptide derived from beta-amyloid  
CC precursor protein (beta-APP). The peptide is a beta-amyloid  
CC peptide and is used to produce a monoclonal antibody. The specification  
CC describes a method for prevention or inhibition of progression of  
CC Alzheimer's disease. The method comprises administering a composition  
CC comprising a recombinant DNA molecule containing a gene encoding a  
CC recombinant antibody end-specific for the N-terminus or the C-terminus  
CC of an amyloid-beta peptide, operably linked to a promoter which is  
CC expressed in the central nervous system. The recombinant antibody

CC molecules prevent the accumulation of beta-amyloid peptides in the  
CC extracellular space, interstitial fluid and cerebrospinal fluid and the  
CC aggregation of such peptides into amyloid deposits in the brain. They  
CC also inhibit the progression of Alzheimer's disease by inhibiting the  
CC interaction of beta-amyloid peptides mediating Alzheimer's disease  
CC induced neurotoxicity and inhibiting the Alzheimer's disease induced  
CC complement activation and cytokine release involved in the inflammatory  
CC process.

SQ Sequence 13 AA:

Query Match 100.0%; Score 47; DB 19; Length 13;  
Best Local Similarity 100.0%; Pred. No. 0.0033;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EISEVKMDAE 10  
Db 1 EISEVKMDAE 10

RESULT 3  
AAB06315  
ID AAB06315 standard; peptide; 16 AA.

AC AAB06315;

DT 03-OCT-2000 (first entry)

DE Human beta-amyloid precursor protein beta-secretase cleavage site.

KW Human; beta-amyloid precursor protein; beta-APP; beta-secretase;  
KW subtilisin-kexin isoenzyme 1; SKI-1;

KW pro-brain-derived neurotrophic factor; PROBNF; anti-lipemic;  
KW cytosolic; vasotropic; SKI-1 inhibitor; hypercholesterolemia;

KW liver steatosis; Ras-dependent cancer; restenosis;  
KW amyloid protein formation.

OS Homo sapiens.

FT Key Location/Qualifiers

FT Cleavage-site 8..9

PN W0200026348-A2.

PD 11-MAY-2000.

PF 04-NOV-1999; 99WO-CA01058.

PR 04-NOV-1998; 98CA-2249648.

PA (RECL-) INST RECH CLINIQUES MONTREAL.

PI Seidah N, Chretien M, Marcinkiewicz M, Laaksonen R, Davignon J;

DR WPI; 2000-365601/31.

PT Novel soluble proteic fragment of subtilisin-kexin isoenzyme for  
PT producing a polypeptide useful for treating hypercholesterolemia, liver  
PT steatosis and amyloidosis, comprises a specific amino acid sequence -  
PS Example 4; Page 51; 119pp: English.

CC The present sequence is the beta-secretase site of human beta-amyloid  
CC precursor protein (beta-APP). The sequence may be cleaved  
CC by a mammalian subtilase, specifically subtilisin-kexin isoenzyme 1  
CC (SKI-1), a type-1 membrane-bound protease. Peptides which bind to and  
CC are cleaved by SKI-1 may be used for monitoring SKI-1 activity, for  
CC screening inhibitors of SKI-1 activity, or for screening enhancers of  
CC SKI-1 activity. Proteic fragments of SKI-1 which bind to the SKI-1  
CC catalytic site may be used as inhibitors of SKI-1 activity. They may be  
CC used to treat diseases involving overexpression of SKI-1 or SKI-1  
CC substrate. Such diseases include hypercholesterolemia, high levels of  
CC fatty acids, lipids or farnesyl pyrophosphate, liver steatosis,

CC Ras-dependent cancer, restenosis and amyloid protein formation.

XX Sequence 16 AA;

Query Match 100.0%; Score 47; DB 21; Length 16;

Best Local Similarity 100.0%; Pred. No. 0.0042;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EISEVKMDAE 10

Db 2 EISEVKMDAE 11

RESULT 4

AAE00608

ID AAE00608 standard; peptide: 18 AA.

AC AAE00608;

DT 02-JUL-2001 (first entry)

DE Beta-amyloid precursor protein beta-secretase cleavage site.

KM Beta-amyloid precursor protein; beta-APP; caspase; beta-secretase;

KW cysteine protease; apoptosis; caspase expression cassette; metastasis;

KM tumour; cathepsin B; urokinase; proliferation; gene therapy;

KW interdomain linker; cleavage site; Alzheimer's disease.

OS Unidentified.

PN MO200129232-A2.

PD 26-APR-2001.

PR 19-OCT-2000; 2000MO-US28941.

PR 20-OCT-1999; 9905-0160559.

PR 14-AUG-2000; 2000US-0225564.

PA (SCIO-) SCIOS INC.

PI Cordell B, Li Y;

DR WPI; 2001-290920/30.

XX Novel fusion polypeptide comprising first and second caspase subunit

PT separated by cleavage site not associated in nature with caspase

PT subunit, useful for cloning gene encoding enzymes involved in

PT proteolytic cleavage -

PS Example 2; Page 26; 116pp; English.

XX The present sequence is a beta-secretase cleavage site of beta-amyloid

CC precursor protein (beta-APP). This sequence is used to construct

CC an artificially engineered chimeric cassette comprising human caspase-3

CC with interdomain linker replaced by swedish mutant beta-secretase

CC cleavage site. This modified caspase-3 plays a pivotal role in

CC Alzheimer's disease. Caspases are a family of cysteine proteases, that

CC participate in the initiation and execution of apoptosis.

CC The present invention relates to a method for functional cloning of genes

CC encoding proteins or enzymes involved in proteolytic cleavage. The

CC invention is based on the use of caspase expression cassettes comprising

CC the coding sequence of a proteolytic cleavage site flanked by sequences

CC encoding two caspase subunits. A fusion polypeptide comprising a first

CC and a second caspase subunit, separated by a cleavage site not associated

CC in nature, is useful for cloning gene encoding enzymes involved in

CC proteolytic cleavage. An expression cassette containing fusion

CC polypeptide is used to identify a mutant cell line deficient in an

CC enzyme of interest and is also useful for diagnosis and suppression of

CC proliferation or metastases of a tumour cell characterized by

CC overexpression of a polypeptide (e.g. Cathepsin B or urokinase,

CC selectively expressed in the tumour cells). DNA encoding fusion

CC polypeptide is used in gene therapy.

XX Sequence 18 AA;

Query Match 100.0%; Score 47; DB 22; Length 18;

Best Local Similarity 100.0%; Pred. No. 0.0048;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EISEVKMDAE 10

Db 4 EISEVKMDAE 13

RESULT 5

AAV69713

ID AAV69713 standard; peptide: 20 AA.

AC AAV69713;

DT 11-APR-2000 (first entry)

DE Beta-APP alpha-secretase substrate [KM]-APP(-10,+10).

KM Nootropic; neuroprotective; beta-amyloid precursor protein; metabolism;

KW cleavage site; beta-secretase; neurodegenerative disease;

KW Alzheimer's disease.

OS Homo sapiens.

PN MO9964587-A1.

PD 16-DEC-1999.

PR 04-JUN-1999; 99MO-FR01326.

PR 05-JUN-1998; 98FR-0007068.

PR 31-MAR-1999; 99US-0122599.

PA (RHON) RHONE-POULENC RORER SA.

PI (DYPA-) UNIV CURIE PARIS VI P & M.

PI Rholam M, Munoz-Climent N, Moutaouakil M, Cohen P, Bertrand P;

DR WPI; 2000-097537/08.

XX Polypeptide with beta-secretase activity, specific for wild-type

PT amyloid precursor protein, useful in treating Alzheimer's disease -

PS Example 3; Page 24; 44pp; French.

XX Peptides AAV69702-Y69718 represent synthetic peptide substrates for a

CC novel polypeptide with beta-secretase activity that can cleave

CC specifically the natural beta-amyloid precursor protein (bAPP). Normal

CC cleavage of the protein occurs between amino acids Met596-Asp597 and

CC Val593-Ile637 (positions 4-5 and 44-45 of AAV69701). The novel

CC polypeptide is used to identify agents that interact specifically with

CC it. These agents regulate metabolism of APP, particularly they slow down

CC or reduce production of beta-amyloid, so can be used to treat

CC neurodegenerative diseases, particularly Alzheimer's disease.

CC Sequence 20 AA;

Query Match 100.0%; Score 47; DB 21; Length 20;

Best Local Similarity 100.0%; Pred. No. 0.0054;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EISEVKMDAE 10

Db 4 EISEVKMDAE 13

RESULT 6

AAW98002

ID AAW98002 standard; protein; 33 AA.

```

XX AC AAW98002:
XX XX
XX DT 21-JUN-1999 (first entry)
XX XX
XX DE Amyloid precursor protein (aa656-678) with Swedish mutation.
XX XX
XX KW Amyloid precursor protein; APP; human; gene targeting;
XX KW homologous recombination; transgenic mouse; transgenic animal;
XX KW animal model; Alzheimer's disease.
XX XX
XX OS Mus musculus.
XX XX
XX PN M09909150-A1.
XX XX
XX PD 25-FEB-1999.
XX XX
XX PF 18-AUG-1997; 97MO-US14507.
XX XX
XX PR 18-AUG-1997; 97MO-US14507.
XX XX
XX PA (FARB ) BAYER CORP.
XX XX
XX PI Wirak DO:
XX XX
XX DR WPI: 1999-181029/15.
XX XX
XX PS Modification of target nucleic acids - by homologous recombination,
XX XX PT used particularly for introducing a humanised amyloid precursor
XX XX PT protein gene into rodents for producing models of Alzheimer's
XX XX PT disease
XX XX
XX PS Disclosure; Page 145; 209pp; English.
XX XX
XX CC This polypeptide comprises residues 656-678 of a murine amyloid
XX CC precursor protein (APP). The invention provides a novel gene
XX CC targeting strategy that facilitates the introduction of one or
XX CC more specific mutations into any gene in a single double reciprocal
XX CC homologous recombination step. The method has been used
XX CC particularly for introducing a humanised APP gene into rodents for
XX CC producing animal models of Alzheimer's disease (AD). 4 independent
XX CC lines of transgenic mice (lines ES5007, ES5103, ES5401 and ES5403)
XX CC have been created using the gene targeting technique applied to
XX CC embryonic stem cells. In each line, the mouse APP gene was modified
XX CC to encode a mouse/human hybrid (m/hAPP) where amino acid residues
XX CC 666-770 of APP770 were encoded by human cDNA sequences instead of
XX CC mouse genomic exons (exons 16-18). Within these residues, only 3
XX CC amino acid differences exist between the mouse and human proteins,
XX CC i.e. Gly-676 to Arg, Phe-681 to Thr and Arg-684 to His. The
XX CC exon-cDNA fusion gene therefore encodes an APP containing a
XX CC humanised beta-amyloid domain. Swedish- and/or London-FAD APP
XX CC mutations have also been introduced (see also AAW97997-W98001).
XX XX
XX SO Sequence 33 AA:

Query Match 100.0%; Score 47; DB 20; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.0095;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EISEVKMDAE 10
DB 10 EISEVKMDAE 19

RESULT 7
AAV69717
ID AAV69717 standard; peptide: 39 AA.
AC AAV69717:
XX AAV69717:
XX 11-APR-2000 (first entry)
XX Beta-APP alpha-secretase substrate [KM]-APP(-20,+20).
DE

```

```

XX XX
XX KW Neotropic; neuroprotective; beta-amyloid precursor protein; metabolism;
XX KW cleavage site; beta-secretase; neurodegenerative disease;
XX KW Alzheimer's disease.
XX XX
XX OS Homo sapiens.
XX XX
XX PN M09964587-A1.
XX XX
XX PD 16-DEC-1999.
XX XX
XX PF 04-JUN-1999; 99WO-FR01326.
XX XX
XX PR 05-JUN-1998; 98FR-0007068.
XX PR 31-MAR-1999; 99US-0122599.
XX XX
XX PA (RHON ) RHONE-POULENC RORER SA.
XX PA (UYPA-) UNIV CURIE PARIS VI P 6 M.
XX XX
XX PI Rhoulam M, Munoz-Gimenez N, Moutaouakil M, Cohen P, Bertrand P;
XX XX DR WPI: 2000-097537/08.
XX XX
XX PS Polypeptide with beta-secretase activity, specific for wild-type
XX XX PT amyloid precursor protein, useful in treating Alzheimer's disease -
XX XX PT Example 3; Page 24; 44pp; French.
XX XX
XX CC Peptides AAV6702-Y69718 represent synthetic peptide substrates for a
XX CC novel polypeptide with beta-secretase activity that can cleave
XX CC specifically the natural beta-amyloid precursor protein (bAPP). Normal
XX CC cleavage of the protein occurs between amino acids Met596-Asp597 and
XX CC Val636-Ile637 (positions 4-5 and 44-45 of AAV6701). The novel
XX CC polypeptide is used to identify agents that interact specifically with
XX CC it. These agents regulate metabolism of APP, particularly they slow down
XX CC or reduce production of beta-amyloid, so can be used to treat
XX CC neurodegenerative diseases, particularly Alzheimer's disease.
XX XX
XX SO Sequence 39 AA:

Query Match 100.0%; Score 47; DB 21; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EISEVKMDAE 10
DB 13 EISEVKMDAE 22

RESULT 8
AAW26512
ID AAW26512 standard; peptide: 45 AA.
AC AAW26512:
XX AAW26512:
XX 06-JAN-1998 (first entry)
XX XX
XX DE Amyloid precursor protein fragment APP-RFP 751 (BAP dell1-28).
XX XX
XX KW Amyloid precursor protein; APP; beta-amyloid protein; BAP;
XX KW substrate; mutelin; secretase; Alzheimer's disease; human.
XX XX
XX OS Chimeric Homo sapiens.
XX OS Chimeric synthetic.
XX XX
XX FH Key Location/Qualifiers
XX FT Cleavage-site 7..8
XX FT /note= "secretase cleavage site"
XX FT Peptide 10..33
XX FT /label= BAP(dell1-28)
XX FT /note= "truncated beta-amyloid protein"
XX FT 20..42
XX FT Domain
XX FT /label= Transmembrane

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XX  XX  US5656477-A.
PN  XX
XX  PD  12-AUG-1997.
XX  PF  01-MAY-1992; 92US-0877675.
XX  PR  20-SEP-1993; 93US-0123659.
XX  PR  01-MAY-1992; 92US-0877675.
XX  PA  (AMCY ) AMERICAN CYANAMID CO.
XX  PI  Jacobsen JS, Vitek MP;
XX  PI  WPI; 1997-414594/38.
XX  DR  Nucleic acid encoding amyloid precursor muten(s) - comprising
PT  reporter gene and coding sequence, for identifying compounds which
PT  modify the activity of proteolytic enzymes which cleave APP
XX  PS  Disclosure; Fig 5A; 84pp; English.
XX  CC  This peptide sequence shows the region of amyloid precursor protein
XX  CC  (APP) that includes a truncated beta-amyloid protein (BAP) lacking
XX  CC  the native secretase cleavage/recognition site. In an attempt to
XX  CC  engineer an APP non-cleavable substrate for secretase, an
XX  CC  APP-reporter (APP-REP) protein that carries the BAP deletion has
XX  CC  been expressed in recombinant host cells. Deletion of these 18
XX  CC  amino acids, however, still resulted in the secretion of an
XX  CC  N-terminal APP-reporter fragment into the cytoplasm. Non-
XX  CC  cleavable APP substrates can be used to detect other putative
XX  CC  abnormal APP processing events. They can also be used to
XX  CC  investigate cellular post-translational modifications to APP in
XX  CC  order to determine the potential influence on normal secretase and
XX  CC  abnormal BAP 'clipping' activities.
XX  SQ  Sequence 45 AA;
XX  Query Match 100.0%; Score 47; DB 18; Length 45;
XX  Best Local Similarity 100.0%; Pred. No. 0.014;
XX  Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY  1 EISEVKMDAE 10
    |||||
DB  3 EISEVKMDAE 12

RESULT 9
AAW4748
ID  AAW4748 standard; Protein; 45 AA.
XX  AC  AAW4748;
XX  DT  01-JUN-1998 (first entry)
XX  DE  APP-REP 751 [BAP delta(11-28)] peptide.
XX  KW  Amyloid precursor protein; APP; APP 751 isoform; deletion; substrate P;
XX  KW  epitope; Met-enkephalin; detection; secretase; beta-amyloid protein; BAP;
XX  KW  Alzheimer's disease; cleavage.
XX  OS  Homo sapiens.
XX  OS  Synthetic.
XX  FH  Key Location/Qualifiers
XX  FH  Cleavage-site 7..8 /note= "putative secretase cleavage site"
XX  FT  Peptide 10..33 /label= BAP(delta11-28)
XX  FT  /note= "truncated beta-amyloid protein"
XX  FT  Domain 20..42 /label= Transmembrane
XX  FT  US5652092-A.
XX  PN  US5652092-A.

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XX  XX  29-JUL-1997.
PN  XX
XX  PD  01-MAY-1992; 92US-0877675.
XX  PF  20-SEP-1993; 93US-0123659.
XX  PR  01-MAY-1992; 92US-0877675.
XX  PR  05-JUN-1995; 95US-0462859.
XX  PA  (AMCY ) AMERICAN CYANAMID CO.
XX  PI  Jacobsen JS, Vitek MP;
XX  PI  WPI; 1997-392937/36.
XX  DR  Screening for compounds which reduce beta-amyloid protein formation
PT  - using cells which express a construct encoding a marker and an
PT  amyloid precursor muten derived from APP isoforms
XX  PS  Disclosure; Fig 5A; 84pp; English.
XX  CC  This peptide sequence shows the region of amyloid precursor protein
XX  CC  (APP) that includes a truncated beta-amyloid protein (BAP) lacking
XX  CC  the native secretase cleavage/recognition site. In an attempt to
XX  CC  engineer an APP non-cleavable substrate for secretase, an
XX  CC  APP-reporter (APP-REP) protein that carries the BAP deletion has
XX  CC  been expressed in recombinant host cells. Deletion of these 18
XX  CC  amino acids, however, still resulted in the secretion of an
XX  CC  N-terminal APP-reporter fragment into the cytoplasm. Non-
XX  CC  cleavable APP substrates can be used to detect other putative
XX  CC  abnormal APP processing events. They can also be used to
XX  CC  investigate cellular post-translational modifications to APP in
XX  CC  order to determine the potential influence on normal secretase and
XX  CC  abnormal BAP 'clipping' activities.
XX  SQ  Sequence 45 AA;
XX  Query Match 100.0%; Score 47; DB 18; Length 45;
XX  Best Local Similarity 100.0%; Pred. No. 0.014;
XX  Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY  1 EISEVKMDAE 10
    |||||
DB  3 EISEVKMDAE 12

RESULT 10
AAW4748
ID  AAW4748 standard; Protein; 45 AA.
XX  AC  AAW4748;
XX  DT  01-JUN-1998 (first entry)
XX  DE  APP-REP 751 [BAP delta(11-28)] peptide.
XX  KW  Amyloid precursor protein; APP; APP 751 isoform; deletion; substrate P;
XX  KW  epitope; Met-enkephalin; detection; secretase; beta-amyloid protein; BAP;
XX  KW  Alzheimer's disease; cleavage.
XX  OS  Homo sapiens.
XX  OS  Synthetic.
XX  FH  Key Location/Qualifiers
XX  FH  Cleavage-site 7..8 /note= "putative secretase cleavage site"
XX  FT  MISC-difference 19..20 /note= "residues 11-28 of the wild type BAP sequence
XX  FT  are deleted from between these positions"
XX  FT  US5693478-A.
XX  PN  US5693478-A.
XX  PD  02-DEC-1997.

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```
XX 05-JUN-1995: 950S-0464247.
XX
PR 20-SEP-1993: 930S-0123659.
PR 01-MAY-1992: 920S-0877675.
PR 05-JUN-1995: 950S-0464247.
XX
PA (AMCY ) AMERICAN CYANAMID CO.
XX
PI Jacobsen JS, Vitek MP;
XX
DR WPI; 1998-031744/03.
XX
PT Amyloid precursor muten reporter molecule assay containing antibody
PT recognized marker - used to study pathways associated with
PT Alzheimer's disease
XX
PS Disclosure; Fig 5A; 84pp; English.
XX
CC This sequence represent the beta-amyloid protein sequence from the
CC construct APP-REP751 (BAP delta(11-28)). The mutant sequence contains
CC a deletion of the wild type BAP residues 11-28. This causes a
CC shortening of the BAP sequence. This may affect cleavage of the BAP by
CC the "secretase" dependent on whether the "secretase" recognises the
CC cleavage site by a positional effect or by sequence. The mutant sequence
CC can be used in a method to study secretase and beta-amyloid protein
CC (BAP)-generating pathways associated with Alzheimer's disease by
CC studying proteolytic cleavage of the reporter polypeptides (e.g.
CC AAM44744 and AAM44745).
XX
SQ Sequence 45 AA:
Query Match 100.0%; Score 47; DB 19; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EISEVKMDAE 10
Db 3 EISEVKMDAE 12

RESULT 11
AAM42977
ID AAM42977 standard; peptide: 45 AA.
XX
AC AAM42977;
XX
DT 01-MAY-1998 (first entry)
XX
DE Deletion beta-amyloid peptide (BAP) derived from APP-REP 751.
XX
KW Beta-amyloid peptide; BAP; extracellular BAP plaque;
KW cerebrovascular deposit; Alzheimers disease; Down's syndrome;
KW amyloid precursor protein; APP; secretase; BAP aggregation;
KW abnormal proteolytic cleavage.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 20..43
FT /note= "putative transmembrane domain"
XX
XX US5703209-A.
XX
XX 30-DEC-1997.
XX
XX
XX 05-JUN-1995: 950S-0464248.
XX
XX
XX 20-SEP-1993: 930S-0123659.
XX
XX 01-MAY-1992: 920S-0877675.
XX
XX
XX (AMCY ) AMERICAN CYANAMID CO.
```

```
PI Jacobsen JS, Vitek MP;
XX
DR WPI; 1998-076482/07.
XX
PT Amyloid precursor protein fusion polypeptides - comprising APP
PT fragment and marker, useful for research and drug screening
XX
PS Disclosure; Fig 5A; 84pp; English.
XX
CC The present sequence represents a beta-amyloid peptide (BAP), with
CC a deletion amino acids 11-28 (numbered according to AAM42976). Abnormal
CC accumulation of extracellular BAP in plaques and cerebrovascular
CC deposits is characteristic in brains of individuals suffering from
CC Alzheimers disease and Down's syndrome. BAP is a poorly soluble,
CC self-aggregating protein which is derived from a larger amyloid precursor
CC protein (APP). APP is expressed as an integral membrane protein, and is
CC cleaved by secretase, between BAP 16lys and 17leu. Cleavage at this site
CC precludes amyloidogenesis and results in the release of the
CC amino-terminal APP fragment. Three major isoforms of APP exist: APP-695,
CC APP-751 and APP-770. These isoforms are derived by alternative splicing.
CC APP-APP 751 is a deletion construct of APP-751, which has a deletion of
CC 276 amino acids to within 15 amino acids of the BAP domain. APP can be
CC used as a substrate for studying abnormal proteolytic cleavage which
CC results in the release of BAP, and also to screen for drugs that will
CC inhibit such cleavage.
XX
SQ Sequence 45 AA:
Query Match 100.0%; Score 47; DB 19; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EISEVKMDAE 10
Db 3 EISEVKMDAE 12

RESULT 12
AAR64168
ID AAR64168 standard; peptide: 53 AA.
XX
AC AAR64168;
XX
DT 02-AUG-1995 (first entry)
XX
DE Variant beta amyloid protein with 10 preceeding amino acids of APP.
XX
KW beta amyloid protein; mutant; variant; detection; amyloid deposition;
KW diagnosis; amyloidosis associated disease; Alzheimer's disease;
KW Down's syndrome; APP; amyloid precursor protein.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..10
FT /note= "the preceeding 10 amino acids of APP"
FT Peptide 11..53
FT /note= "beta amyloid protein variant"
XX
XX W09428412-A.
XX
XX 08-DEC-1994.
XX
XX
XX 27-MAY-1994: 94MO-US05809.
XX
XX
XX 28-MAY-1993: 93US-0069010.
XX
XX
XX (MIRI-) MIRIAM HOSPITAL.
XX
XX PA
XX PT Majocha RE, Marotta CA;
XX
XX
XX WPI; 1995-023013/03.
```



PT Amyloid binding composition comprising labelled amyloid protein  
 PT and carrier - useful for in vivo imaging of amyloid deposits, for  
 PT diagnosing Alzheimer's disease and Down's Syndrome.  
 XX  
 PS Claim 5; Page 43; 58pp; English.  
 CC  
 CC AAR64168 shows the amino acid sequence of the beta amyloid protein  
 CC plus the 10 amino acids preceding the amyloid precursor protein. The  
 CC protein binds amyloid and is useful for in vivo imaging of amyloid  
 CC deposits and hence diagnosis of an amyloidosis-associated disease, such  
 CC as Alzheimer's disease or Down's syndrome. AAR64165 shows the generic  
 CC sequence of the amyloid protein for generation of variants.  
 CC  
 SQ Sequence 53 AA;  
 Query Match 100.0%; Score 47; DB 16; Length 53;  
 Best Local Similarity 100.0%; Pred. No. 0.016;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EISEVKMDAE 10  
 |||||  
 DB 4 EISEVKMDAE 13  
 RESULT 13  
 AAB10910  
 ID AAB10910 standard; peptide: 57 AA.  
 AC AAB10910;  
 XX  
 XX AAB10910;  
 DT 30-JAN-2001 (first entry)  
 XX  
 DE Human amyloid precursor APP770 A-beta1-40/42 protein fragment.  
 XX  
 KM APP; amyloid precursor protein; APP770; human; copper agonist; treatment;  
 KM amyloid-beta-peptide; neurotropic; neuroprotective; Alzheimer's disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN DE1990357-A1.  
 XX  
 PD 07-SEP-2000.  
 XX  
 XX 03-MAR-1999; 99DE-1009357.  
 PF  
 XX  
 PR 03-MAR-1999; 99DE-1009357.  
 XX  
 PA (MULT/) MULTHAUP G.  
 PA (BEYR/) BEYREUTHER K.  
 XX  
 PI Beyreuther K, Multaup G, Masters CL;  
 XX  
 DR WPI: 2000-595035/57.  
 XX  
 XX Copper agonist binds to the copper binding site of amyloid precursor  
 PT protein, useful for treating Alzheimer's disease -  
 XX  
 XX Example 1; Fig 1; 14pp; German.  
 PS  
 CC This invention describes a novel copper agonist (I) capable of binding to  
 CC the copper binding site of an amyloid precursor protein (APP) and/or  
 CC preventing or reducing the release of amyloid-beta-peptides. The  
 CC invention also describes (1) a medicament comprising (1) in combination  
 CC with a carrier; (2) identifying (I), comprising: (a) contacting potential  
 CC (I) with APP; and (b) detecting a reduction of beta-proteins; and (3)  
 CC identifying (1) comprising: (a) contacting APP or the copper-binding  
 CC site-carrying fragment with a solution of, immobilized substance  
 CC libraries of, or low molecular weight substances from microorganisms or  
 CC plants; (b) performing a competitive assay by adding copper ions to form  
 CC complexes with the ligands; (c) identifying the ligands; and (d)  
 CC selecting ligands, which bind the APP copper binding site or which reduce  
 CC the Abeta peptide release. The products of the invention have neurotropic  
 CC and neuroprotective activity. (1) and the resulting medicament are used

CC for preventing or treating Alzheimer's disease.  
 XX  
 SQ Sequence 57 AA;  
 Query Match 100.0%; Score 47; DB 21; Length 57;  
 Best Local Similarity 100.0%; Pred. No. 0.018;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EISEVKMDAE 10  
 |||||  
 DB 7 EISEVKMDAE 16  
 RESULT 14  
 AAR58937  
 ID AAR58937 standard; peptide: 58 AA.  
 XX  
 AC AAR58937;  
 XX  
 DT 15-APR-1995 (first entry)  
 XX  
 DE Amyloid precursor protein residues 551-608.  
 XX  
 KM Amyloid precursor protein; beta amyloid; monoclonal antibody;  
 KM Anti-Alz 90; Alzheimer's disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9419692-A.  
 XX  
 PD 01-SEP-1994.  
 XX  
 PF 17-FEB-1994; 94WO-US01712.  
 XX  
 PR 18-FEB-1993; 93US-0019208.  
 XX  
 PA (GENO ) GEN HOSPITAL CORP.  
 XX  
 PI Nishimoto I;  
 XX  
 DR WPI: 1994-294486/36.  
 XX  
 PT Identifying cpds. useful for treating or preventing Alzheimer's  
 PT disease - by determining whether it interferes with the  
 PT association of the couplone portion of amyloid precursor protein  
 PT to G polypeptide  
 XX  
 PS Disclosure; Page 40-41; 71pp; English.  
 XX  
 CC Beta amyloid is synthesised as part of a larger protein referred to  
 CC as amyloid precursor protein (APP), which has a number of isoforms  
 CC in humans, including APP695 and APP770. APP forms a complex with GO,  
 CC a GTP-binding protein (or "G protein") in brain. It is suggested  
 CC that abnormal APP-co signalling is involved in the Alzheimer's  
 CC disease process. Anti-Alz 90 is a mouse monoclonal antibody  
 CC specific for an epitope corresp. to residues 551-608 of APP,  
 CC a section of APP that is within the extracellular domain.  
 CC  
 SQ Sequence 58 AA;  
 Query Match 100.0%; Score 47; DB 15; Length 58;  
 Best Local Similarity 100.0%; Pred. No. 0.018;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EISEVKMDAE 10  
 |||||  
 DB 40 EISEVKMDAE 49  
 RESULT 15  
 AAW26511  
 ID AAW26511 standard; peptide: 63 AA.  
 XX

```

AC  AAW26511:
XX
DT  06-JAN-1998 (first entry)
XX
DE  Amyloid precursor protein fragment APP-REP 751 (BAP E22Q).
XX
XX  Amyloid precursor protein: APP; beta-amyloid protein; BAP;
KM  substrate; mutelin; secretase; Alzheimer's disease;
XX  hereditary cerebral haemorrhage with amyloidosis; human.
XX
OS  Homo sapiens.
XX
FH  Key Location/Qualifiers
FT  Peptide 10..51
FT /label= BAP(E22Q)
FT /note= "beta-amyloid protein E22Q mutant"
FT Cleavage-site 25..26
FT /note= "secretase cleavage site"
FT Domain 38..61
FT /label= Transmembrane
XX
XX  US5656477-A.
XX  12-AUG-1997.
XX
XX  01-MAY-1992; 92US-0877675.
XX
XX  20-SEP-1993; 93US-0123659.
XX  01-MAY-1992; 92US-0877675.
XX
XX  (AMCY ) AMERICAN CYANAMID CO.
XX
XX  Jacobsen JS, Vitek MP;
XX
XX  WPI: 1997-414594/38.
XX
XX  Nucleic acid encoding amyloid precursor mutelin(s) - comprising
PT  reporter gene and coding sequence, for identifying compounds which
PT  modify the activity of proteolytic enzymes which cleave APP
XX
XX  Disclosure: Fig 5A; 84pp; English.
XX
XX  This peptide sequence shows the region of amyloid precursor protein
CC  (APP) that includes a beta-amyloid protein (BAP) carrying a point
CC  mutation (BAP E22Q) found in patients with hereditary cerebral
CC  haemorrhage with amyloidosis of Dutch origin (HCHWA-D). In an
CC  attempt to engineer an APP non-cleavable substrate for secretase,
CC  an APP-reporter (APP-REP) protein that carries the E22Q mutation
CC  has been expressed in recombinant host cells. This resulted in the
CC  secretion of an N-terminal fragment indistinguishable from that of
CC  APP-REP 751 (see AAW26393-94). Non-cleavable APP substrates can be
CC  used to detect other putative abnormal APP processing events. They
CC  can also be used to investigate cellular post-translational
CC  modifications to APP in order to determine the potential influence
CC  on normal secretase and abnormal BAP 'clipping' activities.
XX
SQ  Sequence 63 AA:

Query Match 100.0%; Score 47; DB 18; Length 63;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EISEVKMDAE 10
DB 3 EISEVKMDAE 12

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Search completed: October 29, 2002, 10:26:42  
 Job time : 23.1429 secs

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OM protein - protein search, using sw model

Run on: October 29, 2002, 10:23:36 ; Search time 10.4286 Seconds  
(without alignments)  
92.140 Million cell updates/sec

Title: US-09-580-018-2  
Perfect score: 47  
Sequence: 1 EISEVKMDAE 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283138 segs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: PIR:1:\*  
2: PIR:2:\*  
3: PIR:3:\*  
4: PIR:4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	100.0	82	P00438	Alzheimer's disease
2	47	100.0	695	A49795	Alzheimer's disease
3	47	100.0	695	A27485	Alzheimer's disease
4	47	100.0	695	S00550	Alzheimer's disease
5	47	100.0	770	ORH044	Alzheimer's disease
6	44	93.6	747	JH0773	Alzheimer's disease
7	38	80.9	33	S23094	beta-amyloid prote
8	38	80.9	37	E60045	Alzheimer's disease
9	38	80.9	57	F60045	Alzheimer's disease
10	38	80.9	57	G60045	Alzheimer's disease
11	38	80.9	57	D60045	Alzheimer's disease
12	38	80.9	57	A60045	Alzheimer's disease
13	38	80.9	57	B60045	Alzheimer's disease
14	38	80.9	389	G84245	MbDH dehydrogenase
15	36	76.6	261	C64572	conserved hypotet
16	36	76.6	261	F71867	hypothetical prote
17	35	74.5	818	AE1598	DNA gyrase-like pr
18	35	74.5	819	AG1235	DNA gyrase-like pr
19	34	72.3	590	A25680	nuclear histone-bi
20	34	72.3	1378	G88637	protein F53H.4 li
21	33	70.2	289	T34241	hypothetical prote
22	33	70.2	370	T48633	hypothetical prote
23	33	70.2	419	D42725	nitrite hydratase
24	33	70.2	626	E82273	accessory coloniza
25	33	70.2	743	D84854	hypothetical prote
26	33	70.2	793	T27133	hypothetical prote
27	33	70.2	800	S54427	gyrase-like protei
28	33	70.2	800	C89911	topoisomerase IV s
29	32	68.1	146	C69136	hypothetical prote

30	32	68.1	389	2	B69096	corrinoid/iron-sul
31	32	68.1	427	2	G84375	adenosylhomocyste
32	32	68.1	427	2	F85436	hypothetical prote
33	32	68.1	470	2	T05258	glycine hydroxymet
34	32	68.1	486	2	AC2424	hypothetical prote
35	32	68.1	632	2	B69310	mRNA 3'-end proces
36	32	68.1	677	2	B69210	protein F20N2.12 f
37	32	68.1	679	2	A96599	hypothetical prote
38	32	68.1	690	2	S41009	protein T05G5.9 f1
39	32	68.1	705	2	E88564	hypothetical prote
40	32	68.1	941	2	B96553	hypothetical prote
41	31	66.0	84	2	T27174	hypothetical prote
42	31	66.0	105	2	PH1526	gamma-aminobutyric
43	31	66.0	178	2	C64168	hypothetical prote
44	31	66.0	178	2	C69206	hypothetical prote
45	31	66.0	182	2	AC0449	conserved hypotet

#### ALIGNMENTS

##### RESULT 1

P00438 Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 30-Sep-1993 #sequence\_revision 19-Oct-1995 #text\_change 19-Oct-1995

C:Accession: P00438; C60045

R:Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.E.

Biochem. Biophys. Res. Commun. 188, 905-911, 1992

A:Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precurs

A:Reference number: P00438; MUID:93075180

A:Accession: P00438

A:Molecule type: DNA

A:Residues: 1-82 <DNA>

A:Cross-references: GB:M83558; GB:M83657

R:Ohnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d

A:Reference number: A60045; MUID:92017079

A:Accession: C60045

A:Molecule type: mRNA

A:Residues: 12-68 <ORF>

A:Cross-references: EMBL:X56129

C:Species: Macaca fascicularis (crab-eating macaque)

C:Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match 100.0%; Score 47; DB 2; Length 82;

Best Local Similarity 100.0%; Pred. No. 0.01;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EISEVKMDAE 10  
Db 10 EISEVKMDAE 19

##### RESULT 2

A49795 Alzheimer's disease amyloid beta protein precursor - crab-eating macaque

C:Species: Macaca fascicularis (crab-eating macaque)

C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999

C:Accession: A49795

R:Podlitsny, M.B.; Toljan, D.R.; Selkoe, D.J.

Am. J. Pathol. 138, 1423-1435, 1991

A:Title: Homology of the amyloid beta protein precursor in monkey and human supports

A:Reference number: A49795; MUID:91273117

A:Accession: A49795

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-695 <POD>

A:Cross-references: GB:M58727; NID:g342062; PIDN:AAA36829.1; PID:g342063

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase

C:Keywords: alternative splicing

Query Match 100.0%; Score 47; DB 1; Length 695;  
 Best Local Similarity 100.0%; Pred. No. 0.12;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EISEVKMDAE 10  
 |||||||||  
 Db 590 EISEVKMDAE 599

RESULT 3  
 A27485  
 Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse  
 N:Alternate names: proteinase nexin II  
 C:Species: Mus musculus (house mouse)  
 C>Date: 31-Mar-1989 #sequence\_revision 31-Mar-1989 #text\_change 13-Aug-1999  
 C:Accession: A27485; S19727; I49485  
 R:Yamada, T.; Sasaki, H.; Furuya, H.; Miyata, T.; Goto, I.; Sakaki, Y.  
 Biochem. Biophys. Res. Commun. 149, 665-671, 1987  
 A:Title: Complementary DNA for the mouse homolog of the human amyloid beta protein precursor  
 A:Reference number: A27485; MUID:88106489  
 A:Accession: A27485  
 A:Molecule type: mRNA  
 A:Residues: 1-695 <YAM>  
 C:Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques is  
 A:Experimental source: brain  
 R:de Strooper, B.; van Leuven, F.; van den Berghe, H.  
 Biochim. Biophys. Acta 1129, 141-143, 1991  
 A:Title: The amyloid beta protein precursor or proteinase nexin II from mouse is closer  
 A:Reference number: S19727; MUID:92096458  
 A:Accession: S19727  
 A:Molecule type: mRNA  
 A:Residues: 1-210, 'G', 212-220, 'S', 222-396, 'A', 398-402, 'T', 404-448, 'A', 450-695 <STR>  
 A:Cross-references: EMBL:X59379  
 R:Izumii, R.; Yamada, T.; Yoshikai, S.; Sasaki, H.; Hattori, M.; Sakaki, Y.  
 Gene 112, 189-199, 1992  
 A:Title: Positive and negative regulatory elements for the expression of the Alzheimer's  
 A:Reference number: I49485; MUID:92209998  
 A:Accession: I49485  
 A>Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-19 <RES>  
 A:Cross-references: GB:DI0603; NID:9220328; PIDN:BA01456.1; PID:9220329  
 C:Genetics:  
 A:Map position: 16C3  
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase A  
 C:Keywords: alternative splicing; amyloid; transmembrane protein

Query Match 100.0%; Score 47; DB 2; Length 695;  
 Best Local Similarity 100.0%; Pred. No. 0.12;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EISEVKMDAE 10  
 |||||||||  
 Db 590 EISEVKMDAE 599

RESULT 4  
 S00550  
 Alzheimer's disease amyloid beta protein precursor - rat  
 N:Alternate names: beta-A4 amyloid protein  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 13-Aug-1999  
 C:Accession: S00550; A41245; A39820; S46251  
 R:Shivers, B.D.; Hildlich, C.; Multhaup, G.; Salbaum, M.; Beyreuther, K.; Seeburg, P.H.  
 EMBO J. 7, 1365-1370, 1988  
 A:Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brain  
 A:Reference number: S00550; MUID:88312583  
 A:Accession: S00550  
 A:Molecule type: mRNA  
 A:Residues: 1-695 <SHI>  
 A:Cross-references: EMBL:X07648; NID:955616; PIDN:CAA30488.1; PID:955617  
 R:Schubert, D.; Schroeder, R.; Lacorbiere, M.; Salton, T.; Cole, G.  
 Science 241, 223-226, 1988

A:Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan co  
 A:Reference number: A41245; MUID:88264430  
 A:Accession: A41245  
 A:Molecule type: protein  
 A:Residues: 18-37, 'X', 39-40, 'X', 42-44 <SCH>  
 A:Note: Evidence for heparan sulfate attachment  
 R:Hesse, L.; Behner, D.; Masters, C.L.; Multhaup, G.  
 FEBS Lett. 349, 109-116, 1994  
 A:Title: The beta-A4 amyloid precursor protein binding to copper.  
 A:Reference number: S46251; MUID:94320627  
 A:Accession: S46251  
 A:Contents: annotation; copper binding sites  
 A:Note: rat peptides were isolated but not sequenced  
 R:Potempska, A.; Styles, J.; Mehta, P.; Kim, K.S.; Miller, D.L.  
 J. Biol. Chem. 266, 8464-8469, 1991  
 A:Title: Purification and tissue level of the beta-amyloid peptide precursor of rat b  
 A:Reference number: A39820; MUID:91217087  
 A:Accession: A39820  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 18-32 <POT>  
 A:Experimental source: brain  
 C:Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques is  
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase  
 C:Keywords: alternative splicing; amyloid; glycoprotein; transmembrane protein  
 F:625-648/Domain: transmembrane #status predicted <TM>

Query Match 100.0%; Score 47; DB 2; Length 695;  
 Best Local Similarity 100.0%; Pred. No. 0.12;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EISEVKMDAE 10  
 |||||||||  
 Db 590 EISEVKMDAE 599

RESULT 5  
 Q0RU04  
 Alzheimer's disease amyloid beta protein precursor [validated] - human  
 N:Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor xia inh  
 N:Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vascu  
 protein precursor splice form APP(770)  
 C:Species: Homo sapiens (man)  
 C>Date: 30-Jun-1987 #sequence\_revision 28-Jul-1995 #text\_change 15-Sep-2000  
 C:Accession: S02260; S05194; A32277; A32860; A35486; I39452; I39453; I59562;  
 4668; A28883; A29302; A60805; J00038; S05011; A60355; S25076; S38252;  
 R:Lemaire, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.;  
 Nucleic Acids Res. 17, 517-522, 1989  
 A:Title: The PrEA4(695) precursor protein of Alzheimer's disease A4 amyloid is encode  
 A:Reference number: S02260; MUID:89128427  
 A:Accession: S02260  
 A:Molecule type: DNA  
 A:Residues: 1-288, 'V', 365-770 <LEM1>  
 A:Cross-references: EMBL:X13466  
 R:Lemaire, H.G.  
 submitted to the EMBL Data Library, November 1988  
 A:Reference number: S05194  
 A:Accession: S05194  
 A:Molecule type: DNA  
 A:Residues: 1-14, 'VW', 17-288, 'V', 365-770 <LEM2>  
 A:Cross-references: EMBL:X13466; NID:935598; PIDN:CAA11830.1; PID:9871360  
 A:Note: alternative splice form APP(695)  
 R:La Fauce, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.  
 Biochem. Biophys. Res. Commun. 159, 297-304, 1989  
 A:Title: Characterization of the 5'-end region and the first two exons of the beta-pr  
 A:Reference number: A32277; MUID:89165870  
 A:Accession: A32277  
 A:Molecule type: DNA  
 A:Residues: 1-75 <LAF>  
 A:Cross-references: GB:M24546; GB:M24547; NID:9441202; PIDN:AAC13654.1; PID:9516074  
 R:Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.  
 Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989  
 A:Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows simila

A:Reference number: A33260; MUID:89392030  
A:Accession: A33260  
A:Molecule type: DNA  
A:Residues: 656-737 <COH>  
A:Cross-references: GB:M9270; NID:q178863; PIDN:AA51768.1; PID:q178665  
R:Prelli, F.; Levy, E.; van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B.  
Biochem. Biophys. Res. Commun. 170, 301-307, 1990  
A:Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid of  
A:Reference number: A35486; MUID:90321244  
A:Accession: A35486  
A:Molecule type: DNA  
A:Residues: 672-710 <PREI>  
A:Note: 693-Gln was found in DNA isolated from HCMA-D patients  
R:Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.  
Gene 87, 257-263, 1990  
A:Title: Genomic organization of the human amyloid beta-protein precursor gene.  
A:Reference number: 139451; MUID:90236318  
A:Accession: 139451  
A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMF  
A:Molecule type: DNA  
A:Residues: 1-770 <YOSI>  
A:Cross-references: GB:M3112; NID:q178613; PIDN:AAB59502.1; PID:q178616  
A:Accession: 139451  
A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMF  
A:Molecule type: DNA  
A:Residues: 1-530, QWIMPYIPAPWEAKVGR <YOS2>  
A:Cross-references: GB:M34875; NID:q178608; PIDN:AAB59501.1; PID:q178615  
R:Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.  
Gene 102, 291-292, 1991  
A:Reference number: A59020; MUID:91340168  
A:Accession: A59020  
A:Status: annotation; erratum  
A:Note: revised physical map for reference 139451  
R:Levy, E.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van Duine  
Science 248, 1124-1126, 1990  
A:Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemorrh  
A:Reference number: 139453; MUID:90260663  
A:Accession: 139453  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 656-737 <LEV>  
A:Cross-references: GB:M37896; NID:q178618; PIDN:AA51727.1; PID:q178620  
R:Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.  
Science 254, 97-99, 1991  
A:Title: A mutation in the amyloid precursor protein associated with hereditary Alzheim  
A:Reference number: 159562; MUID:92022553  
A:Accession: 159562  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 689-716, 'F', 718-737 <MUR>  
A:Cross-references: GB:S57665; NID:q926720; PIDN:AAB19991.1; PID:q236721  
R:Kamilo, K.; Orr, H.T.; Payami, H.; Wijman, E.M.; Alonso, M.E.; Pulst, S.M.; Anderson,  
arakis, S.E.; Korenberg, J.R.; Sharma, V.; Kukull, W.; Larson, E.; Heston, L.L.; Martin,  
Am. J. Hum. Genet. 51, 998-1014, 1992  
A:Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for the  
A:Reference number: A44017; MUID:99035397  
A:Accession: A44017  
A:Molecule type: DNA  
A:Residues: 687-692, 'G', 694-718 <RAM1>  
A:Cross-references: GB:S45135; NID:q9257377; PIDN:AAB23645.1; PID:q257378  
A:Experimental source: familial Alzheimer disease family SB  
A:Note: sequence extracted from NCBI backbone (NCBIP:115376)  
R:Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.H.;  
Nature 325, 733-736, 1987  
A:Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surfac  
A:Reference number: A03134; MUID:87144572

A:Accession: A03134  
A:Molecule type: mRNA  
A:Residues: 1-288, 'V', 365-770 <KAN>  
A:Cross-references: GB:Y00264; NID:q28525; PIDN:CAA6374.1; PID:q28526  
A:Note: alternative splice form App(695)  
R:Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.  
Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987  
A:Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascula  
A:Reference number: A29030; MUID:87231971  
A:Accession: A29030  
A:Molecule type: mRNA  
A:Residues: 284-288, 'V', 365-646, 'E', 648-770 <ROB>  
A:Cross-references: GB:M6765; NID:q178539; PIDN:AA51722.1; PID:q178540  
A:Note: the authors translated the codon GAG for residue 647 as Asp  
R:Goldhaber, D.; Lerman, M.I.; McBride, O.W.; Saffioti, U.; Gajdusek, D.C.  
Science 235, 877-880, 1987  
A:Title: Characterization and chromosomal localization of a cDNA encoding brain amylo  
A:Reference number: A47584; MUID:87120328  
A:Accession: A47584  
A:Molecule type: mRNA  
A:Residues: 674-756, 'S', 758-770 <GOL>  
A:Cross-references: GB:M15533; NID:q178706; PIDN:AA35540.1; PID:q178707  
A:Experimental source: brain  
R:Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van  
Science 235, 680-684, 1987  
A:Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near  
A:Reference number: A47585; MUID:87120329  
A:Accession: A47585  
A:Molecule type: mRNA  
A:Residues: 674-703 <TAN1>  
A:Cross-references: GB:M15532; NID:q177957; PIDN:AA51564.1; PID:q177958  
R:Dyrks, T.; Weidemann, A.; Mulhapp, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Mue  
EMBO J. 7, 949-957, 1988  
A:Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 p  
A:Reference number: S02638; MUID:86296437  
A:Accession: S02638  
A:Molecule type: mRNA  
A:Residues: 672-678 <DYR>  
R:Tanzi, R.E.; McClatchey, A.I.; Lampert, E.D.; Villa-Komaroff, L.; Gusella, J.F.; N  
Nature 331, 528-530, 1988  
A:Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA assoc  
A:Reference number: S00707; MUID:8612640  
A:Accession: S00707  
A:Molecule type: mRNA  
A:Residues: 286-344, 'I', 365-366 <TAN2>  
A:Cross-references: EMBL:X06982; NID:q28817; PIDN:CAA30042.1; PID:q929612  
A:Experimental source: promyelocytic leukemia cell line HL60  
A:Note: alternative splice form App(751)  
R:Ponte, P.; Gonzalez-Pedro, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.;  
Nature 331, 525-527, 1988  
A:Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inh  
A:Reference number: S00925; MUID:8812639  
A:Accession: S00925  
A:Molecule type: mRNA  
A:Residues: 1-344, 'I', 365-770 <PO2>  
A:Cross-references: GB:X06989; EMBL:Y00297; NID:q28720; PIDN:CAA30050.1; PID:q28721  
R:Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.  
Nature 331, 530-532, 1988  
A:Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibi  
A:Reference number: A38949; MUID:8812641  
A:Accession: A38949  
A:Molecule type: mRNA  
A:Residues: 287-367 <KIT>  
A:Cross-references: GB:X06981; NID:q28816; PIDN:CAA30041.1; PID:q929611  
A:Experimental source: glioblastoma cell line  
A:Note: alternative splice form App(770)  
R:Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ash  
Brain Res. Mol. Brain Res. 4, 121-131, 1988  
A:Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of thre  
A:Reference number: A30320  
A:Accession: A30320  
A:Status: not compared with conceptual translation

A:Molecule type: mRNA  
 A:Residues: 284-288, 'V', 365-770 <VIT1>  
 A:Accession: B30320  
 A>Status: not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 122-288, 'V', 365-770 <VIT2>  
 A:Accession: C30320  
 A>Status: not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 606-770 <VIT3>  
 R:Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta, C.A.  
 Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988  
 A:Title: Molecular cloning of amyloid CDNA derived from mRNA of the Alzheimer disease  
 A:Reference number: A31087; MUID:88124954  
 A:Accession: A31087  
 A:Molecule type: mRNA  
 A:Residues: 507-770 <ZAI>  
 A:Cross-references: GB:M18734; NID:g178572; PIDN:AA51726.1; PID:g178573  
 A>Note: The authors translated the codon GAA for residue 599 as Gly, ACC for residue 603  
 8 as Val, GTC for residue 609 as Asn, AAT for residue 610 as Gly, and GGT for residue 65  
 A>Note: the cited Genbank accession number, J03594, is not in release 101.0  
 R:Masters, C.L.; Multhaup, G.; Simms, G.; Potgiesser, J.; Martins, R.N.; Beyreuther, K.

Query Match  
 Best Local Similarity 100.0%; Score 47; DB 1; Length 770;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EISEVKMAE 10  
 |||||||||

Db 665 EISEVKMAE 674

RESULT 6  
 JH0773 Alzheimer's disease amyloid beta protein precursor - African clawed frog  
 C:Species: Xenopus laevis (African clawed frog)  
 C>Date: 10-Jun-1993 #sequence\_revision 10-Jun-1993 #text\_change 13-Aug-1999  
 C:Accession: JH0773  
 R:Okado, H.; Okamoto, H.  
 Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992  
 A:Title: A Xenopus homologue of the human beta-amyloid precursor protein: developmental  
 A:Reference number: JH0773; MUID:93129227  
 A:Accession: JH0773  
 A:Molecule type: mRNA  
 A:Residues: 1-747 <OKA>  
 A:Cross-references: GB:S52417; NID:g263150; PIDN:AA824853.1; PID:g263151  
 A:Experimental source: larva  
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinase  
 C:Keywords: alternative splicing; amyloid  
 F:287-337/Domain: animal kunitz-type proteinase inhibitor homology <BPI>

Query Match  
 Best Local Similarity 93.6%; Score 44; DB 2; Length 747;  
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 EISEVKMAE 10  
 |||||||||

Db 642 EISEVKMAE 651

RESULT 7  
 S23094 beta-amyloid protein precursor - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 03-May-1996  
 C:Accession: S23094  
 R:Kojima, S.; Omori, M.  
 FEBS Lett. 304, 57-60, 1992  
 A:Title: Two-way cleavage of beta-amyloid protein precursor by multicatalytic proteinase  
 A:Reference number: S23094; MUID:92316198  
 A:Accession: S23094  
 A:Molecule type: protein  
 A:Residues: 1-33 <KOU>

C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinase  
 Query Match  
 Best Local Similarity 80.9%; Score 38; DB 2; Length 33;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 SEVKMDAE 10  
 |||||||

Db 1 SEVKMDAE 8

RESULT 8  
 E60045 Alzheimer's disease amyloid beta/A4 protein precursor - sheep (fragment)  
 C:Species: Ovis sp. (sheep)  
 C>Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 28-Jul-1995  
 C:Accession: E60045  
 R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
 Brain Res. Mol. Brain Res. 10, 299-305, 1991  
 A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d  
 A:Reference number: A60045; MUID:92017079  
 A:Accession: E60045  
 A:Molecule type: mRNA  
 A:Residues: 1-57 <JOH>  
 A:Cross-references: EMBL:X56130  
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinase  
 C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match  
 Best Local Similarity 100.0%; Score 38; DB 2; Length 57;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 SEVKMDAE 10  
 |||||||

Db 1 SEVKMDAE 8

RESULT 9  
 F60045 Alzheimer's disease amyloid beta/A4 protein precursor - pig (fragment)  
 C:Species: Sus scrofa domestica (domestic pig)  
 C>Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 13-Aug-1999  
 C:Accession: F60045  
 R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
 Brain Res. Mol. Brain Res. 10, 299-305, 1991  
 A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d  
 A:Reference number: A60045; MUID:92017079  
 A:Accession: F60045  
 A:Molecule type: mRNA  
 A:Residues: 1-57 <JOH>  
 A:Cross-references: EMBL:X56127; NID:g1895; PIDN:CAA39592.1; PID:g1896  
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinase  
 C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match  
 Best Local Similarity 80.9%; Score 38; DB 2; Length 57;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 SEVKMDAE 10  
 |||||||

Db 1 SEVKMDAE 8

RESULT 10  
 G60045 Alzheimer's disease amyloid beta/A4 protein precursor - guinea pig (fragment)  
 C:Species: Cavia porcellus (guinea pig)  
 C>Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 28-Jul-1995  
 C:Accession: G60045  
 R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
 Brain Res. Mol. Brain Res. 10, 299-305, 1991  
 A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d  
 A:Reference number: A60045; MUID:92017079

A:Accession: G60045  
A:Molecule type: mRNA  
A:Residues: 1-57 <JOH>  
A:Cross-references: EMBL:X56126  
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase  
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match  
Best Local Similarity 80.9%; Score 38; DB 2; Length 57;  
Matches 8; Conservativity 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SEVKMDAE 10  
|||||  
Db 1 SEVKMDAE 8

RESULT 11  
D60045  
Alzheimer's disease amyloid beta/A4 protein precursor - bovine (fragment)  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 28-Jul-1995  
C:Accession: D60045

R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
Brain Res. Mol. Brain Res. 10, 299-305, 1991  
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog  
A:Reference number: A60045; MUID:92017079  
A:Accession: D60045  
A:Molecule type: mRNA  
A:Residues: 1-57 <JOH>  
A:Cross-references: EMBL:X56124  
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase  
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match  
Best Local Similarity 80.9%; Score 38; DB 2; Length 57;  
Matches 8; Conservativity 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SEVKMDAE 10  
|||||  
Db 1 SEVKMDAE 8

RESULT 12  
A60045  
Alzheimer's disease amyloid beta/A4 protein precursor - dog (fragment)  
C:Species: Canis lupus familiaris (dog)  
C:Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 28-Jul-1995  
C:Accession: A60045  
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
Brain Res. Mol. Brain Res. 10, 299-305, 1991  
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog  
A:Reference number: A60045; MUID:92017079  
A:Accession: A60045  
A:Molecule type: mRNA  
A:Residues: 1-57 <JOH>  
A:Cross-references: EMBL:X56125  
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase  
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match  
Best Local Similarity 80.9%; Score 38; DB 2; Length 57;  
Matches 8; Conservativity 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SEVKMDAE 10  
|||||  
Db 1 SEVKMDAE 8

RESULT 13  
B60045  
Alzheimer's disease amyloid beta/A4 protein precursor - polar bear (fragment)  
C:Species: Ursus maritimus (polar bear)  
C:Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 13-Aug-1999

C:Accession: B60045  
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
Brain Res. Mol. Brain Res. 10, 299-305, 1991  
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d  
A:Reference number: A60045; MUID:92017079  
A:Accession: B60045  
A:Molecule type: mRNA  
A:Residues: 1-57 <JOH>  
A:Cross-references: EMBL:X56128; NID:92165; PIDN:CAA39593.1; PID:92166  
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase  
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match  
Best Local Similarity 80.9%; Score 38; DB 2; Length 57;  
Matches 8; Conservativity 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SEVKMDAE 10  
|||||  
Db 1 SEVKMDAE 8

RESULT 14  
G84245  
NADH dehydrogenase [imported] - Halobacterium sp. NRC-1  
C:Species: Halobacterium sp. NRC-1  
C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001  
C:Accession: G84245  
R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Bergquist, B.; Pan, M.; Shukla, H.D.; Lasky  
; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Ja  
Jung, K.H.; Alam, M.; Freltas, T.  
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000  
A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Edhardt, H.; Lowe, T.M.;  
A:Title: Genome sequence of Halobacterium species NRC-1.  
A:Reference number: A84160; MUID:20504483  
A:Accession: G84245  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-389 <STO>  
A:Cross-references: GB:AE004437; NID:q10580455; PIDN:AA619331.1; GSPDB:GN00138  
C:Genetics:  
A:Gene: yj1D

Query Match  
Best Local Similarity 80.9%; Score 38; DB 2; Length 389;  
Matches 7; Conservativity 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 EISEVKMDAE 10  
||:|||||  
Db 251 ELSDEVMDAE 260

RESULT 15  
C64572  
conserved hypothetical protein HP0419 - Helicobacter pylori (strain 26695)  
C:Species: Helicobacter pylori  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jun-2000  
C:Accession: C64572  
R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Sutton, R.A.; Sutton, G.G.; Fleischmann, R  
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKe  
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey,  
Nature 388, 539-547, 1997  
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser  
A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.  
A:Reference number: A64520; MUID:97394467  
A:Accession: C64572  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-261 <TOM>  
A:Cross-references: GB:AF000557; GB:AE000511; NID:92313514; PIDN:AA007484.1; PID:9231  
C:Superfamily: conserved hypothetical protein HP0419; bioC homology  
F:36-161/Domain: bioC homology <BIOC>

Query Match  
76.6%; Score 36; DB 1; Length 261;

Best Local Similarity 60.0%; Pred. No. 7.7;  
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 EISEVKMDAE 10  
|||::|::|  
Db 29 EISQIKIDSE 38

Search completed: October 29, 2002, 10:30:58  
Job time : 11.4286 secs



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OM protein - protein search, using sw model

Run on: October 29, 2002, 10:22:36 ; Search time 5 seconds  
(without alignments)  
77.439 Million cell updates/sec

Title: US-09-580-018-2  
Perfect score: 47  
Sequence: 1 EISEVKMDAE-10

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues  
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SWISSPROT-40\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	100.0	751	A4_SAISC	Q95241 saimiri sci
2	47	100.0	770	A4_HUMAN	P05067 homo sapien
3	47	100.0	770	A4_MOUSE	P12023 mus musculu
4	47	100.0	770	A4_RAT	P08592 rattus norv
5	42	89.4	58	A4_CANFA	Q28280 canis fami1
6	42	89.4	59	A4_BOVIN	Q28053 bos tauris
7	38	80.9	57	A4_PIG	Q29023 sus scrofa
8	38	80.9	57	A4_URSWA	Q29149 ursus marit
9	38	80.9	58	A4_RABIT	Q28748 oryctolagus
10	38	80.9	58	A4_SHEEP	Q28757 ovis aries
11	34	72.3	589	H1BN_XENLA	P06180 xenopus lae
12	33	70.2	419	A47K_PSECU	P31521 pseudomona
13	33	70.2	800	PARC_STRAU	P50073 staphylococ
14	32	68.1	705	YNP9_CAEEL	P34562 caenorhabdi
15	32	68.1	793	TL21_CHICK	Q9dd78 gallus gall
16	31	66.0	178	YJGA_HAEIN	P45076 haemophilus
17	31	66.0	183	YJGA_ECOLI	P26650 escherichia
18	31	66.0	214	SC14_SCHCO	P35795 schizophyll
19	31	66.0	227	C7B6_HUMAN	Q92520 homo sapien
20	31	66.0	249	YXEO_BKCSU	P54554 bacillus su
21	31	66.0	334	HBP2_HUMAN	O75031 homo sapien
22	31	66.0	343	SNXG_HUMAN	O51768 homo sapien
23	31	66.0	451	HENM_PARDE	P51676 paracoccus
24	31	66.0	993	RPN1_YEAST	P38764 saccharomyc
25	31	66.0	1012	CX05_HUMAN	O75665 homo sapien
26	31	66.0	1682	MSP1_PLAF3	P19598 plasmodium
27	30	63.8	80	EX7S_PSEAE	O9hwy5 pseudomona
28	30	63.8	127	ILBP_PIG	P10289 sus scrofa
29	30	63.8	296	H1S1_YARLI	O99145 yarrowia 11
30	30	63.8	304	PH85_KIULA	O92241 kluyveromyc
31	30	63.8	305	PH85_YEAST	P17157 saccharomyc
32	30	63.8	332	MDHC_BETVU	O9sm18 beta vulgar
33	30	63.8	464	SPN5_SCHPO	P48010 schizosacch

34	30	63.8	483	1	YC02_YEAST	P25632 saccharomyc
35	30	63.8	488	1	GAB4_CHICK	P24045 gallus gall
36	30	63.8	538	1	THSH_METTH	O26885 methanobact
37	30	63.8	554	1	NU5K_API11	P34855 apis mellif
38	30	63.8	656	1	V091_FOWPV	O72896 fowlpox vir
39	30	63.8	704	1	HSB5_TRYCR	P06660 trypanosoma
40	30	63.8	722	1	MESD_LEUME	Q10418 leucostoc
41	30	63.8	763	1	DPO3_SULSH	O05706 sulfolobus
42	30	63.8	789	1	V1B4_AGR79	P05353 agrobacteri
43	30	63.8	856	1	CLPB_HELPJ	O9zmh1 helicobacte
44	30	63.8	856	1	CLPB_HELPJ	P71404 helicobacte
45	30	63.8	1514	1	NX1A_RAT	O63372 rattus norv

## ALIGNMENTS

```

RESULT 1
A4_SAISC STANDARD; PRT; 751 AA.
ID A4_SAISC
AC Q95241:
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein precursor [Contains: Beta-
DE amyloid protein (Beta-Ap) (A-beta)].
GN App.
OS Saimiri sciureus (Common squirrel monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.
OX NCBI_Taxid=9521;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver, and Kidney;
RX MEDLINE=96108492; PubMed=8532114;
RA Levy E., Amorim A., Frangione B., Walker L.C.;
RT "Beta-amyloid precursor protein gene in squirrel monkeys with
RT cerebral amyloid angiopathy."
RL Neurobiol. Aging 16:805-808(1995).
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
CC WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
CC NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
CC PHOSPHORYLATION (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -!- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
DR EMBL: S81024; AAD14347.1; -.
DR HSSP: P05067; IAPP.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PRINTS: PR00759; BASICPASE.
DR SMART: SM00006; A4_EXTRA; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS00279; BPTI_KUNITZ_2; 1.

```

KW Glycoprotein; Amyloid; Neurope; Transmembrane; Alternative splicing;  
 KM Signal: Serine protease inhibitor.  
 FT CHAIN 1 17 A4 PROTEIN.  
 FT SIGNAL 18 751 BETA-AMYLOID PROTEIN (POTENTIAL).  
 FT CHAIN 653 695 EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 18 680 POTENTIAL.  
 FT TRASMEM 681 704 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 705 751 BPT/KUNITZ INHIBITOR.  
 FT SITE 287 345 CLATHRIN-BINDING (BY SIMILARITY).  
 FT SITE 740 743 REACTIVE BOND.  
 FT ACT-SITE 301 302 BY SIMILARITY.  
 FT DISULFID 291 341 BY SIMILARITY.  
 FT DISULFID 300 324 BY SIMILARITY.  
 FT DISULFID 316 337 BY SIMILARITY.  
 FT CARBOHYD 523 523 N-LINKED (GLCNAC. . .) (PROBABLE).  
 FT CARBOHYD 552 552 N-LINKED (GLCNAC. . .) (PROBABLE).  
 SO SEQUENCE 751 AA; 84893 MM; 6C3EA31089569049 CRC64;

Query Match 100.0%; Score 47; DB 1; Length 751;  
 Best Local Similarity 100.0%; Freq. No. 0.085;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EISEVXMDAE 10  
 |||||  
 DB 646 EISEVXMDAE 655

RESULT 2  
 A4\_HUMAN STANDARD; PRT; 770 AA.  
 ID A4\_HUMAN  
 AC P05067; P09000; Q16011;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 01-NOV-1991 (Rel. 20, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Alzheimer's disease amyloid A4 protein precursor (Protease nexin-II)  
 DE (PN-II) (APP) [contains: Beta-amyloid protein (beta-Ap4) (A-beta)].  
 GN APP OR A4 OR CVAP OR Aβ1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=871144572; PubMed=2881207;  
 RA Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L.,  
 RA Grzeschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.;  
 RT "The precursor of Alzheimer's disease amyloid A4 protein resembles a  
 RT cell-surface receptor".  
 RL Nature 325:733-736(1987).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=88122639; PubMed=2893289;  
 RA Ponte P., Gonzalez-Dewhitt P., Schilling J., Miller J., Hsu D.,  
 RA Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F.,  
 RA Cordell B.;  
 RT "A new A4 amyloid mRNA contains a domain homologous to serine  
 RT proteinase inhibitors".  
 RL Nature 331:525-527(1988).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=89128427; PubMed=2783775;  
 RA Lemaire H.-G., Salbaum J.M., Multhaup G., Kang J., Bayney R.M.,  
 RA Unterbeck A., Beyreuther K., Mueller-Hill B.,  
 RT "The Pream(695) precursor protein of Alzheimer's disease A4 amyloid  
 RT is encoded by 16 exons".  
 RL Nucleic Acids Res. 17:517-522(1989).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=97263807; PubMed=9108164;  
 RA Hattori M., Tsukahara F., Furuhara Y., Tanahashi H., Hirose M.,  
 RA Saio M., Tsukuni S., Sakaki Y.;  
 RT "A novel method for making nested deletions and its application for

RT sequencing of a 300 kb region of human APP locus.";  
 RL Nucleic Acids Res. 25:1802-1808(1997).  
 RN [5]  
 RP SEQUENCE OF 286-345 AND 365-366 FROM N.A.  
 RX MEDLINE=88122640; PubMed=2893290;  
 RA Tanzi R.E., McClatchey A.I., Lamperti E.D., Villa-Komaroff L.,  
 RA Gusella J.F., Neve R.L.;  
 RT "Protease inhibitor domain encoded by an amyloid protein precursor  
 RT mRNA associated with Alzheimer's disease".  
 RL Nature 331:528-530(1988).  
 RN [6]  
 RP SEQUENCE OF 287-367 FROM N.A.  
 RX MEDLINE=88122641; PubMed=2893291;  
 RA Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.;  
 RT "Novel precursor of Alzheimer's disease amyloid protein shows  
 RT protease inhibitory activity".  
 RL Nature 331:530-532(1988).  
 RN [7]  
 RP SEQUENCE OF 284-289 AND 365-770 FROM N.A.  
 RX MEDLINE=87231971; PubMed=3035574;  
 RA Robakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;  
 RT "Molecular cloning and characterization of a cDNA encoding the  
 RT cerebrovascular and the neuritic plaque amyloid peptides".  
 RL Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).  
 RN [8]  
 RP SEQUENCE OF 507-770 FROM N.A.  
 RX MEDLINE=88124954; PubMed=2893379;  
 RA Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,  
 RA Marotta C.A.;  
 RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer  
 RT disease brain: coding and noncoding regions of the fetal precursor  
 RT mRNA are expressed in the cortex".  
 RL Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).  
 RN [9]  
 RP SEQUENCE OF 672-681.  
 RX MEDLINE=88035004; PubMed=3312495;  
 RA Partridge W.M., Vinters H.V., Yang J., Eisenberg J., Choi T.B.,  
 RA Tountoulout W.W., Huebner V., Shively J.E.;  
 RT "Amyloid angiopathy of Alzheimer's disease: amino acid composition  
 RT and partial sequence of a 4,200-dalton peptide isolated from cortical  
 RT microvessels".  
 RL J. Neurochem. 49:1394-1401(1987).  
 RN [10]  
 RP SEQUENCE OF 739-770 FROM N.A.  
 RX MEDLINE=90236318; PubMed=2110105;  
 RA Yoshikawa S.-I., Sasaki H., Doh-Ura K., Furuya H., Sakaki Y.;  
 RT "Genomic organization of the human amyloid beta-protein precursor  
 RT gene".  
 RL Gene 87:257-263(1990).  
 RN [11]  
 RP SEQUENCE OF 1-10 FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=89016647; PubMed=3140222;  
 RA Schon E.A., Mita S., Sadlock J., Herbert J.;  
 RT "A cDNA specifying the human amyloid beta precursor protein (ABP)  
 RT encodes a 95-kDa polypeptide".  
 RL Nucleic Acids Res. 16:9351-9351(1988).  
 RN [12]  
 RP SEQUENCE OF 18-50.  
 RX MEDLINE=87250462; PubMed=3597385;  
 RA van Nostrand W.E., Cunningham D.D.;  
 RT "Purification of protease nexin II from human fibroblasts".  
 RL J. Biol. Chem. 262:8508-8514(1987).  
 RN [13]  
 RP IDENTITY OF APP WITH NEXIN-II.  
 RX MEDLINE=89384866; PubMed=2506449;  
 RA Oltersdorf T., Fritz L.C., Schenk D.B., Lieberburg I.,  
 RA Johnson-Wood K.L., Beattie E.C., Ward P.J., Blacher R.W., Dovey H.F.,  
 RA Sinha S.;  
 RT "The secreted form of the Alzheimer's amyloid precursor protein with  
 RT the Kunitz domain is protease nexin-II".  
 RL Nature 341:144-147(1989).  
 RN [14]

RP PROTEASE-SPECIFICITY OF INHIBITOR DOMAIN.  
 RX MEDLINE=90211252; PubMed=1969731; Kido H., Fukutomi A., Schilling J., Wang Y., Cordell B., Katunuma N.  
 RT "Protease-specificity of kunitz inhibitor domain of Alzheimer's disease amyloid protein precursor."  
 RL Biochem. Biophys. Res. Commun. 167:716-721(1990).  
 RN [15]  
 RP COMPLEX WITH G(O).  
 RX MEDLINE=93188965; PubMed=8446172; Nishimoto I., Okamoto T., Matsunura Y., Takahashi S., Okamoto T., Murayama Y., Ogata E.;  
 RA "Alzheimer amyloid protein precursor complexes with brain GTP-binding protein G(O)."  
 RL Nature 362:75-79(1993).  
 RN [16]  
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 28-133.  
 RX MEDLINE=92155582; PubMed=10201399; Rossgjohn J., Caprai R., Fell S.C., Henry A., McKinstiry M.J., Garlatis D., Hesse L., Multhaupt G., Beyreuther K., Masters C.L., Parker M.W.;  
 RA "Crystal structure of the N-terminal, growth factor-like domain of Alzheimer amyloid protein precursor protein."  
 RL Nat. Struct. Biol. 6:327-331(1999).  
 RN [17]  
 RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF 287-344.  
 RX MEDLINE=91104913; PubMed=2125487; Hydes T.R., Randal M., Kennedy L.A., Eigenbrodt G., Kosiakof A.A.;  
 RA "X-ray crystal structure of the protease inhibitor domain of Alzheimer's amyloid beta-protein precursor."  
 RL Biochemistry 29:10018-10022(1990).  
 RN [18]  
 RP STRUCTURE BY NMR OF 289-344.  
 RX MEDLINE=92031488; PubMed=1718421; Heald S.L., Tilton R.F. Jr., Hammond L.S., Lee A., Bayney R.M., Ramack M.E., Ramabhadran T.V., Dreyer R.N., Davis G., Unterbeck A., Tamburini P.P.;  
 RA "Sequential NMR resonance assignment and structure determination of the kunitz-type inhibitor domain of the Alzheimer's beta-amyloid precursor protein."  
 RL Biochemistry 30:10467-10478(1991).  
 RN [19]  
 RP STRUCTURE BY NMR OF 672-699.  
 RX MEDLINE=94281210; PubMed=7516706; Talafous J., Marchynski K.J., Klopman G., Zagorski M.G.;  
 RA "Solution structure of residues 1-28 of the amyloid beta-peptide."  
 RL Biochemistry 33:7788-7796(1994).  
 RN [20]  
 RP STRUCTURE BY NMR OF 696-706.  
 RX MEDLINE=97128622; PubMed=8973180; Kohno T., Kobayashi K., Maeda T., Sato K., Takashima A.;  
 RA "Three-dimensional structures of the amyloid beta peptide (25-35) in membrane-mimicking environment."  
 RL Biochemistry 35:16094-16104(1996).  
 RN [21]  
 RP STRUCTURE BY NMR OF 672-711.  
 RX MEDLINE=98359783; PubMed=9663002; Coles M., Bicknell W., Watson A.A., Fairlie D.P., Craik D.J.;  
 RA "Solution structure of amyloid beta-peptide(1-40) in a water-miscible environment. Is the membrane-spanning domain where we think it is?"  
 RL Biochemistry 37:11064-11077(1998).  
 RN [22]  
 RP STRUCTURE BY NMR OF 672-699.  
 RX MEDLINE=20400066; PubMed=10940222; Poulsen S., Watson A.A., Craik D.J.;  
 RA "Solution structures in aqueous SDS micelles of two amyloid beta peptides of Abeta(1-28) mutated at the alpha-secretase cleavage site."  
 RL J. Struct. Biol. 130:142-152(2000).  
 RN [23]  
 RP STRUCTURE BY NMR OF 681-706.  
 RX MEDLINE=20400065; PubMed=10940721; Zhang S., Iwata K., Tachemman M.J., Peng J.W., Li S., Stimson E.R., Lu Y., Felix A.M., Maggio J.E., Lee J.P.;

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RT "The Alzheimer's peptide a beta adopts a collapsed coil structure in
RL water.";
RL J. Struct. Biol. 130:130-141(2000).
RN [24]
RP STGNAL SEQUENCE CLEAVAGE SITE, AND TOPOLOGY.
RX MEDLINE=6826437; PubMed=2900137;
RA Dykx T., Weidmann A., Mulhaup G., Salbaum J.M., Lemaire H.-G.,
RA Kang J., Mueller-Hill B., Masters C.L., Beyreuther K.;
RT "Identification, transmembrane orientation and biogenesis of the
RT amyloid A4 precursor of Alzheimer's disease.";
OY 1 EISEVKMDAE 10
|||
Db 665 EISEVKMDAE 674

Query Match 100.0%; Score 47; DB 1; Length 770;
Best Local Similarity 100.0%; Pred. NO. 0.087;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0

RESULT 3
A4_MOUSE STANDARD: PRT; 770 AA.
ID A4_MOUSE
AC P12023;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog precursor
DE (Amyloidogenic glycoprotein) (AG).
GN APP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.
RC STRAIN-BALB/C; TISSUE=Brain;
RX MEDLINE=92096458; PubMed=1756177;
RA de Strooper B., van Duven F., van den Bergh H.;
RT "The amyloid beta protein precursor or proteolase nexin II from mouse
RL is closer related to its human homolog than previously reported.";
RL Biochim. Biophys. Acta 1129:141-143(1991).
RN [2]
RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=88106489; PubMed=3322280;
RA Yamada T., Sasaki H., Furuya H., Miyata T., Goto I., Sakaki Y.;
RT "Complementary DNA for the mouse homolog of the human amyloid beta
RL protein precursor.";
RL Biochem. Biophys. Res. Commun. 149:665-671(1987).
RN [3]
RP REVISIONS.
RA Yamada T.;
RL Submitted (MAR-1988) to the EMBL/Genbank/DBJ databases.
RN [4]
RP SEQUENCE OF 289-364 FROM N.A.
RC STRAIN=CD-1; TISSUE=Placenta;
RX MEDLINE=89345111; PubMed=2569710;
RA Fukuchi K., Martin G.M., Deeb S.S.;
RT "Sequence of the protease inhibitor domain of the A4 amyloid protein
RL precursor of Mus domestica.";
RL Nucleic Acids Res. 17:5396-5396(1989).
RN [5]
RP SEQUENCE OF 1-19 FROM N.A.
RX MEDLINE=92209998; PubMed=1555768;
RA Izumi R., Yamada T., Yoshikata S.I., Sasaki H., Hattori M.,
RA Sakai Y.;
RT "Positive and negative regulatory elements for the expression of the
RL Alzheimer's disease amyloid precursor-encoding gene in mouse.";
RL Gene 112:189-195(1992).
RN [6]
RP SEQUENCE OF 281-380 FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE=Brain, and Kidney;

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RX MEDLINE=89149813; PubMed=2493250;
RA Yamada T., Sasaki H., Dohura K., Goto I., Sakaki Y.;
RT "Structure and expression of the alternatively-spliced forms of mRNA
RT for the mouse homolog of Alzheimer's disease amyloid beta protein
RT precursor."
RL Biochem. Biophys. Res. Commun. 158:906-912(1989).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS; APP(395), APP(695),
CC APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE
CC SPLICING.
CC -1- TISSUE SPECIFICITY: AAA(770) IS EXPRESSED IN KIDNEY, AAA(751) IS
CC WIDELY EXPRESSED. AAA(695) IS EXPRESSED IN BRAIN, KIDNEY AND
CC LIVER.
CC -1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
CC WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
CC NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
CC PHOSPHORYLATION (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
CC -----
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CC -----
DR EMBL: X59379; -; NOT_ANNOTATED_CDS.
DR EMBL: M18373; AAA37139.1; -.
DR EMBL: X15210; CAA33280.1; -.
DR EMBL: D10603; BAA01456.1; -.
DR EMBL: M24397; AAA39929.1; -.
DR PIR: A27485; A27485.
DR PIR: S04855; S04855.
DR PIR: S19727; S19727.
DR HSSP: P05067; IQCM.
DR MGD: MGI:88059; APP.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam: PF00014; Kunitz_BPTI.
DR PRINTS: PR00203; AMYLOIDA4.
DR PRINTS: PR00739; BASICPTASE.
DR SMART: SM00006; A4_EXTRA; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS0279; BPTI_KUNITZ_2; 1.
DR GlycoProfile: Amyloid; Neurone; Transmembrane; Signal;
KW Alternative splicing; Serine protease inhibitor.
FT SIGNAL 1 17
FT CHAIN 18 770
FT FT ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN
FT FT EXTRACELLULAR (POTENTIAL).
FT FT POTENTIAL.
FT FT CYTOPLASMIC (POTENTIAL).
FT FT EQUIVALENT OF BETA-AMYLOID PROTEIN.
FT FT BPTI/KUNITZ INHIBITOR.
FT FT CLATHRIN-BINDING (BY SIMILARITY).
FT FT SITE 759 762
FT FT DISULFID 291 341
FT FT DISULFID 300 324
FT FT DISULFID 316 337
FT FT CARBOHYD 542 542
FT FT CARBOHYD 571 571
FT FT VARSPLIC 289 289
FT FT VARSPLIC 290 364
FT FT VARSPLIC 346 380
FT SEQUENCE 770 AA; 86752 MW; 2650DE0890CAFA7A CRC64;
Query Match 100.0%; Score 47; DB 1; Length 770;

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Best Local Similarity 100.0%; Pred. No. 0.087;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EISEVKMDAE 10
DB 665 EISEVKMDAE 674
RESULT 4
ID A4_RAT STANDARD: PRT; 770 AA.
AC P08592;
DT 01-DEC-1988 (rel. 08, Created)
DT 16-OCT-1992 (rel. 24, Last sequence update)
DE Alzheimer's disease amyloid A4 protein homolog precursor
DE (Amyloidogenic glycoprotein) (AG).
GN APP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=88312583; PubMed=2900758;
RA Shivers B.D., Hilbich C., Multhaup G., Salbaum J.M., Beyreuther K.,
RA Seeburg P.H.;
RT "Alzheimer's disease amyloidogenic glycoprotein: expression pattern
RT in rat brain suggests a role in cell contact."
RN EMBL J. 7:1365-1370(1988).
RP SEQUENCE OF 289-364 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=89183625; PubMed=2648331;
RA Kang J., Mueller-Hill B.;
RT "The sequence of the two extra exons in rat preA4."
RL Nucleic Acids Res. 17:2130-2130(1989).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS; APP(395), APP(563), APP(695),
CC APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE
CC SPLICING.
CC -1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
CC WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
CC NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
CC PHOSPHORYLATION (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
CC -----
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CC -----
DR EMBL: X07648; CAA30488.1; -.
DR EMBL: X14066; CAA32229.1; -.
DR PIR: S00550; S00550.
DR PIR: S03607; S03607.
DR HSSP: P05067; IAAP.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam: PF00014; Kunitz_BPTI.
DR Pfam: PF00014; Kunitz_BPTI.
DR PRINTS: PR00203; AMYLOIDA4.
DR PRINTS: PR00739; BASICPTASE.
DR SMART: SM00006; A4_EXTRA; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00320; A4_INTRA; 1.

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QY      2 ISEVKMDAE 10
      1 ISEVKMDAE 9

RESULT 7
AA_PIG
ID      AA_PIG          STANDARD:      PRT:      57 AA.
AC      Q29023;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE      protein (Beta-Ap4) (A-beta)] (Fragment).
GN      APP.
OS      Sus scrofa (Pig).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX      NCBI_TaxID=9823;

RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Brain;
RX      MEDLINE=92017079; PubMed=1656157;
RA      Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT      "Conservation of the sequence of the Alzheimer's disease amyloid
RT      peptide in dog, polar bear and five other mammals by cross-species
RT      polymerase chain reaction analysis.";
RL      Brain Res. Mol. Brain Res. 10:299-305(1991).
CC      -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC      INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC      G(O) (BY SIMILARITY).
CC      -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC      -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL: X56127; CAA39592.1; -
DR      HSSP: P05067; 1BA4.
DR      InterPro: IPR001868; A4_APP.
DR      PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR      PROSITE: PS00320; A4_INTRA; PARTIAL.
KW      Glycoprotein; Amyloid; Neurone; Transmembrane.
FT      NON_TER      1
FT      CHAIN      6 48
FT      DOMAIN      <1 33
FT      TRANSMEM      34 57
FT      NON_TER      57 57
FT      POTENTIAL.
SQ      SEQUENCE      57 AA; 6172 MW; 84209D88BEA82DFA CRC64;

Query Match      80.9%; Score 38; DB 1; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      3 SEVKMDAE 10
      1 SEVKMDAE 8

RESULT 8
AA_URSMA
ID      AA_URSMA          STANDARD:      PRT:      57 AA.
AC      Q29149;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      30-MAY-2000 (Rel. 39, Last annotation update)
DE      Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid

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DE      protein (Beta-Ap4) (A-beta)] (Fragment).
GN      APP.
OS      Ursus maritimus (Polar bear) (Thalartos maritimus).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.
OX      NCBI_TaxID=29073;

RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Brain;
RX      MEDLINE=92017079; PubMed=1656157;
RA      Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT      "Conservation of the sequence of the Alzheimer's disease amyloid
RT      peptide in dog, polar bear and five other mammals by cross-species
RT      polymerase chain reaction analysis.";
RL      Brain Res. Mol. Brain Res. 10:299-305(1991).
CC      -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC      INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC      G(O) (BY SIMILARITY).
CC      -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC      -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL: X56128; CAA39593.1; -
DR      HSSP: P05067; 1A4L.
DR      InterPro: IPR001868; A4_APP.
DR      PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR      PROSITE: PS00320; A4_INTRA; PARTIAL.
KW      Glycoprotein; Amyloid; Neurone; Transmembrane.
FT      NON_TER      1
FT      CHAIN      6 48
FT      DOMAIN      <1 33
FT      TRANSMEM      34 57
FT      NON_TER      57 57
FT      POTENTIAL.
SQ      SEQUENCE      57 AA; 6172 MW; 84209D88BEA82DFA CRC64;

Query Match      80.9%; Score 38; DB 1; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      3 SEVKMDAE 10
      1 SEVKMDAE 8

RESULT 9
AA_RABIT
ID      AA_RABIT          STANDARD:      PRT:      58 AA.
AC      Q28748;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE      protein (Beta-Ap4) (A-beta)] (Fragment).
GN      APP.
OS      Oryctolagus cuniculus (Rabbit).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX      NCBI_TaxID=9986;

RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Brain;
RX      MEDLINE=92017079; PubMed=1656157;
RA      Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT      "Conservation of the sequence of the Alzheimer's disease amyloid
RT      peptide in dog, polar bear and five other mammals by cross-species
RT      polymerase chain reaction analysis.";

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RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -i- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -----
CC -i- SUBCELLULAR LOCATION: Type I membrane protein.
CC -----
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CC -----
DR EMBL: X56129; CAA39594.1; -.
DR HSSP: P05067; IBA4.
DR InterPro: IPR001868; A4_APP.
DR PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR PROSITE: PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.
FT CHAIN 1 48 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 34 57 POTENTIAL.
FT DOMAIN 58 >58 CYTOPLASMIC (POTENTIAL).
FT NON_TER 58 58
SQ SEQUENCE 58 AA; 6300 MW; F434209D8EBA82D CRC64;

Query Match
Best Local Similarity 80.9%; Score 38; DB 1; Length 58;
Matches 8; Conservative 0; Pred. No. 0.38; Mismatches 0; Indels 0; Gaps 0;

OY 3 SEVKMDAE 10
Db 1 SEVKMDAE 8

RESULT 10
A4_SHEEP
ID A4_SHEEP STANDARD; PRT; 58 AA.
AC Q28757;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-Ap) (A-beta)] (Fragment).
GN A4p.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=92017079; PubMed=1656157;
RA "Johnstone E.M., Chaney M.O., Morris F.H., Pascual R., Little S.P.;
RA "Conservation of the sequence of the Alzheimer's disease amyloid
RA peptide in dog, polar bear and five other mammals by cross-species
RA polymerase chain reaction analysis."
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -i- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -----
CC -i- SUBCELLULAR LOCATION: Type I membrane protein.
CC -----
CC -i- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
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CC -----
DR EMBL: X56130; CAA39595.1; -.
DR HSSP: P05067; IAML.
DR InterPro: IPR001868; A4_APP.
DR PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR PROSITE: PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.
FT CHAIN 1 48 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 34 57 POTENTIAL.
FT DOMAIN 58 >58 CYTOPLASMIC (POTENTIAL).
FT NON_TER 58 58
SQ SEQUENCE 58 AA; 6300 MW; F434209D8EBA82D CRC64;

Query Match
Best Local Similarity 80.9%; Score 38; DB 1; Length 58;
Matches 8; Conservative 0; Pred. No. 0.38; Mismatches 0; Indels 0; Gaps 0;

OY 3 SEVKMDAE 10
Db 1 SEVKMDAE 8

RESULT 11
H1BN_XENLA
ID H1BN_XENLA STANDARD; PRT; 589 AA.
AC P06180;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE Histone-binding protein NI/NZ.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
RC TISSUE=Oocyte;
RX MEDLINE=87161764; PubMed=3549279;
RA Kleinschmidt J.A., Dingwall C., Maier G., Franke W.W.;
RA "Molecular characterization of a karyophilic, histone-binding
RA protein: cDNA cloning, amino acid sequence and expression of nuclear
RA protein NI/NZ of Xenopus laevis."
RL EMO J. 5:3547-3552(1986).
CC -i- FUNCTION: THIS PROTEIN IS INVOLVED IN NUCLEOSOME ASSEMBLY. IT
CC IS BOUND TO H3 AND H4 IN THE ABSENCE OF DNA, BUT RELEASED FROM
CC H3 AND H4 IN THE PRESENCE OF DNA.
CC -----
CC -i- SUBCELLULAR LOCATION: Nuclear.
CC -----
CC -i- SIMILARITY: WITH RABBIT NUCLEAR AUTOANTIGENIC SPERM PROTEIN.
CC -----
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CC -----
DR EMBL: X04712; CAA28419.1; -.
DR PIR: A25680; A25680.
DR InterPro: IPR001440; TPR.
DR Pfam: PF00515; TPR; 3.
KW Nuclear protein; Chromosomal protein.
FT INT_MET 0
FT DOMAIN 107 118 ASP/GLU-RICH (ACIDIC).
FT DOMAIN 289 325 ASP/GLU-RICH (ACIDIC).
FT DOMAIN 530 536 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
SQ SEQUENCE 589 AA; 64897 MW; AC28927B4D4E245B CRC64;

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Query Match          72.3%; Score 34; DB 1; Length 589;
Best Local Similarity 60.0%; Pred. No. 27;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EISEVKMDAE 10
   1111111111
Db 259 EVAEEKMDSE 268

RESULT 12
P47K.PSECL          STANDARD:      PRT: 419 AA.
ID P47K.PSECL
AC P31521;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 47 kDa protein (P47K).
OS Pseudomonas chlororaphis (Pseudomonas aureofaciens).
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=333;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-B23;
RC MEDLINE-91193202; PubMed-2013568;
RA Nishiyama M., Horinouchi S., Kobayashi M., Nagasawa T., Yamada H.,
RA Bepu T.;
RT "Cloning and characterization of genes responsible for metabolism of
RT nitrile compounds from Pseudomonas chlororaphis B23."
RL J. Bacteriol. 173:2465-2472(1991).
CC -I- FUNCTION: THE PRESENCE OF P47K IS CRITICAL FOR THE EXPRESSION
CC OF THE NITRILE HYDRATASE GENES. MAY STABILIZE OR ACTIVATE THE
CC NITRILE HYDRATASE PROTEINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D90216; BAA14247.1; -.
DR PIR: D42725; D42725.
DR InterPro: IPR003495; COBW.
DR Pfam: PF02492; COBW; 1.
SQ SEQUENCE 419 AA; 46666 MW; PF5113800E27FF0C CRC64;

Query Match          70.2%; Score 33; DB 1; Length 419;
Best Local Similarity 60.0%; Pred. No. 30;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EISEVKMDAE 10
   1111111111
Db 45 DMSVNDLDAE 54

RESULT 13
PARC.STAU          STANDARD:      PRT: 800 AA.
ID PARC.STAU
AC P50073; P95682; P95683;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Topoisomerase IV subunit A (EC 5.99.1.-).
GN PARC OR GRLA.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-FDA 574;

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RX MEDLINE=95089700; PubMed=79971176;
RA Ferrero L., Cameron B., Manse B., Lagneaux D., Crouzet J.,
RA Femechon A., Blanche F.;
RT "Cloning and primary structure of Staphylococcus aureus DNA
RT topoisomerase IV: a primary target of fluoroquinolones."
RL Mol. Microbiol. 13:641-653(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-KMP9, AND RM4220;
RC MEDLINE=96300529; PubMed=8723458;
RA Yamagishi J., Kojima T., Oyama Y., Fujimoto K., Hattori H.,
RA Nakamura S., Inoue M.;
RT "Alterations in the DNA topoisomerase IV grlA gene responsible for
RT quinolone resistance in Staphylococcus aureus."
RL Antimicrob. Agents Chemother. 40:1157-1163(1996).
RN [3]
RP NOTAGENESIS.
RC STRAIN-RM4220;
RC MEDLINE=96104899; PubMed=7492103;
RA Ferrero L., Cameron B., Crouzet J.;
RT "Analysis of gyrA and grlA mutations in stepwise-selected
RT ciprofloxacin-resistant mutants of Staphylococcus aureus."
RL Antimicrob. Agents Chemother. 39:1554-1558(1995).
CC -I- FUNCTION: TOPOISOMERASE IV IS ESSENTIAL FOR CHROMOSOME
CC SEGREGATION. IT HAS RELAXATION OF SUPERCOILED DNA ACTIVITY.
CC PERFORMS THE DECATENATION EVENTS REQUIRED DURING THE REPLICATION
CC OF A CIRCULAR DNA MOLECULE (BY SIMILARITY).
CC -I- SUBUNIT: COMPOSED OF TWO SUBUNITS: GRLA AND GRLB.
CC -I- SIMILARITY: STRONG, WITH THE A SUBUNIT OF GRLAS.
CC -----
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CC -----
DR EMBL: L25288; AAA53116.1; -.
DR EMBL: D67074; BAA11085.1; -.
DR EMBL: D67075; BAA11087.1; -.
DR HSSP: P09097; 1AB4.
DR InterPro: IPR002205; DNA_topoisoIV.
DR Pfam: PF00521; DNA_topoisoIV; 1.
DR SMART: SM00434; TOP4c; 1.
KW Topoisomerase; Isomerase; DNA-binding; Antibiotic resistance.
FT ACT_SITE 119 119
FT VARIANT 410 410
FT MOTAGEN 80 80
FT MOTAGEN 84 80
FT MOTAGEN 84 84
FT CONFLICT 267 267
FT CONFLICT 567 567
FT CONFLICT 594 594
FT CONFLICT 594 594
FT CONFLICT 688 688
SQ SEQUENCE 800 AA; 90997 MW; ABE9273684755D87 CRC64;

Query Match          70.2%; Score 33; DB 1; Length 800;
Best Local Similarity 60.0%; Pred. No. 58;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 EISEVKMDAE 10
   1111111111
Db 486 EIEIKIKDKE 495

RESULT 14
YNP9.CAEEL          STANDARD:      PRT: 705 AA.
ID YNP9.CAEEL
AC P34562;
DT 01-FEB-1994 (Rel. 28, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Hypothetical 80.6 kDa protein T0565.9 in chromosome III.

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GN T05G5.9.
OC Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloterinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=BRISTOL N2;
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Pavello A., Fraser A.,
RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
RA Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,
RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showkeen R.,
RA Sims M., Smalton N., Smith A., Smith M., Sonhammer E., Staden R.,
RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
RA Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
RA Woldman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL Nature 368:32-38(1994).
RN [2]
RP REVISIONS.
RA Durbin R.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -----
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CC -----
CC EMBL: Z27079; CAAB1596.1; -
DR PTR: S41009; S41009
DR Wormpep: T05G5.9; CE21153.
DR InterPro: IPR000237; GRIP.
DR Pfam: PF01465; GRIP.
DR KW Hypothetical protein; Coiled coil.
FT DOMAIN 75 137 COILED COIL (POTENTIAL).
FT DOMAIN 160 509 COILED COIL (POTENTIAL).
FT DOMAIN 562 641 COILED COIL (POTENTIAL).
SO SEQUENCE 705 AA; 80637 MW; 9EB9873F5FC04966 CRC64;

Query Match 68.1%; Score 32; DB 1; Length 705;
Best Local Similarity 60.0%; Pred. No. 81;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 EISHYKMDAE 10
Db 108 ELEQVKMDAE 117

RESULT 15
ID TL21-CHICK STANDARD; PRT; 793 AA.
AC O9DD78;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Toll-like receptor 2 type 1 precursor.
GN TL2-1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;

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RX PubMed=11590137;
RA Fukui A., Inoue N., Matsumoto M., Nomura M., Yamada K., Matsuda Y.,
RA Toyoshima K., Seya T.;
RT "Molecular cloning and functional characterization of chicken
RT Toll-like receptors. A single chicken Toll covers multiple molecular
RT patterns.";
RL J. Biol. Chem. 276:47143-47149(2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Takahashi T.;
RT "Molecular cloning and expression analysis of the chick Toll-like
RT receptor 2 in embryonic ventricular myocytes.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC - FUNCTION: Participates in the innate immune response to microbial
CC agents. Acts via MyD88 and TRAF6, leading to NF-kappa-B
CC activation, cytokine secretion and the inflammatory response (By
CC similarity). Does not respond to LPS and responds with less
CC ability than TL2-2 to mycoplasma macrophage-activating
CC lipopeptide-2MD (MALP-2).
CC - SUBUNIT: Binds MyD88 via their respective TIR domains. Binds TL2-
CC via their respective extracellular domains (By similarity).
CC - SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC - TISSUE SPECIFICITY: Highly expressed in ovary. Detected at lower
CC levels in heart, lung, gizzard and testis.
CC - PTM: N-glycosylated. TL2-1 is more heavily glycosylated than
CC TL2-2.
CC - SIMILARITY: BELONGS TO THE TOLL-LIKE RECEPTOR FAMILY.
CC - SIMILARITY: CONTAINS 1 TIR DOMAIN
CC - SIMILARITY: CONTAINS 13 LEUCINE-RICH REPEATS (LRR).
CC -----
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CC -----
CC EMBL: AB050005; BAB16843.1; -
DR EMBL: AB046119; BAB16113.2; -
DR InterPro: IPR001611; LRR.
DR InterPro: IPR000483; LRR_Cterm.
DR InterPro: IPR003592; LRR_out.
DR InterPro: IPR003591; LRR_typ.
DR InterPro: IPR000157; TIR.
DR Pfam: PF00360; LRR; 4.
DR Pfam: PF01463; LRRCT; 1.
DR Pfam: PF01582; TIR; 1.
DR PRINTS: PR00019; LEURICRPT.
DR SMART: SM00370; LRR; 4.
DR SMART: SM00082; LRRCT; 1.
DR SMART: SM00369; LRR_TYP; 6.
DR SMART: SM00255; TIR; 1.
DR PROSITE: PS50104; TIR; 1.
KW Receptor; Immune response; Inflammatory response; Signal;
KW Transmembrane; Repeat; Leucine-rich repeat; Glycoprotein.
FT SIGNAL 1 25
FT CHAIN 26 793
FT DOMAIN 26 597
FT TRANSMEM 598 618
FT DOMAIN 619 793
FT REPEAT 62 85
FT REPEAT 86 109
FT REPEAT 111 133
FT REPEAT 135 158
FT REPEAT 159 182
FT REPEAT 184 206
FT REPEAT 206 370
FT REPEAT 344 370
FT REPEAT 395 419
FT REPEAT 421 445
FT REPEAT 447 465
FT REPEAT 465 485
FT REPEAT 486 509

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FT REPEAT 511 530 LRR 13.  
FT DOMAIN 648 793 TIR.  
FT CARBOHYD 48 48 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 120 120 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 161 161 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 254 254 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 325 325 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 402 402 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 451 451 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 793 AA: 90766 MM: 2BF659D9305D4562 CRC64:

Query Match 58.1% Score 32; DB 1; Length 793;  
Best Local Similarity 50.0%; Pred. No. 91;  
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 EISEVKMDAE 10  
I:|:|:|  
DB 238 EVREIKLDIE 247

Search completed: October 29, 2002, 10:27:26  
Job time : 7 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 29, 2002, 10:23:11 ; Search time 18 Seconds

(without alignments)  
96.108 Million cell updates/sec

Title: us-09-580-018-2  
Perfect score: 47  
Sequence: 1 EISEVKMDAE 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTRMBL\_19:  
1: sp\_archaea:  
2: sp\_bacteria:  
3: sp\_fungi:  
4: sp\_human:  
5: sp\_invertebrate:  
6: sp\_mammal:  
7: sp\_mhc:  
8: sp\_organelle:  
9: sp\_phage:  
10: sp\_plant:  
11: sp\_protent:  
12: sp\_virus:  
13: sp\_vertebrate:  
14: sp\_unclassified:  
15: sp\_virus:  
16: sp\_bacteriaph:  
17: sp\_archaeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	100.0	79	11	035463
2	47	100.0	82	4	P78438
3	47	100.0	82	4	016014
4	47	100.0	82	4	016019
5	47	100.0	82	4	016020
6	47	100.0	607	11	099K32
7	47	100.0	695	6	095K37
8	47	100.0	695	11	P97487
9	47	100.0	695	11	060496
10	47	100.0	770	6	09TU10
11	46	97.9	534	13	093296
12	46	97.9	569	13	09PVL1
13	46	97.9	695	13	09DCJ8
14	46	97.9	751	13	09DCJ7
15	44	93.6	693	13	098SG0
16	44	93.6	695	13	098SF9

17	44	93.6	747	13	091963	Q91963 xenopus. ap
18	38	80.9	389	17	09HR27	Q9hr27 halobacteri
19	36	76.6	261	16	025173	Q25173 helicobacte
20	36	76.6	261	16	092KH1	Q92kh1 helicobacte
21	35	74.5	818	16	092C65	Q92c65 listeria in
22	34	72.3	141	2	044749	Q44749 borrelia bu
23	34	72.3	141	2	044784	Q44784 borrelia bu
24	34	72.3	141	2	09R3H3	Q9r3h3 borrelia bu
25	34	72.3	141	2	09R9H8	Q9r9h8 borrelia bu
26	34	72.3	141	2	09S0J3	Q9s0j3 borrelia bu
27	34	72.3	141	2	09S0A9	Q9s0a9 borrelia bu
28	34	72.3	141	2	09S037	Q9s037 borrelia bu
29	34	72.3	141	2	09R2Y5	Q9r2y5 borrelia bu
30	34	72.3	141	2	086117	Q86117 borrelia bu
31	34	72.3	141	2	007496	Q07496 borrelia bu
32	34	72.3	141	2	044779	Q44779 borrelia bu
33	34	72.3	141	2	044788	Q44788 borrelia bu
34	34	72.3	321	3	001213	Q01213 mucor muced
35	34	72.3	869	5	09V610	Q9v610 drosophila
36	34	72.3	1378	5	045075	Q45075 caenorhabdi
37	33	70.2	63	16	09A063	Q9a063 streptococc
38	33	70.2	289	5	019813	Q19813 caenorhabdi
39	33	70.2	324	12	09Q8M9	Q9q8m9 myxoma viru
40	33	70.2	370	10	09LYK0	Q9lyk0 arabidopsis
41	33	70.2	626	2	056633	Q56633 vibrio chol
42	33	70.2	626	2	09ACW8	Q9acw8 vibrio chol
43	33	70.2	626	16	09KT07	Q9kt07 vibrio chol
44	33	70.2	699	13	057394	Q57394 narke japon
45	33	70.2	743	10	09SLB2	Q9slb2 arabidopsis

## ALIGNMENTS

RESULT 1  
035463  
AC 035463;  
DT 01-JAN-1998 (TREMBLrel. 05, created)  
DT 01-JAN-1998 (TREMBLrel. 05, last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)  
DE ALZHEIMER'S AMYLOID BETA PROTEIN (FRAGMENT).  
GN BETA APP.  
OS Cricetus griseus (Chinese hamster).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Cricetinae;  
OC Cricetulus.  
OX NCBI\_TaxID=10029;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Sambamurti K., Plinix I., Gandhi S.;  
RL Submitted (Oct-1997) to the EMBL/Genbank/DBJ databases.  
DR EMBL: AF030413; AAB86608.1; -  
DR HSSP: P05067; 1BA4.  
FT NON\_TER 1  
FT NON\_TER 79  
SQ SEQUENCE 79 AA; 8538 MW; 37F2C6C3BFF3F597 CRC64;

Query Match 100.0%; Score 47; DB 11; Length 79;  
Best Local Similarity 100.0%; Pred. No. 0.053;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 1 EISEVKMDAE 10  
Db 14 EISEVKMDAE 23  
RESULT 2  
P78438 PRELIMINARY: PRT; 82 AA.  
AC P78438;  
DT 01-MAY-1997 (TREMBLrel. 03, created)  
DT 01-MAY-1997 (TREMBLrel. 03, last sequence update)

01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
DE AMYLOID PROTEIN (BETA-AMYLOID PROTEIN) (FRAGMENT).  
GN APP.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89392030; PubMed=2675837;  
RA Johnstone E.M., Chaney M.O., Moore R.E., Ward K.E., Norris F.H.,  
RA Little S.P.;  
RT "Alzheimer's disease amyloid peptide is encoded by two exons and shows  
RT similarity to soybean trypsin inhibitor.";  
RL Biochem. Biophys. Res. Commun. 163:1248-1255(1989).  
RN [2]  
RP SEQUENCE OF 19-48 FROM N.A.  
RX MEDLINE=87120329; PubMed=2949367;  
RA Tanzi R.E., Gusella J.F., Watkins P.C., Bruns G.A., George-Hyslop P.,  
RA Van Keuren M.L., Patterson D., Pagan S., Kurlit D.M., Nave R.L.;  
RT "Amyloid beta protein gene: cDNA, mRNA distribution, and genetic  
RT linkage near the Alzheimer locus.";  
RL Science 235:880-884(1987).  
RN [3]  
RP SEQUENCE OF 32-63 FROM N.A.  
RX MEDLINE=93035397; PubMed=1415269;  
RA Kamino K., Orr H.T., Payami H., Wajsbom E.M., Alonso M.E., Pulst S.M.,  
RA Anderson L., O'dahl S., Nemens E., White J.A.;  
RT "Linkage and mutational analysis of familial Alzheimer disease  
RT kindreds for the APP gene region.";  
RL Am. J. Hum. Genet. 51:998-1014(1992).  
DR EMBL: M29270; AAAS1768.1; -;  
DR EMBL: M29269; AAAS1768.1; JOINED.  
DR EMBL: M15532; AAAS1564.1; -;  
DR EMBL: S45136; AAB23646.1; -;  
DR HSSP: P05067; 1BA4. 1  
FT NON\_TER 1  
SQ SEQUENCE 82 AA; 8994 MW; 8DA9E42B813A070E CRC64;

Query Match 100.0%; Score 47; DB 4; Length 82;  
Best Local Similarity 100.0%; Pred. No. 0.055;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EISEVKMDAE 10  
Db 10 EISEVKMDAE 19

RESULT 3  
Q16014 PRELIMINARY; PRT; 82 AA.  
AC Q16014;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE BETA-AMYLOID PEPTIDE (FRAGMENT).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93236601; PubMed=8476439;  
RA Denman R.B., Rosenzweig R., Miller D.L.;  
RT "A system for studying the effect(s) of familial Alzheimer disease  
RT mutations on the processing of the beta-amyloid peptide precursor.";  
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).  
DR EMBL: S60721; AAB26263.2; -;  
DR HSSP: P05067; 1BA4. 1  
FT NON\_TER 1  
SQ SEQUENCE 82 AA; 8972 MW; F534AA5B3EA9230A CRC64;

Query Match 100.0%; Score 47; DB 4; Length 82;  
Best Local Similarity 100.0%; Pred. No. 0.055;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EISEVKMDAE 10  
Db 11 EISEVKMDAE 20

RESULT 4  
Q16019 PRELIMINARY; PRT; 82 AA.  
AC Q16019;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE BETA-AMYLOID PEPTIDE (FRAGMENT).  
GN BETA APP.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93236601; PubMed=8476439;  
RA Denman R.B., Rosenzweig R., Miller D.L.;  
RT "A system for studying the effect(s) of familial Alzheimer disease  
RT mutations on the processing of the beta-amyloid peptide precursor.";  
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).  
DR EMBL: S61380; AAB26264.2; -;  
DR HSSP: P05067; 1BA4. 1  
FT NON\_TER 1  
SQ SEQUENCE 82 AA; 8938 MW; F534AA5DE579230A CRC64;

Query Match 100.0%; Score 47; DB 4; Length 82;  
Best Local Similarity 100.0%; Pred. No. 0.055;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EISEVKMDAE 10  
Db 11 EISEVKMDAE 20

RESULT 5  
Q16020 PRELIMINARY; PRT; 82 AA.  
AC Q16020;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE BETA-AMYLOID PEPTIDE (FRAGMENT).  
GN BETA APP.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93236601; PubMed=8476439;  
RA Denman R.B., Rosenzweig R., Miller D.L.;  
RT "A system for studying the effect(s) of familial Alzheimer disease  
RT mutations on the processing of the beta-amyloid peptide precursor.";  
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).  
DR EMBL: S61383; AAB26265.2; -;  
DR HSSP: P05067; 1BA4. 1  
FT NON\_TER 1  
SQ SEQUENCE 82 AA; 8882 MW; F534AA5AED5D9230A CRC64;

OY 1 EISEVKMDAE 10  
 |||||||||  
 DB 11 EISEVKMDAE 20

## RESULT 6

ID 099K32 PRELIMINARY; PRT; 607 AA.  
 AC 099K32;  
 DT 01-JUN-2001 (TREMBlrel. 17, Created)  
 DT 01-JUN-2001 (TREMBlrel. 17, last sequence update)  
 DE 01-DEC-2001 (TREMBlrel. 19, last annotation update)  
 DE HYPOTHETICAL 68.4 KDA PROTEIN (FRAGMENT).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=MAMMARY TUMOR. MAP-TGF ALPHA MODEL. 7 MONTHS OLD, CROSS  
 RC TISSUE.  
 RA Strausberg R.;  
 RL Submitted (MAR-2001) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: BC005490; AAH05490.1; -.  
 DR HSSP: P05067; 1AAP.  
 DR InterPro: IPR001868; A4\_APP.  
 DR InterPro: IPR002223; Kunitz-BPTI.  
 DR Pfam: PF00014; Kunitz-BPTI. 1.  
 DR PRINTS: PR00203; AMYLOIDA4.  
 DR PRINTS: PR00759; BASICPTASE.  
 DR SMART: SM00131; KU. 1.  
 DR PROSITE: PS00319; A4\_EXTRA; 1.  
 DR PROSITE: PS00320; A4\_INTRA; 1.  
 DR PROSITE: PS00280; BPTI\_KUNITZ\_1; 1.  
 DR PROSITE: PS0279; BPTI\_KUNITZ\_2; 1.  
 KM Hypothetical protein; Serine protease inhibitor.  
 FT NON\_TER 1  
 SQ SEQUENCE 607 AA; 68391 MW; BFR02214CHA7D172 CRC64;

Query Match 100.0%; Score 47; DB 11; Length 607;  
 Best Local Similarity 100.0%; Pred. No. 0.41;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EISEVKMDAE 10  
 |||||||||  
 DB 502 EISEVKMDAE 511

RESULT 7  
 ID 095KN7 PRELIMINARY; PRT; 695 AA.  
 AC 095KN7;  
 DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)  
 DE AMYLOID B-PROTEIN PRECURSOR.  
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecinae; Macaca.  
 NCBI\_TaxID=9541;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=CEREBELLUM;  
 RX MEDLINE=91273117; PubMed=1905108;  
 RA Podlasky M.B., Tolan D.R., Selkoe D.J.;  
 RT "Homology of the amyloid beta protein precursor in monkey and human  
 RT supports a primate model for beta amyloidosis in Alzheimer's  
 RT disease";  
 RL Am. J. Pathol. 138:1423-1435(1991).  
 DR EMBL: M58727; AAA36829.1; -.  
 FT SIGNAL 1 17 POTENTIAL.

FT CHAIN 597 636 POTENTIAL.  
 SQ SEQUENCE 695 AA; 78663 MW; 4F6EA0139F969D56 CRC64;

Query Match 100.0%; Score 47; DB 6; Length 695;  
 Best Local Similarity 100.0%; Pred. No. 0.47;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EISEVKMDAE 10  
 |||||||||  
 DB 590 EISEVKMDAE 599

## RESULT 8

ID P97487 PRELIMINARY; PRT; 695 AA.  
 AC P97487; P97942;  
 DT 01-MAY-1997 (TREMBlrel. 03, Created)  
 DT 01-MAY-1997 (TREMBlrel. 03, last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)  
 DE HIPPOCAMPAL AMYLOID PROTEIN.  
 GN APP.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SAMP8; TISSUE=HIPPOCAMPUS;  
 RA Flood J.F., Kumar V.B., Sasser T., Word I., Morley J.E.;  
 RL Submitted (JAN-1997) to the EMBL/Genbank/DBJ databases.  
 RN [2]  
 RP SEQUENCE OF 581-662 FROM N.A.  
 RC STRAIN=129SV;  
 RA Wragg M.A., Busfield F., Duff K., Korenblat K., Capocchi M.,  
 RA Long J.F., Goate A.M.;  
 RL Submitted (DEC-1996) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: U84012; AAB41502.1; -.  
 DR EMBL: U82624; AAB40919.1; -.  
 DR HSSP: P05067; 1MWP.  
 DR MGD: MGI:88059; APP.  
 DR InterPro: IPR001868; A4\_APP.  
 DR Pfam: PF02177; A4\_EXTRA; 1.  
 DR PRINTS: PR00203; AMYLOIDA4.  
 DR SMART: SM00006; A4\_EXTRA; 1.  
 DR PROSITE: PS00319; A4\_EXTRA; 1.  
 DR PROSITE: PS00320; A4\_INTRA; 1.  
 SQ SEQUENCE 695 AA; 78414 MW; 9A5FBE2ED261236E CRC64;

Query Match 100.0%; Score 47; DB 11; Length 695;  
 Best Local Similarity 100.0%; Pred. No. 0.47;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EISEVKMDAE 10  
 |||||||||  
 DB 590 EISEVKMDAE 599

RESULT 9  
 ID 060496 PRELIMINARY; PRT; 695 AA.  
 AC 060496;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)  
 DE PUTATIVE AMYLOID PRECURSOR PROTEIN.  
 OS Cavia sp.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Hystriognathi; Cavidae; Cavia.  
 NCBI\_TaxID=10143;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=BRAIN;  
 RX MEDLINE=97236426; PubMed=9116031;

```
RA Beck M., Mueller D., Bigl V.;  
RT "Amyloid precursor protein in Guinea pigs - complete cDNA sequence and  
alternative splicing."  
RL Biochim. Biophys. Acta 1351:17-21(1997).  
DR EMBL: X97631; CAA66230.1; -.  
DR HSSP: P05067; 1BA4.  
DR InterPro: IPR001868; A4_APP.  
DR Pfam: PF02177; A4_EXTRA; 1.  
DR PRINTS: PR00203; AMYLOIDA4.  
DR SMART: SM00006; A4_EXTRA; 1.  
DR PROSITE: PS00319; A4_EXTRA; 1.  
DR PROSITE: PS00320; A4_INTRA; 1.  
SQ SEQUENCE 695 AA; 78701 MW; 5196A0C4017F16AB CRC64;  
  
Query Match 100.0%; Score 47; DB 11; Length 695;  
Best Local Similarity 100.0%; Pred. No. 0.47;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 EISEVKMDAE 10  
Db 590 EISEVKMDAE 599  
  
RESULT 10  
Q9TU10 PRELIMINARY; PRT; 770 AA.  
AC Q9TU10; 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE AMYLOID PRECURSOR PROTEIN.  
OS Sus scrofa (Pig)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI_TaxID=9823;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Kimura A., Takahashi T.;  
RT "Amyloid precursor protein 770."  
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AB032550; BAA84580.1; -.  
DR HSSP: P05067; 1AAP.  
DR InterPro: IPR001868; A4_APP.  
DR InterPro: IPR002223; Kunitz_BPTI.  
DR Pfam: PF02177; A4_EXTRA; 1.  
DR PRINTS: PR00203; AMYLOIDA4.  
DR PRINTS: PR00759; BASICPTASE.  
DR SMART: SM00006; A4_EXTRA; 1.  
DR SMART: SM00131; KU; 1.  
DR PROSITE: PS00319; A4_EXTRA; 1.  
DR PROSITE: PS00320; A4_INTRA; 1.  
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.  
DR PROSITE: PS02789; BPTI_KUNITZ_2; 1.  
KW Serine protease inhibitor.  
SQ SEQUENCE 770 AA; 86961 MW; 5FALDPCB2BC583E CRC64;  
  
Query Match 100.0%; Score 47; DB 6; Length 770;  
Best Local Similarity 100.0%; Pred. No. 0.52;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 EISEVKMDAE 10  
Db 665 EISEVKMDAE 674  
  
RESULT 11  
Q93296 PRELIMINARY; PRT; 534 AA.  
AC Q93296; 01-NOV-1998 (TREMBLrel. 08, Created)  
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
```

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DE AMYLOID PROTEIN (FRAGMENT).  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98337885; PubMed=9671674;  
RA Barnes N.Y., Li L., Yoshikawa K., Schwartz L.M., Oppenheim R.W.,  
RA Milligan C.E.;  
RT "Increased production of amyloid precursor protein provides a  
substrate for caspase-3 in dying motoneurons."  
RL J. Neurosci. 18:5869-5880(1998).  
DR EMBL: AF042098; AAC25052.1; -.  
DR HSSP: P05067; 1BA4.  
DR InterPro: IPR001868; A4_APP.  
DR PRINTS: PR00203; AMYLOIDA4.  
DR PROSITE: PS00319; A4_EXTRA; 1.  
DR PROSITE: PS00320; A4_INTRA; 1.  
FT NON_TER 1  
SQ SEQUENCE 534 AA; 60597 MW; FB53ECC2B66DAC92 CRC64;  
  
Query Match 97.9%; Score 46; DB 13; Length 534;  
Best Local Similarity 90.0%; Pred. No. 0.57;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 EISEVKMDAE 10  
Db 429 EISEVKMDAE 438  
  
RESULT 12  
Q9PVL1 PRELIMINARY; PRT; 569 AA.  
AC Q9PVL1; 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE AMYLOID PROTEIN (FRAGMENT).  
GN APP.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=BRAIN;  
RA Coulson E.J., Pallag K., Beyreuther K., Masters C.L.;  
RT "What the evolution of the amyloid protein precursor supergene family  
tells us about its function."  
RL Neurochem. Int. 0:0-0(2000).  
DR EMBL: AF030341; AAF12698.1; -.  
DR HSSP: P05067; 1BA4.  
DR InterPro: IPR001868; A4_APP.  
DR Pfam: PF02177; A4_EXTRA; 1.  
DR PRINTS: PR00203; AMYLOIDA4.  
DR SMART: SM00006; A4_EXTRA; 1.  
DR PROSITE: PS00319; A4_EXTRA; 1.  
DR PROSITE: PS00320; A4_INTRA; 1.  
FT NON_TER 1  
SQ SEQUENCE 569 AA; 64753 MW; 0AB8B851863A19D CRC64;
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Query Match 97.9%; Score 46; DB 13; Length 569;  
Best Local Similarity 90.0%; Pred. No. 0.61;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 EISEVKMDAE 10  
Db 465 EISEVKMDAE 474
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RESULT 13
ID 09DGJ8 PRELIMINARY; PRT; 695 AA.
AC 09DGJ8;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)
DE BETA-AMYLOID PRECURSOR PROTEIN 695 ISOFORM.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Sarasa M., Rodolose A., Sorribas V.;
RT "Cloning of full-length chicken beta-amyloid precursor protein
RT isoforms";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF289218; MAG0593.1; -.
DR HSSP: P05067; IBA4.
DR InterPro: IPR001868; A4_APP.
DR Pfam: PF02177; A4_EXTRA; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR SMART: SM00006; A4_EXTRA; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
SQ SEQUENCE 695 AA; 78565 MW; F201ED02AEC86D95 CRC64;

Query Match 97.9%; Score 46; DB 13; Length 695;
Best Local Similarity 90.0%; Pred. No. 0.74;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 EISEVKMDAE 10
DB 590 EVSEVKMDAE 599

RESULT 14
ID 09DGJ7 PRELIMINARY; PRT; 751 AA.
AC 09DGJ7;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)
DE BETA-AMYLOID PRECURSOR PROTEIN 751 ISOFORM.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Sarasa M., Rodolose A., Sorribas V.;
RT "Cloning of full-length chicken beta-amyloid precursor protein
RT isoforms";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF289219; MAG00594.1; -.
DR HSSP: P05067; IBA4.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PRINTS: PR00759; BASICPTASE.
DR SMART: SM00006; A4_EXTRA; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00260; BPTI_KUNITZ_1; 1.
DR PROSITE: PS0279; BPTI_KUNITZ_2; 1.
DR Serine protease inhibitor.
SQ SEQUENCE 751 AA; 84705 MW; E78E9413A8033084 CRC64;

Query Match 97.9%; Score 46; DB 13; Length 751;
Best Local Similarity 90.0%; Pred. No. 0.8;

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 EISEVKMDAE 10
DB 646 EVSEVKMDAE 655

RESULT 15
ID 098SG0 PRELIMINARY; PRT; 693 AA.
AC 098SG0;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)
DE BETA-AMYLOID PRECURSOR PROTEIN A.
GN APP.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Van den Hurk W.H.;
RL Thesis (2001), Department of Biological Sciences,
RL University of Nijmegen, Nijmegen, Netherlands.
DR EMBL: AJ298150; CAC37193.1; -.
DR HSSP: P05067; 1H23.
DR InterPro: IPR001868; A4_APP.
DR Pfam: PF02177; A4_EXTRA; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR SMART: SM00006; A4_EXTRA; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
DR Signal.
KM SIGNAL.
FT SIGNAL.
SQ SEQUENCE 693 AA; 78568 MW; CAFIDF55C1AB653 CRC64;

Query Match 93.6%; Score 44; DB 13; Length 693;
Best Local Similarity 90.0%; Pred. No. 1.9;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 EISEVKMDAE 10
DB 588 EISEVKMDSE 597

Search completed: October 29, 2002, 10:29:38
Job time : 19.1429 secs

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OY 1 EISEVKMDAE 10  
|  
Db 2 EISEVKMDAE 11

## RESULT 2

US-08-541-902-11  
; Sequence 11, Application US/08541902  
; Patent No. 5707620  
; GENERAL INFORMATION:  
; APPLICANT: Travis, James  
; APPLICANT: Potempa, Jan S.  
; APPLICANT: Barr, Philip J.  
; APPLICANT: Pavloff, Nadine  
; APPLICANT: Pike, Robert N.  
; TITLE OF INVENTION: Lysine-specific Porphyromonas gingivalis  
; TITLE OF INVENTION: Protease  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Greenlee and Winner, P.C.  
; STREET: 5370 Manhattan Circle, Suite 201  
; CITY: Boulder  
; STATE: CO  
; COUNTRY: US  
; ZIP: 80303

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/541.902  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/141.324  
; FILING DATE: 21-OCT-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Feiber, Donna M.  
; REGISTRATION NUMBER: 33,878  
; REFERENCE/DOCKET NUMBER: 44-93  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 303-499-8080  
; TELEFAX: 303-499-8089

INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 27 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
US-08-541-902-11

Query Match 100.0%; Score 47; DB 1; Length 27;  
Best Local Similarity 100.0%; Pred. No. 0.0025;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EISEVKMDAE 10  
|  
Db 2 EISEVKMDAE 11

## RESULT 3

US-08-462-859A-5  
; Sequence 5, Application US/08462859A  
; Patent No. 5652092  
; GENERAL INFORMATION:  
; APPLICANT: Jacobsen, J. S.  
; APPLICANT: Vitek, M. P.  
; TITLE OF INVENTION: NO. 5652092el Amyloid Precursor and Method of

;; TITLE OF INVENTION: using Same to Access Agents which Down-Regulate Formation  
;; TITLE OF INVENTION: of B-Amyloid Peptide  
;; NUMBER OF SEQUENCES: 19  
;; CORRESPONDENCE ADDRESSES:  
;; ADDRESSEE: American Cyanamid Company  
;; STREET: One Cyanamid Plaza  
;; CITY: Wayne  
;; STATE: New Jersey  
;; COUNTRY: United States  
;; ZIP: 07470-8426

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/462.859A  
; FILING DATE: 05-JUN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Barnhard, Elizabeth M.  
; REGISTRATION NUMBER: 31,088  
; REFERENCE/DOCKET NUMBER: 31,844-04  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (201)831-3346  
; TELEFAX: (201)831-3305  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 45 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-462-859A-5

Query Match 100.0%; Score 47; DB 1; Length 45;  
Best Local Similarity 100.0%; Pred. No. 0.0043;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EISEVKMDAE 10  
|  
Db 3 EISEVKMDAE 12

## RESULT 4

US-08-123-659A-5  
; Sequence 5, Application US/08123659A  
; Patent No. 5656477  
; GENERAL INFORMATION:  
; APPLICANT: Jacobsen, J. S.  
; APPLICANT: Vitek, M. P.  
; TITLE OF INVENTION: NO. 5656477el Amyloid Precursor and Method of  
; TITLE OF INVENTION: Using Same to Access Agents which Down-Regulate Formation  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Anne Rosenblum  
; STREET: 163 Delaware Avenue, Suite 212  
; CITY: Delmar  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 12054  
COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/123.659A  
; FILING DATE: 20-SEP-1993  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Rosenblum, Anne M.

REGISTRATION NUMBER: 30,419  
REFERENCE/DOCKET NUMBER: 31,844-01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (518)475-0611  
TELEFAX: (518)475-0619  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 45 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-123-659A-5

Query Match 100.0%; Score 47; DB 1; Length 45;  
Best Local Similarity 100.0%; Pred. No. 0.0043;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EISEVKMDAE 10  
|||||  
DB 3 EISEVKMDAE 12

RESULT 5

US-08-464-247A-5  
Sequence 5, Application US/08464247A  
Patent No. 5693478  
GENERAL INFORMATION:  
APPLICANT: Jacobsen, J. S.  
APPLICANT: Vittek, M. P.  
TITLE OF INVENTION: No. 5693478el Amyloid Precursor and Method of  
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation  
TITLE OF INVENTION: of B-Amyloid Peptide  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: American Cyanamid Company  
STREET: One Campus Drive  
CITY: Parsippany  
STATE: New Jersey  
COUNTRY: United States  
ZIP: 07054  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/464,247A  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Barnhard, Elizabeth M.  
REGISTRATION NUMBER: 31,088  
REFERENCE/DOCKET NUMBER: 31,844-03  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-683-4117  
TELEFAX: 201-683-2158  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 45 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-464-247A-5

Query Match 100.0%; Score 47; DB 1; Length 45;  
Best Local Similarity 100.0%; Pred. No. 0.0043;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EISEVKMDAE 10  
|||||  
DB 3 EISEVKMDAE 12

RESULT 6  
US-08-464-248A-5  
Sequence 5, Application US/08464248A  
Patent No. 5703209  
GENERAL INFORMATION:  
APPLICANT: Jacobsen, J. S.  
APPLICANT: Vittek, M. P.  
TITLE OF INVENTION: No. 5703209el Amyloid Precursor and Method of  
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation  
TITLE OF INVENTION: of B-Amyloid Peptide  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: American Cyanamid Company  
STREET: One Campus Drive  
CITY: Parsippany  
STATE: New Jersey  
COUNTRY: United States  
ZIP: 07470-8426  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/464,248A  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Barnhard, Elizabeth M.  
REGISTRATION NUMBER: 31,088  
REFERENCE/DOCKET NUMBER: 31,844-02  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (201)831-3246  
TELEFAX: (201)831-3305  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 45 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-464-248A-5

Query Match 100.0%; Score 47; DB 1; Length 45;  
Best Local Similarity 100.0%; Pred. No. 0.0043;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 3 EISEVKMDAE 12

RESULT 7  
US-08-371-930-25  
Sequence 25, Application US/08371930  
Patent No. 5578451  
GENERAL INFORMATION:  
APPLICANT: Nishimoto, Ikuo  
TITLE OF INVENTION: ALZHEIMER'S DISEASE THERAPEUTICS  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
COMPUTER: IBM PS/2 Model 502 or 555X  
OPERATING SYSTEM: MS-DOS (Version 5.0)  
SOFTWARE: Wordperfect (Version 5.1)

;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/371,930  
;; FILING DATE:  
;; CLASSIFICATION: 436  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/019,208  
;; FILING DATE: February 18, 1993  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Clark, Paul T.  
;; REGISTRATION NUMBER: 30,162  
;; REFERENCE/DOCKET NUMBER: 00786/154001  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (617) 542-5070  
;; TELEFAX: (617) 542-8906  
;; TELEX: 200154  
;; INFORMATION FOR SEQ ID NO: 25:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 58  
;; TYPE: amino acid  
;; STRANDEDNESS:  
;; TOPOLOGY: linear  
;; US-08-371-930-25

Query Match 100.0%; Score 47; DB 1; Length 58;  
Best Local Similarity 100.0%; Pred. No. 0.0058;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EISEVKMDAE 10  
|||||  
Db 40 EISEVKMDAE 49

RESULT 8  
PCT-US94-01712-25  
;; Sequence 25, Application PC/TUS9401712  
;; GENERAL INFORMATION:  
;; APPLICANT: Nishimoto, Ikuo  
;; TITLE OF INVENTION: ALZHEIMER'S DISEASE THERAPEUTICS  
;; NUMBER OF SEQUENCES: 30  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Fish & Richardson  
;; STREET: 225 Franklin Street  
;; CITY: Boston  
;; STATE: Massachusetts  
;; COUNTRY: U.S.A.  
;; ZIP: 02110-2804  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
;; COMPUTER: IBM PS/2 Model 50x or 55SX  
;; OPERATING SYSTEM: MS-DOS (Version 5.0)  
;; SOFTWARE: WordPerfect (Version 5.1)  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: PCT/US94/01712  
;; FILING DATE:  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/019,208  
;; FILING DATE: February 18, 1993  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Clark, Paul T.  
;; REGISTRATION NUMBER: 30,162  
;; REFERENCE/DOCKET NUMBER: 00786/154001  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (617) 542-5070  
;; TELEFAX: (617) 542-8906  
;; TELEX: 200154  
;; INFORMATION FOR SEQ ID NO: 25:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 58  
;; TYPE: amino acid  
;; STRANDEDNESS:  
;; TOPOLOGY: linear  
;; PCT-US94-01712-25

Query Match 100.0%; Score 47; DB 5; Length 58;  
Best Local Similarity 100.0%; Pred. No. 0.0058;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EISEVKMDAE 10  
|||||  
Db 40 EISEVKMDAE 49

RESULT 9  
US-08-462-859A-3  
;; Sequence 3, Application US/08462859A  
;; Patent No. 5652092  
;; GENERAL INFORMATION:  
;; APPLICANT: Jacobsen, J. S.  
;; TITLE OF INVENTION: No. 5652092el Amyloid Precursor and Method of  
;; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation  
;; NUMBER OF SEQUENCES: 19  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: American Cyanamid Company  
;; STREET: One Cyanamid Plaza  
;; CITY: Wayne  
;; STATE: New Jersey  
;; COUNTRY: United States  
;; ZIP: 07470-8426  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/462,859A  
;; FILING DATE: 05-JUN-1995  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Barnard, Elizabeth M.  
;; REGISTRATION NUMBER: 31,088  
;; REFERENCE/DOCKET NUMBER: 31,844-04  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (201)851-3246  
;; TELEFAX: (201)851-3305  
;; INFORMATION FOR SEQ ID NO: 3:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 63 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS:  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; US-08-462-859A-3

Query Match 100.0%; Score 47; DB 1; Length 63;  
Best Local Similarity 100.0%; Pred. No. 0.0063;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EISEVKMDAE 10  
|||||  
Db 3 EISEVKMDAE 12

RESULT 10  
US-08-462-859A-4  
;; Sequence 4, Application US/08462859A  
;; Patent No. 5652092  
;; GENERAL INFORMATION:  
;; APPLICANT: Jacobsen, J. S.  
;; TITLE OF INVENTION: No. 5652092el Amyloid Precursor and Method of  
;; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation  
;; NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:  
ADDRESSEE: American Cyanamid Company  
STREET: One Cyanamid Plaza  
CITY: Wayne  
STATE: New Jersey  
COUNTRY: United States  
ZIP: 07470-8426  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/462,859A  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Barnhard, Elizabeth M.  
REGISTRATION NUMBER: 31,088  
REFERENCE/DOCKET NUMBER: 31,844-04  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (201)831-3246  
TELEFAX: (201)831-3305  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 63 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-462-859A-4

Query Match  
Best Local Similarity 100.0%; Score 47; DB 1; Length 63;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EISEVKMDAE 10  
Db 3 EISEVKMDAE 12

RESULT 11  
US-08-123-659A-3  
Sequence 3, Application US/08123659A  
Patent No. 5656477  
GENERAL INFORMATION:  
APPLICANT: Jacobsen, J. S.  
TITLE OF INVENTION: No. 5656477el Amyloid Precursor and Method of  
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Anne Rosenblum  
STREET: 163 Delaware Avenue, Suite 212  
CITY: Delmar  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 12054  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/123,659A  
FILING DATE: 20-SEP-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Rosenblum, Anne M.  
REGISTRATION NUMBER: 30,419  
REFERENCE/DOCKET NUMBER: 31,844-01  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (518)475-0611  
TELEFAX: (518)475-0619  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 63 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-123-659A-3

Query Match  
Best Local Similarity 100.0%; Score 47; DB 1; Length 63;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EISEVKMDAE 10  
Db 3 EISEVKMDAE 12

RESULT 12  
US-08-123-659A-4  
Sequence 4, Application US/08123659A  
Patent No. 5656477  
GENERAL INFORMATION:  
APPLICANT: Jacobsen, J. S.  
TITLE OF INVENTION: No. 5656477el Amyloid Precursor and Method of  
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Anne Rosenblum  
STREET: 163 Delaware Avenue, Suite 212  
CITY: Delmar  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 12054  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/123,659A  
FILING DATE: 20-SEP-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Rosenblum, Anne M.  
REGISTRATION NUMBER: 30,419  
REFERENCE/DOCKET NUMBER: 31,844-01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (518)475-0611  
TELEFAX: (518)475-0619  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 63 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-123-659A-4

Query Match  
Best Local Similarity 100.0%; Score 47; DB 1; Length 63;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EISEVKMDAE 10  
Db 3 EISEVKMDAE 12

RESULT 13  
US-08-464-247A-3  
Sequence 3, Application US/08464247A

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Patent No. 5693478
GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
APPLICANT: Vittek, M. P.
TITLE OF INVENTION: No. 5693478e1 Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
TITLE OF INVENTION: of B-Amyloid Peptide
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESS: American Cyanamid Company
STREET: One Campus Drive
CITY: Parsippany
STATE: New Jersey
COUNTRY: United States
ZIP: 07054
COMPUTER READABLE FORM:
MEDIUM TYPE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,247A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,844-03
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-683-2158
TELEFAX: 201-683-4117
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 63 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-247A-3

Query Match      100.0%; Score 47; DB 1; Length 63;
Best Local Similarity 100.0%; Pred. No. 0.0063;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 3 EISEVKMDAE 12

RESULT 14
US-08-464-247A-4
Sequence 4, Application US/08464247A
Patent No. 5693478
GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
APPLICANT: Vittek, M. P.
TITLE OF INVENTION: No. 5693478e1 Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
TITLE OF INVENTION: of B-Amyloid Peptide
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESS: American Cyanamid Company
STREET: One Campus Drive
CITY: Parsippany
STATE: New Jersey
COUNTRY: United States
ZIP: 07054
COMPUTER READABLE FORM:
MEDIUM TYPE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/08/464,247A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,844-03
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-683-2158
TELEFAX: 201-683-4117
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 63 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-247A-4

Query Match      100.0%; Score 47; DB 1; Length 63;
Best Local Similarity 100.0%; Pred. No. 0.0063;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 EISEVKMDAE 10
Db 3 EISEVKMDAE 12

RESULT 15
US-08-464-248A-3
Sequence 3, Application US/08464248A
Patent No. 5703209
GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
APPLICANT: Vittek, M. P.
TITLE OF INVENTION: No. 5703209e1 Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
TITLE OF INVENTION: of B-Amyloid Peptide
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESS: American Cyanamid Company
STREET: One Cyanamid Plaza
CITY: Wayne
STATE: New Jersey
COUNTRY: United States
ZIP: 07470-8426
COMPUTER READABLE FORM:
MEDIUM TYPE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,248A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,844-02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201)831-3246
TELEFAX: (201)831-3305
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 63 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-248A-3

Query Match      100.0%; Score 47; DB 1; Length 63;
Best Local Similarity 100.0%; Pred. No. 0.0063;
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Matches	10;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
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Job time : 9 secs





GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 29, 2002, 10:22:21 ; Search time 23.1429 Seconds  
(without alignments)  
47.995 Million cell updates/sec

Title: US-09-580-018-3  
Perfect score: 48  
Sequence: ITSEVKDAEF-10

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Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 11073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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9	48	100.0	11	22	AA62668
10	48	100.0	11	22	AA62668
11	48	100.0	11	22	AA62668

12	48	100.0	23	22	AA62668	Asp2 substrate w/1
13	48	100.0	33	20	AA62668	Amyloid precursor
14	48	100.0	39	21	AA62668	Beta-APP alpha-sec
15	48	100.0	45	18	AA62668	Amyloid precursor
16	48	100.0	45	18	AA62668	Amyloid precursor
17	48	100.0	45	19	AA62668	Amyloid precursor
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21	48	100.0	57	21	AA62668	Amyloid-beta precu
22	48	100.0	58	15	AA62668	Human amyloid prec
23	48	100.0	63	18	AA62668	Amyloid precursor
24	48	100.0	63	18	AA62668	Amyloid precursor
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27	48	100.0	63	19	AA62668	Beta-amyloid pepti
28	48	100.0	63	19	AA62668	Peptide derived fr
29	48	100.0	67	19	AA62668	Novel human diagno
30	48	100.0	93	22	AA62668	Familial Alzheimer
31	48	100.0	112	17	AA62668	London-FAD APP pol
32	48	100.0	115	20	AA62668	Flag-amyloid prote
33	48	100.0	117	19	AA62668	Deduced sequence i
34	48	100.0	162	9	AA62668	Beta-amyloid-relat
35	48	100.0	162	12	AA62668	Deduced from clone
36	48	100.0	162	14	AA62668	Beta-amyloid precu
37	48	100.0	249	15	AA62668	Protein sequence i
38	48	100.0	264	10	AA62668	Sequence of amy 37
39	48	100.0	264	10	AA62668	Amyloid precursor
40	48	100.0	264	10	AA62668	Amyloid precursor
41	48	100.0	264	10	AA62668	APP-REP 751 protei
42	48	100.0	264	10	AA62668	Amyloid precursor
43	48	100.0	264	10	AA62668	APP-REP 751 amyloi
44	48	100.0	264	10	AA62668	Amyloid precursor
45	48	100.0	264	10	AA62668	Amyloid precursor

## ALIGNMENTS

RESULT 1	AA62668	standard; peptide; 10 AA.
ID	AA62668	
XX	AA62668	
AC	AA62668	
XX	AA62668	
DT	17-SEP-2001 (first entry)	
XX	17-SEP-2001	
DE	Beta-sheet breaker peptide inhibitor assay related peptide #3.	
XX	Beta-sheet breaker peptide; protein conformational disease; amyloid;	
KW	Alzheimer's disease; FAF; Down' syndrome; amyloidosis disorder;	
KM	pilon disease; prion associated neurodegenerative disease.	
XX	Synthetic.	
OS	Synthetic.	
PN	WO200134631-A2.	
XX	17-MAY-2001.	
PD	04-NOV-2000: 2000WO-US30416.	
PF	05-NOV-1999: 99US-0163911.	
PR	05-NOV-1999: 99US-0163911.	
XX	(AXON-) AXONYX INC.	
PA	Soto-Jara C;	
PI	Soto-Jara C;	
XX	WPI; 2001-408068/43.	
DR	New peptide analogues and mimetics, useful by oral administration for	
XX	the treatment of Alzheimer's and prion disease by stabilization of the	
PT	conformation of amyloidogenic peptide	
XX		

PS Examples; Page 28; 48pp; English.  
XX  
CC The present invention relates to beta-sheet breaker peptide analogues  
CC capable of inhibiting beta-pleated sheet formation in amyloid  
CC beta-peptide. These are obtained by modification of a beta-sheet breaker  
CC peptide. They can be used to reduce the formation of amyloid or  
CC amyloid-like deposits involving abnormal folding into beta-sheet  
CC structures or conformational change in prion Pr protein. They are thus  
CC useful in the treatment of Alzheimer's disease, FAF, Down's syndrome,  
CC other amyloidosis disorders, prion diseases such as kuru,  
CC Creutzfeldt-Jakob disease, Gerstmann-Strauslert-Scheinker syndrome, prion  
CC associated human neurodegenerative diseases, scrapie, spongiform  
CC encephalopathy, transmissible milk encephalopathy and chronic wasting  
CC disease of mule deer and elk. The present sequence is a peptide described  
CC in the exemplification of the invention.  
XX  
SQ Sequence 10 AA:  
Query Match 100.0%; Score 48; DB 22; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.00077;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ISEVKMDAEF 10  
DB 1 ISEVKMDAEF 10  
RESULT 2  
AAB46207  
ID AAB46207 standard; peptide: 10 AA.  
XX  
AC AAB46207;  
XX  
DT 04-APR-2001 (first entry)  
XX  
DE Human APP derived immunogenic peptide #3.  
XX  
KW Amyloid deposit; APP: Abeta; brain; human; clearing response; nootropic;  
KW Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;  
KW amyloid precursor protein; Alzheimer's disease.  
XX  
OS Homo sapiens.  
XX  
PN WO200072880-A2.  
XX  
PD 07-DEC-2000.  
XX  
PF 26-MAY-2000; 2000WO-US14810.  
XX  
PR 28-MAY-1999; 99US-0322289.  
XX  
PA (NEUR-) NEURALAB LTD.  
XX  
PI Schenk DB, Bard F, Vasquez NJ, Yednock T;  
XX  
DR WPI; 2001-032104/04.  
XX  
PT Preventing or treating a disease associated with amyloid deposits,  
PT especially Alzheimer's disease, comprises administering amyloid  
PT specific antibody -  
XX  
PS Disclosure; Figure 19; 143pp; English.  
XX  
CC This invention describes a novel method of preventing or treating a  
CC disease associated with amyloid deposits of amyloid precursor protein  
CC (APP) Abeta fragments in the brain of a patient, which comprises  
CC administering to the patient: (a) an antibody that binds to Abeta, the  
CC antibody binds to an amyloid deposit and induces a clearing response (Fc  
CC receptor mediated phagocytosis) against it (b) a polypeptide containing  
CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent  
CC that induces an immunogenic response against residues 1-3 to 7-11 of  
CC Abeta. The products of the invention have nootropic and neuroprotective  
CC activity. The method is also useful for monitoring a course of treatment

CC being administered to a patient e.g. active and passive immunization. The  
CC methods are useful for prophylactic and therapeutic treatment of  
CC Alzheimer's disease.  
XX  
SQ Sequence 10 AA:  
Query Match 100.0%; Score 48; DB 22; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.00077;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ISEVKMDAEF 10  
DB 1 ISEVKMDAEF 10  
RESULT 3  
AAB75143  
ID AAB75143 standard; peptide: 11 AA.  
XX  
AC AAB75143;  
XX  
DT 08-AUG-2001 (first entry)  
XX  
DE APP beta-secretase cleavage site spanning peptide SEQ ID NO.1.  
XX  
KW Amyloid precursor protein; APP; Asp 1; endorepsin 1; inhibition;  
KW transmembrane aspartyl proteinase; APP Swedish variant; nootropic;  
KW neuroprotective; beta-secretase cleavage site; Alzheimer's disease;  
KW beta amyloid protein-related disease; antiAlzheimer.  
XX  
OS Homo sapiens.  
XX  
PN WO200131054-A1.  
XX  
PD 03-MAY-2001.  
XX  
PF 19-OCT-2000; 2000WO-GB04028.  
XX  
PR 22-OCT-1999; 99GB-0025136.  
XX  
PA (SMK ) SMITHKLINE BEECHAM PLC.  
PA (SMK ) SMITHKLINE BEECHAM CORP.  
XX  
PI Christie G, Hussain I, Powell DJ;  
XX  
DR WPI; 2001-328654/34.  
XX  
PT Identifying inhibitors of Asp 1-mediated cleavage, for treating or  
PT preventing beta-amyloid protein-related disease, comprises measuring  
PT the extent of substrate cleavage in a reaction system containing Asp 1  
PT and a substrate -  
XX  
PS Disclosure; Page 3; 31pp; English.  
XX  
CC The present invention describes a method of screening for compounds  
CC which inhibit Asp 1-mediated cleavage of a polypeptide or protein  
CC substrate. The method comprises providing a reaction system comprising  
CC Asp 1 and substrate, and measuring the extent of cleavage of the  
CC substrate in the presence of test compound compared with that in the  
CC presence of the test compound. Also described are: (1) a method of  
CC screening for compounds which inhibit Asp 1 mediated cleavage of a  
CC polypeptide or protein substrate comprising providing a reaction system  
CC comprising Asp 1 and a labeled active site ligand, and measuring the  
CC extent of binding of the labeled ligand in the presence of test compound  
CC compared with that in the presence of the test compound; (2) a compound  
CC identified by the method; (3) a pharmaceutical composition comprising the  
CC compound of (2) and a carrier; (4) a method of inhibiting Asp 1 modulated  
CC amyloid precursor protein (APP) cleavage, or treating or prophylaxis of  
CC beta-amyloid protein-related disease, comprising administering to a  
CC patient a compound of (2); (5) a compound which is an inhibitor of Asp 1  
CC modulated APP cleavage; and (6) a method for treating or prophylaxis of  
CC beta-amyloid protein-related disease comprising administering a compound  
CC of (2) or (5). The compound which inhibits Asp 1 mediated cleavage of a

CC polypeptide or protein is useful in therapy, in the preparation of a  
 CC medicament for inhibiting Asp 1-mediated APP cleavage and for the  
 CC treatment or prophylaxis of beta-amyloid protein-related disease,  
 CC including Alzheimer's disease. The present sequence represents an APP  
 CC beta-secretase cleavage site spanning peptide which can be used as a  
 CC substrate in the method of the invention.

XX Sequence 11 AA:

Query Match 100.0%; Score 48; DB 22; Length 11;

Best Local Similarity 100.0%; Pred. No. 0.00086;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISEVKMDAEF 10

Db 1 ISEVKMDAEF 10

RESULT 4

ABR75144

AC AAB75144;

DT 08-AUG-2001 (first entry)

DE Asp 1 substrate sequence SEQ ID NO:3.

XX Amyloid precursor protein; APP; Asp 1; endorepsin 1; inhibition;  
 XX transmembrane aspartyl proteinase; APP Swedish variant; nontropic;  
 XX neuroprotective; beta-secretase cleavage site; Alzheimer's disease;  
 XX beta amyloid protein-related disease; antiAlzheimer.  
 OS Homo sapiens.

XX Key Location/Qualifiers

FT Modified-site 1 /note="N-terminally attached to maltose binding protein  
 FT (MBP)"

XX WO200131054-A1.

XX 03-MAY-2001.

XX 19-OCT-2000; 2000WO-GB04028.

XX 22-OCT-1999; 99GB-0025136.

XX (SMIR ) SMITHKLINE BEECHAM PLC.  
 XX (SMIR ) SMITHKLINE BEECHAM CORP.

XX Christle G, Hussain I, Powell DJ;

XX WPI; 2001-328654/34.

XX Identifying inhibitors of Asp 1-mediated cleavage, for treating or  
 XX preventing beta-amyloid protein-related disease, comprises measuring  
 XX the extent of substrate cleavage in a reaction system containing Asp 1  
 XX and a substrate -

XX Disclosure; Page 3; 31pp; English.

XX The present invention describes a method of screening for compounds  
 XX which inhibit Asp 1-mediated cleavage of a polypeptide or protein  
 XX substrate. The method comprises providing a reaction system comprising  
 XX Asp 1 and substrate, and measuring the extent of cleavage of the  
 XX substrate in the presence of test compound compared with that in the  
 XX presence of the test compound. Also described are: (1) a method of  
 XX screening for compounds which inhibit Asp 1 mediated cleavage of a  
 XX polypeptide or protein substrate comprising providing a reaction system  
 XX comprising Asp 1 and a labeled active site ligand, and measuring the  
 XX extent of binding of the labeled ligand in the presence of test compound  
 XX compared with that in the presence of the test compound; (2) a compound

CC identified by the method; (3) a pharmaceutical composition comprising the  
 CC compound of (2) and a carrier; (4) a method of inhibiting Asp 1 mediated  
 CC amyloid precursor protein (APP) cleavage, or treating or prophylaxis of  
 CC beta-amyloid protein-related disease, comprising administering to a  
 CC patient a compound of (2); (5) a compound which is an inhibitor of Asp 1  
 CC mediated APP cleavage; and (6) a method for treating or prophylaxis of  
 CC beta-amyloid protein-related disease comprising administering a compound  
 CC of (2) or (5). The compound which inhibits Asp 1 mediated cleavage of a  
 CC polypeptide or protein is useful in therapy, in the preparation of a  
 CC medicament for inhibiting Asp 1-mediated APP cleavage and for the  
 CC treatment or prophylaxis of beta-amyloid protein-related disease,  
 CC including Alzheimer's disease. The present sequence represents an Asp 1  
 CC substrate sequence which is given in the exemplification of the present  
 CC invention.

XX Sequence 11 AA:

Query Match 100.0%; Score 48; DB 22; Length 11;

Best Local Similarity 100.0%; Pred. No. 0.00086;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISEVKMDAEF 10

Db 1 ISEVKMDAEF 10

RESULT 5

ABR7468

AC AAB7468;

DT 03-AUG-2001 (first entry)

DE Asp2 substrate wild-type beta-site peptide sequence.

XX Asp2; endorepsin 2; memapsin 2; beta-amyloid protein;  
 XX Alzheimer's disease; cortical Lewy body disease; Parkinson's disease;  
 XX Asp2 inhibitor.  
 OS Unidentified.

XX Key Location/Qualifiers

FT Modified-site 1 /label="OTHER  
 FT /note="optionally bound to maltose binding protein"

XX WO200129563-A1.

XX 26-APR-2001.

XX 19-OCT-2000; 2000WO-GB04039.

XX 21-OCT-1999; 99GB-0024957.

XX (SMIR ) SMITHKLINE BEECHAM PLC.  
 XX (SMIR ) SMITHKLINE BEECHAM CORP.

XX Christle G, Hussain I, Powell DJ;

XX WPI; 2001-300381/31.

XX Screening for inhibitors of Asp 2 mediated polypeptide cleavage  
 XX comprising measuring substrate cleavage or ligand binding with a system  
 XX comprising Asp 2 and a substrate or labelled ligand in the presence or  
 XX absence of a test compound -

XX Disclosure; Page 3; 34pp; English.

XX The present invention describes a method of screening for compounds which  
 XX inhibit Asp2 (also known as memapsin 2 and endorepsin 2) mediated  
 XX cleavage of a protein substrate, involving measuring the extent of  
 XX cleavage of the substrate in the presence and absence of the test

CC compound. Asp2 is thought to be involved in the cleavage of amyloid  
CC precursor protein which is excised to produce beta-amyloid. Beta-amyloid  
CC is involved in the pathogenesis of Alzheimer's disease, Parkinson's  
CC disease, cortical Lewy body disease and vascular and cerebrovascular  
CC diseases, and Asp2 inhibitors could be useful in their treatment. The  
CC present sequence is an example of an Asp2 substrate.

CC Sequence 11 AA;

Query Match 100.0%; Score 48; DB 22; Length 11;

Best Local Similarity 100.0%; Pred. No. 0.00086; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISEVKMDAEF 10  
1 ISEVKMDAEF 10

RESULT 6  
AAW70869  
ID AAW70869 standard; peptide; 13 AA.

XX AAW70869;

XX 04-FEB-1999 (first entry)

DE Beta-amyloid peptide to create a monoclonal antibody.

KW Beta-amyloid precursor protein; beta-APP; beta-amyloid peptide;  
antibody; amyloid deposit; Alzheimer's disease.

XX Synthetic.

XX Homo sapiens.

XX MO9844955-A1.

XX 15-OCT-1998.

PF 09-APR-1998; 98WO-US06900.

PR 09-APR-1997; 97US-0041850.

PA (MCIN/) MCINNIS P A.  
PA (MIND-) MINDSET LTD.

PI Chain DG;

DR WPI; 1998-594476/50.

PT Preventing or inhibiting progression of Alzheimer's Disease -  
PT comprises use of recombinant DNA encoding an antibody specific for  
PT the N- or C-terminus of an amyloid-beta peptide

PS Example 1; Page 47; 58pp; English.

CC The present sequence represents a peptide derived from beta-amyloid  
CC precursor protein (beta-APP). The peptide is a beta-amyloid  
CC peptide and is used to produce a monoclonal antibody. The specification  
CC describes a method for prevention or inhibition of progression of  
CC Alzheimer's disease. The method comprises administering a composition  
CC comprising a recombinant DNA molecule containing a gene encoding a  
CC recombinant antibody end-specific for the N-terminus or the C-terminus  
CC of an amyloid-beta peptide, operably linked to a promoter which is  
CC expressed in the central nervous system. The recombinant antibody  
CC molecules prevent the accumulation of beta-amyloid peptides in the  
CC extracellular space, interstitial fluid and cerebrospinal fluid and the  
CC aggregation of such peptides into amyloid deposits in the brain. They  
CC also inhibit the progression of Alzheimer's disease by inhibiting the  
CC interaction of beta-amyloid peptides mediating Alzheimer's disease  
CC induced neurotoxicity and inhibiting the Alzheimer's disease induced  
CC complement activation and cytokine release involved in the inflammatory  
CC process.

SQ Sequence 13 AA;

Query Match 100.0%; Score 48; DB 19; Length 13;

Best Local Similarity 100.0%; Pred. No. 0.001; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISEVKMDAEF 10  
2 ISEVKMDAEF 11

RESULT 7  
AAB06315  
ID AAB06315 standard; peptide; 16 AA.

XX AAB06315;

DT 03-OCT-2000 (first entry)

DE Human beta-amyloid precursor protein beta-secretase cleavage site.

KW Human; beta-amyloid precursor protein; beta-APP; beta-secretase;  
subtilisin-kexin isoenzyme 1; SKI-1;

KW pro-brain-derived neurotrophic factor; PROBDNF; antilipemic;  
cytostatic; vasotropic; SKI-1 inhibitor; hypercholesterolaemia;

KW liver steatosis; Ras dependent cancer; restenosis;  
amyloid protein formation.

XX Homo sapiens.

OS Key Location/Qualifiers

FT Cleavage-site 8..9

PN WO200026348-A2.

XX 11-MAY-2000.

PF 04-NOV-1999; 99WO-CA01058.

PR 04-NOV-1998; 98CA-2249648.

PA (RECL-) INST RECH CLINIQUES MONTREAL.

PI Seidah N, Chretien M, Marcinkiewicz M, Laaksonen R, Davignon J;

DR WPI; 2000-365601/31.

PT Novel soluble proteic fragment of subtilisin-kexin isoenzyme for  
PT producing a polypeptide useful for treating hypercholesterolemia, liver  
PT steatosis and amyloidosis, comprises a specific amino acid sequence -

PS Example 4; Page 51; 119pp; English.

CC The present sequence is the beta-secretase site of human beta-amyloid  
CC precursor protein (beta-APP). The sequence may be cleaved  
CC by a mammalian subtilase, specifically subtilisin-kexin isoenzyme 1  
CC (SKI-1), a type-1 membrane-bound proteinase. Peptides which bind to and  
CC are cleaved by SKI-1 may be used for monitoring SKI-1 activity, for  
CC screening inhibitors of SKI-1 activity, or for screening enhancers of  
CC SKI-1 activity. Proteic fragments of SKI-1 which bind to the SKI-1  
CC catalytic site may be used as inhibitors of SKI-1 activity. They may be  
CC used to treat diseases involving overexpression of SKI-1 or SKI-1

CC substrate. Such diseases include hypercholesterolaemia, high levels of  
CC fatty acids, lipids or farnesyl pyrophosphate, liver steatosis,  
CC Ras-dependent cancer, restenosis and amyloid protein formation.

SQ Sequence 16 AA;

Query Match 100.0%; Score 48; DB 21; Length 16;

Best Local Similarity 100.0%; Pred. No. 0.0013; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISEVKMDAEF 10

DB 3 ISEVKMDAEF 12

# RESULT 8

AAE06317  
ID AAE06317 standard; peptide: 16 AA.

AC AAE06317;

DT 03-OCT-2000 (first entry)

DE Human beta-amyloid precursor protein beta-epsilon1-secretase site.

XX Human; beta-amyloid precursor protein; beta-APP;

XX beta-epsilon1-secretase; subtilisin-kexin isoenzyme 1; SKI-1;

XX pro-brain-derived neurotrophic factor; proBDNF; antilipemic;

XX cytosolic; vasotropic; SKI-1 inhibitor; hypercholesterolaemia;

XX liver steatosis; Ras-dependent cancer; restenosis;

XX amyloid protein formation.

XX Homo sapiens.

XX Key

XX Cleavage-site 8..9

XX WO200026348-A2.

XX 11-MAY-2000.

XX 04-NOV-1999; 99WO-CA01058.

XX PF 04-NOV-1999; 98CA-2249648.

XX PR 04-NOV-1998; 98CA-2249648.

XX PA (RECL-) INST RECH CLINIQUES MONTREAL.

XX PI Seidah N, Chretien M, Marcinkiewicz M, Laaksonen R, Davignon J;

XX DR WPI; 2000-365601/31.

XX PT Novel soluble proteic fragment of subtilisin-kexin isoenzyme for

XX producing a polypeptide useful for treating hypercholesterolemia, liver

XX steatosis and amyloidosis, comprises a specific amino acid sequence -

XX Example 4; Page 51; 119pp; English.

XX The present sequence is the beta-epsilon1-secretase site of human

XX beta-amyloid precursor protein (beta-APP). The sequence may be cleaved

XX by a mammalian subtilase, specifically subtilisin-kexin isoenzyme 1

XX (SKI-1), a type-1 membrane-bound proteinase. Peptides which bind to and

XX are cleaved by SKI-1 may be used for monitoring SKI-1 activity, for

XX screening inhibitors of SKI-1 activity, or for screening enhancers of

XX SKI-1 activity. Proteic fragments of SKI-1 which bind to the SKI-1

XX catalytic site may be used as inhibitors of SKI-1 activity. They may be

XX used to treat diseases involving overexpression of SKI-1 or SKI-1

XX substrate. Such diseases include hypercholesterolemia, high levels of

XX fatty acids, lipids or farnesyl pyrophosphate, liver steatosis,

XX Ras-dependent cancer, restenosis and amyloid protein formation.

XX SQ Sequence 16 AA;

XX Query Match 100.0%; Score 48; DB 21; Length 16;

XX Best Local Similarity 100.0%; Pred. No. 0.0013;

XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 1 ISEVKMDAEF 10

XX DB 1 ISEVKMDAEF 10

XX RESULT 9

XX AAE00608

XX ID AAE00608 standard; peptide: 18 AA.

XX AAE00608;

AC AAE00608;

DT 02-JUL-2001 (first entry)

DE Beta-amyloid precursor protein beta-secretase cleavage site.

XX Beta-amyloid precursor protein; beta-APP; caspase; beta-secretase;

XX cysteine protease; apoptosis; caspase expression cassette; metastasis;

XX tumour; cathepsin B; urokinase; proliferation; gene therapy;

XX interdomain linker; cleavage site; Alzheimer's disease.

XX Unidentified.

XX WO200129232-A2.

XX 26-APR-2001.

XX 19-OCT-2000; 2000WO-US28941.

XX 20-OCT-1999; 99US-0160559.

XX 14-AUG-2000; 2000US-0225564.

XX (SCIO-) SCIOS INC.

XX Cordell B, Li Y;

XX WPI; 2001-290920/30.

XX Novel fusion polypeptide comprising first and second caspase subunit

XX separated by cleavage site not associated in nature with caspase

XX subunit, useful for cloning gene encoding enzymes involved in

XX proteolytic cleavage -

XX Example 2; Page 26; 116pp; English.

XX The present sequence is a beta-secretase cleavage site of beta-amyloid

XX precursor protein (beta-APP). This sequence is used to construct

XX an artificially engineered chimeric cassette comprising human caspase-3

XX with interdomain linker replaced by Swedish mutant beta-secretase

XX cleavage site. This modified caspase-3 plays a pivotal role in

XX Alzheimer's disease. Caspases are a family of cysteine proteases, that

XX participate in the initiation and execution of apoptosis.

XX The present invention relates to a method for functional cloning of genes

XX encoding proteins or enzymes involved in proteolytic cleavage. The

XX invention is based on the use of caspase expression cassettes comprising

XX the coding sequence of a proteolytic cleavage site flanked by sequences

XX encoding two caspase subunits. A fusion polypeptide comprising a first

XX and a second caspase subunit, separated by a cleavage site not associated

XX in nature, is useful for cloning gene encoding enzymes involved in

XX proteolytic cleavage. An expression cassette containing fusion

XX polypeptide is used to identify a mutant cell line deficient in an

XX enzyme of interest and is also useful for diagnosis and suppression of

XX proliferation or metastases of a tumour cell characterised by

XX overexpression of a polypeptide (e.g. Cathepsin B or urokinase,

XX selectively expressed in the tumour cells). DNA encoding fusion

XX polypeptide is used in gene therapy.

XX SQ Sequence 18 AA;

XX Query Match 100.0%; Score 48; DB 22; Length 18;

XX Best Local Similarity 100.0%; Pred. No. 0.0015;

XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 1 ISEVKMDAEF 10

XX DB 5 ISEVKMDAEF 14

XX RESULT 10

XX AAY69713

XX ID AAY69713 standard; peptide: 20 AA.

AC AAY69713;  
 XX  
 DT 11-APR-2000 (first entry)  
 XX  
 DE Beta-APP alpha-secretase substrate [KM]-APP(-10,+10).  
 XX  
 KM Nootropic; neuroprotective; beta-amyloid precursor protein; metabolism;  
 KM cleavage site; beta-secretase; neurodegenerative disease;  
 KM Alzheimer's disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W09964587-A1.  
 XX  
 PD 16-DEC-1999.  
 XX  
 PF 04-JUN-1999; 99WO-FR01326.  
 XX  
 PR 05-JUN-1998; 98FR-0007068.  
 PR 31-MAR-1999; 99US-0122599.  
 XX  
 PA (RHON ) RHONE-POULENC RORER SA.  
 PA (UYPA-) UNITV CURIE PARIS VI P 8 M.  
 XX  
 PI Rholam M, Munoz-Gimenez N, Moutaouakil M, Cohen P, Bertrand P;  
 DR WPI; 2000-097537/08.  
 XX  
 PT Polypeptide with beta-secretase activity, specific for wild-type  
 PT amyloid precursor protein, useful in treating Alzheimer's disease -  
 XX  
 PS Example 3; Page 24; 44pp; French.  
 XX  
 CC Peptides AAY69702-Y69718 represent synthetic peptide substrates for a  
 CC novel polypeptide with beta-secretase activity that can cleave  
 CC specifically the natural beta-amyloid precursor protein (bAPP). Normal  
 CC cleavage of the protein occurs between amino acids Met596-Asp597 and  
 CC Val636-Ile637 (positions 4-5 and 44-45 of AAY69701). The novel  
 CC polypeptide is used to identify agents that interact specifically with  
 CC it. These agents regulate metabolism of APP, particularly they slow down  
 CC or reduce production of beta-amyloid, so can be used to treat  
 CC neurodegenerative diseases, particularly Alzheimer's disease.  
 CC  
 SQ Sequence 20 AA;  
 XX  
 SQ  
 Query Match 100.0%; Score 48; DB 21; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 0.0017;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 ISEVKMDAEF 10  
 |||||||||  
 DB 5 ISEVKMDAEF 14  
 |||||||||  
 RESULT 11  
 AAB75147  
 ID AAB75147 standard; peptide: 23 AA.  
 XX  
 AC AAB75147;  
 XX  
 DT 08-AUG-2001 (first entry)  
 XX  
 DE Asp 1 substrate sequence SEQ ID NO:6.  
 XX  
 KM Amyloid precursor protein; APP; Asp 1; endocrepisin 1; inhibition;  
 KM transmembrane aspartyl protease; APP Swedish variant; neurotropic;  
 KM neuroprotective; beta-secretase cleavage site; Alzheimer's disease;  
 KM beta amyloid protein-related disease; antialzheimer.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers

FT Modified-site 1  
 FT /note="N-terminally attached to maltose binding protein  
 FT (MBP)"  
 XX  
 XX W0200131054-A1.  
 XX  
 PN 03-MAY-2001.  
 XX  
 PD 19-OCT-2000; 2000MO-GB04028.  
 XX  
 PF 22-OCT-1999; 99GB-0025136.  
 XX  
 PR (SMIK ) SMITHKLINE BEECHAM PLC.  
 PA (SMIK ) SMITHKLINE BEECHAM CORP.  
 XX  
 PI Christie G, Hussain I, Powell DJ;  
 XX  
 DR WPI; 2001-328654/34.  
 XX  
 PT Identifying inhibitors of Asp 1-mediated cleavage, for treating or  
 PT preventing beta-amyloid protein-related disease, comprises measuring  
 PT the extent of substrate cleavage in a reaction system containing Asp 1  
 PT and a substrate -  
 XX  
 PS Disclosure; Page 3; 31pp; English.  
 XX  
 CC The present invention describes a method of screening for compounds  
 CC which inhibit Asp 1-mediated cleavage of a polypeptide or protein  
 CC substrate. The method comprises providing a reaction system comprising  
 CC Asp 1 and substrate, and measuring the extent of cleavage of the  
 CC substrate in the presence of test compound compared with that in the  
 CC presence of the test compound. Also described are: (1) a method of  
 CC screening for compounds which inhibit Asp 1 mediated cleavage of a  
 CC polypeptide or protein substrate comprising providing a reaction system  
 CC comprising Asp 1 and a labeled active site ligand, and measuring the  
 CC extent of binding of the labeled ligand in the presence of test compound  
 CC compared with that in the presence of the test compound; (2) a compound  
 CC identified by the method; (3) a pharmaceutical composition comprising the  
 CC compound of (2) and a carrier; (4) a method of inhibiting Asp 1 modulated  
 CC amyloid precursor protein (APP) cleavage, or treating or prophylaxis of  
 CC beta-amyloid protein-related disease, comprising administering to a  
 CC patient a compound of (2); (5) a compound which is an inhibitor of Asp 1  
 CC modulated APP cleavage; and (6) a method for treating or prophylaxis of  
 CC beta-amyloid protein-related disease comprising administering a compound  
 CC of (2) or (5). The compound which inhibits Asp 1 mediated cleavage of a  
 CC polypeptide or protein is useful in therapy, in the preparation of a  
 CC medicament for inhibiting Asp 1-modulated APP cleavage and for the  
 CC treatment or prophylaxis of beta-amyloid protein-related disease.  
 CC including Alzheimer's disease. The present sequence represents an Asp 1  
 CC substrate sequence which is given in the exemplification of the present  
 CC invention.  
 CC  
 SQ Sequence 23 AA;  
 XX  
 SQ  
 Query Match 100.0%; Score 48; DB 22; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 0.002;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 ISEVKMDAEF 10  
 |||||||||  
 DB 1 ISEVKMDAEF 10  
 |||||||||  
 RESULT 12  
 AAB97473  
 ID AAB97473 standard; Protein; 23 AA.  
 XX  
 AC AAB97473;  
 XX  
 DT 03-AUG-2001 (first entry)  
 XX  
 DE Asp2 substrate wild-type beta-site-C-terminal Q-tag fusion peptide.  
 XX

KW Asp2, endocrepisin 2; memapsin 2; beta-amyloid protein;  
 KW Alzheimer's disease; cortical Lewy body disease; Parkinson's disease;  
 KW Asp2 inhibitor.  
 XX Synthetic.  
 OS  
 FH Key Location/Qualifiers  
 FT Modified-site 1 /label= OTHER  
 FT /note= "bound to maltose binding protein"  
 XX  
 PN W0200129563-A1.  
 XX  
 XX 26-APR-2001.  
 PD  
 XX 19-OCT-2000; 2000WO-GB04039.  
 PF  
 XX 21-OCT-1999; 99GB-0024957.  
 PR  
 XX (SMIK ) SMITHKLINE BEECHAM PLC.  
 PA (SMIK ) SMITHKLINE BEECHAM CORP.  
 XX  
 PI Christie G, Hussain I, Powell DJ;  
 DR WPI; 2001-300381/31.  
 XX  
 XX Screening for inhibitors of Asp 2 mediated polypeptide cleavage  
 PT comprises measuring substrate cleavage or ligand binding with a system  
 PT comprising Asp 2 and a substrate or labelled ligand in the presence or  
 PT absence of a test compound -  
 XX  
 PS Disclosure; Page 4; 34pp; English.  
 XX  
 CC The present invention describes a method of screening for compounds which  
 CC inhibit Asp2 (also known as memapsin 2 and endocrepisin 2) mediated  
 CC cleavage of a substrate in the presence and absence of the test  
 CC compound. Asp2 is thought to be involved in the cleavage of amyloid  
 CC precursor protein which is excised to produce beta-amyloid. Beta-amyloid  
 CC is involved in the pathogenesis of Alzheimer's disease. Parkinson's  
 CC disease, cortical Lewy body disease and vascular and cerebrovascular  
 CC diseases, and Asp2 inhibitors could be useful in their treatment. The  
 CC present sequence is an example of an Asp2 substrate.  
 CC  
 XX  
 SQ Sequence 23 AA;  
 QY 1 ISEVKMDAEF 10  
 Db 1 ISEVKMDAEF 10  
 XX  
 RESULT 13  
 AAM98002  
 ID AAM98002 standard; Protein; 33 AA.  
 XX  
 AC AAM98002;  
 XX  
 DT 21-JUN-1999 (first entry)  
 XX  
 DE Amyloid precursor protein (aa656-678) with Swedish mutation.  
 XX  
 KW Amyloid precursor protein; APP; human; gene targeting;  
 KW homologous recombination; transgenic mouse; transgenic animal;  
 KW animal model; Alzheimer's disease.  
 XX  
 OS Mus musculus.  
 XX  
 XX W09909150-A1.  
 PN  
 XX

PD 25-FEB-1999.  
 XX  
 PF 18-AUG-1997; 97WO-US14507.  
 XX  
 PR 18-AUG-1997; 97WO-US14507.  
 XX  
 PA (FARR ) BAYER CORP.  
 XX  
 PI Mirak DO;  
 XX  
 DR WPI; 1999-181029/15.  
 XX  
 XX Modification of target nucleic acids - by homologous recombination,  
 PT used particularly for introducing a humanized amyloid precursor  
 PT protein gene into rodents for producing models of Alzheimer's  
 PT disease  
 XX  
 PS Disclosure; Page 145; 209pp; English.  
 XX  
 CC This polypeptide comprises residues 656-678 of a murine amyloid  
 CC precursor protein (APP). The invention provides a novel gene  
 CC targeting strategy that facilitates the introduction of one or  
 CC more specific mutations into any gene in a single double reciprocal  
 CC homologous recombination step. The method has been used  
 CC particularly for introducing a humanised APP gene into rodents for  
 CC producing animal models of Alzheimer's disease (AD). 4 independent  
 CC lines of transgenic mice (lines ES5007, ES5103, ES5401 and ES5403)  
 CC have been created using the gene targeting technique applied to  
 CC embryonic stem cells. In each line, the mouse APP gene was modified  
 CC to encode a mouse/human hybrid (m/hAPP) where amino acid residues  
 CC 666-770 of APP770 were encoded by human cDNA sequences instead of  
 CC mouse genomic exons (exons 16-18). Within these residues, only 3  
 CC amino acid differences exist between the mouse and human proteins,  
 CC i.e. Gly-676 to Arg, Phe-681 to Thr and Arg-684 to His. The  
 CC exon-cDNA fusion gene therefore encodes an APP containing a  
 CC humanised beta-amyloid domain. Swedish- and/or London-FAD APP  
 CC mutations have also been introduced (see also AAM97997-W98001).  
 CC  
 XX  
 SQ Sequence 33 AA;  
 QY 1 ISEVKMDAEF 10  
 Db 11 ISEVKMDAEF 20  
 XX  
 ID AAY69717 standard; peptide; 39 AA.  
 XX  
 AC AAY69717;  
 XX  
 DT 11-APR-2000 (first entry)  
 XX  
 DE Beta-APP alpha-secretase substrate [KM]-APP(-20,+20).  
 XX  
 KW Nootropic; neuroprotective; beta-amyloid precursor protein; metabolism;  
 KW cleavage site; beta-secretase; neurodegenerative disease;  
 KW Alzheimer's disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W09964587-A1.  
 XX  
 PD 16-DEC-1999.  
 XX  
 XX 04-JUN-1999; 99WO-FR01326.  
 XX  
 PF 05-JUN-1998; 98FR-0007068.  
 PR 31-MAR-1999; 99US-0122599.  
 XX

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XX (RHON ) RHONE-POULENC, RORER SA.
PA (UYRA-) UNIV CURIE PARIS VI P & M.
XX
XX Rhojam M, Munoz-Glamez N, Moutaouakil M, Cohen P, Bertrand P;
PI WPI; 2000-097537/08.
XX
XX Polypeptide with beta-secretase activity, specific for wild-type
PT amyloid precursor protein, useful in treating Alzheimer's disease -
XX
XX Example 3; Page 24; 44pp; French.
XX
XX Peptides AAV69702-Y69718 represent synthetic peptide substrates for a
CC novel polypeptide with beta-secretase activity that can cleave
CC specifically the natural beta-amyloid precursor protein (BAP). Normal
CC cleavage of the protein occurs between amino acids Met596-Asp597 and
CC Val636-Ile637 (positions 4-5 and 44-45 of AAV69701). The novel
CC polypeptide is used to identify agents that interact specifically with
CC it. These agents regulate metabolism of APP, particularly they slow down
CC or reduce production of beta-amyloid, so can be used to treat
CC neurodegenerative diseases, particularly Alzheimer's disease.
XX
SQ Sequence 39 AA;
Query Match 100.0%; Score 48; DB 21; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.0037;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ISEVKMDAEF 10
Db 14 ISEVKMDAEF 23

```

RESULT 15

```

AAW26512
ID AAW26512 standard; Peptide: 45 AA.
XX
XX AAW26512;
AC
XX
XX 06-JAN-1998 (first entry)
DE Amyloid precursor protein fragment APP-REP 751 (BAP del11-28).
XX
XX Amyloid precursor protein; APP; beta-amyloid protein; BAP;
KW substrate; muten; secretase; Alzheimer's disease; human.
XX
XX Chimeric Homo sapiens.
OS Chimeric synthetic.
XX
XX Key Location/Qualifiers
FH Cleavage-site 7..8
FT /note= "secretase cleavage site"
FT Peptide 10..33
FT /label= BAP(del11-28)
FT /note= "truncated beta-amyloid protein"
FT Domain 20..42
FT /label= Transmembrane
XX
XX US5656477-A.
XX
XX 12-AUG-1997.
XX
XX 01-MAY-1992; 92US-0877675.
XX
XX 20-SEP-1993; 93US-0123659.
XX
XX 01-MAY-1992; 92US-0877675.
XX
XX (AMCY ) AMERICAN CYANAMID CO.
XX
XX Jacobsen JS, Vitek MP;
XX
XX WPI; 1997-414594/38.

```

```

XX Nucleic acid encoding amyloid precursor muten(s) - comprising
PT reporter gene and coding sequence, for identifying compounds which
PT modify the activity of proteolytic enzymes which cleave APP
XX
XX Disclosure; Fig 5A; 84pp; English.
XX
XX This peptide sequence shows the region of amyloid precursor protein
CC (APP) that includes a truncated beta-amyloid protein (BAP) lacking
CC the native secretase cleavage/recognition site. In an attempt to
CC engineer an APP non-cleavable substrate for secretase, an
CC APP-reporter (APP-REP) protein that carries the BAP deletion has
CC been expressed in recombinant host cells. Deletion of these 18
CC amino acids, however, still resulted in the secretion of an
CC N-terminal APP-reporter fragment into the cytoplasm. Non-
CC cleavable APP substrates can be used to detect other putative
CC abnormal APP processing events. They can also be used to
CC investigate cellular post-translational modifications to APP in
CC order to determine the potential influence on normal secretase and
CC abnormal BAP 'clipping' activities.
XX
SQ Sequence 45 AA;
Query Match 100.0%; Score 48; DB 18; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.0044;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ISEVKMDAEF 10
Db 4 ISEVKMDAEF 13

```

Search completed: October 29, 2002, 10:26:43  
Job time : 24.1429 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 29, 2002, 10:23:36 ; Search time 10.4286 Seconds  
(without alignments)  
92.140 Million cell updates/sec

Title: US-09-580-018-3  
Perfect score: 48  
Sequence: 1 ISEVKMDAEF 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR-71:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	100.0	82	P00438	Alzheimer's disease
2	48	100.0	695	A49795	Alzheimer's disease
3	48	100.0	695	A27485	Alzheimer's disease
4	48	100.0	695	S00550	Alzheimer's disease
5	48	100.0	770	ORH04	Alzheimer's disease
6	44	91.7	33	S23094	beta-amyloid prote
7	44	91.7	57	E60045	Alzheimer's disease
8	44	91.7	57	F60045	Alzheimer's disease
9	44	91.7	57	G60045	Alzheimer's disease
10	44	91.7	57	D60045	Alzheimer's disease
11	44	91.7	57	A60045	Alzheimer's disease
12	44	91.7	57	B60045	Alzheimer's disease
13	42	87.5	747	JH0773	Alzheimer's disease
14	34	70.8	142	E89026	hypothetical prote
15	34	70.8	400	E69446	conserved hypotet
16	34	70.8	626	AF0358	transcription anti
17	34	70.8	700	E84131	chondroitin sulfat
18	34	70.8	3562	A47171	hypothetical prote
19	33	68.8	242	C96606	NBDH dehydrogenase
20	33	68.8	389	G84245	accessory coloniza
21	33	68.8	626	E82273	conserved hypotet
22	32	66.7	261	C64572	hypothetical prote
23	32	66.7	261	F71867	taurine transport
24	32	66.7	281	AH3629	hypothetical prote
25	32	66.7	282	T26112	hypothetical prote
26	32	66.7	347	T31922	PMO-protein - Chlo
27	32	66.7	354	S51143	44.7K vira protein
28	32	66.7	400	S70187	probable trehalase
29	32	66.7	426	G75187	

30	32	66.7	470	2	C75591	threonine synthase
31	32	66.7	793	2	T27133	hypothetical prote
32	32	66.7	929	2	T52517	hypothetical prote
33	32	66.7	941	2	B96553	hypothetical prote
34	32	66.7	1378	2	G88637	protein F53H1.4 11
35	32	66.7	1456	1	WMGCPV	RNA-directed RNA p
36	32	66.7	1906	2	AD2443	hypothetical prote
37	32	66.7	4563	1	LPHUB	apolipoprotein B-1
38	31	64.6	84	2	T27174	hypothetical prote
39	31	64.6	105	2	PH1526	gamma-aminobutyric
40	31	64.6	178	2	G64168	hypothetical prote
41	31	64.6	182	2	AC0449	conserved hypotet
42	31	64.6	182	2	B97000	hypothetical prote
43	31	64.6	183	2	S56460	probable alpha hel
44	31	64.6	183	2	C91280	probable alpha hel
45	31	64.6	183	2	C86121	probable alpha hel

## ALIGNMENTS

## RESULT 1

P00438 Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)

C:Species: Oryctolagus cuniculus (domestic rabbit)

C>Date: 30-Sep-1993 #sequence\_revision 19-Oct-1995 #text\_change 19-Oct-1995

C:Accession: P00438; C60045

R:Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.E.

Biochem. Biophys. Res. Commun. 188, 905-911, 1992

A>Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precurs

A:Reference number: P00438; MUID:93075180

A:Accession: P00438

A:Molecule type: DNA

A:Residues: 1-82 <DAV>

A:Cross-references: GB:M83558; GB:M83657

R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A>Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d

A:Reference number: A60045; MUID:92017079

A:Accession: C60045

A:Molecule type: mRNA

A:Residues: 12-68 <JOB>

A:Cross-references: EMBL:X56129

C:Superfamily: Alzheimer's disease amyloid beta protein: animal Knittz-type proteinas

C:Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match 100.0%; Score 48; DB 2; Length 82;

Best Local Similarity 100.0%; Pred. No. 0.0043;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ISEVKMDAEF 10  
DB 11 ISEVKMDAEF 20

## RESULT 2

A49795 Alzheimer's disease amyloid beta protein precursor - crab-eating macaque

C:Species: Macaca fascicularis (crab-eating macaque)

C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999

C:Accession: A49795

R:Podlisy, M.B.; Tolan, D.R.; Selkoe, D.J.

Am. J. Pathol. 138, 1423-1435, 1991

A>Title: Homology of the amyloid beta protein precursor in monkey and human supports

A:Reference number: A49795; MUID:91273117

A:Accession: A49795

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-695 <POD>

A:Cross-references: GB:M58727; NID:g342062; PIDN:AAA36829.1; PTD:g342063

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Knittz-type proteinas

C:Keywords: alternative splicing

Query Match 100.0%; Score 48; DB 1; Length 695;  
 Best Local Similarity 100.0%; Pred. No. 0.048;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ISEVKMDAEF 10  
 |||||||||  
 Db 591 ISEVKMDAEF 600

## RESULT 3

A27485

Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse

N:Alternate names: proteinase nexin II

C:Species: Mus musculus (house mouse)

C:Date: 31-Mar-1989 #sequence revision 31-Mar-1989 #text change 13-Aug-1999

C:Accession: A27485; S19727; I49485

R:Yamada, T.; Sasaki, H.; Futuya, H.; Miyata, T.; Goto, I.; Sasaki, Y.

Biochem. Biophys. Res. Commun. 149, 665-671, 1987

A:Title: Complementary DNA for the mouse homolog of the human amyloid beta protein precursor

A:Reference number: A27485; MUID:88106489

A:Accession: A27485

A:Molecule type: mRNA

A:Residues: 1-695 <XAM>

A:Cross-references: GB:M18373; NID:9191568; PIDN:AAA37139.1; PID:9309085

A:Experimental source: brain

R:de Strooper, B.; van Leeuwen, F.; van den Berghe, H.

Biochim. Biophys. Acta 1129, 141-143, 1991

A:Title: The amyloid beta protein precursor or proteinase nexin II from mouse is closer

A:Reference number: S19727; MUID:92096458

A:Accession: S19727

A:Molecule type: mRNA

A:Residues: 1-210, G', 212-220, 'S', 222-396, 'A', 398-402, 'T', 404-448, 'A', 450-695 <STR>

A:Cross-references: EMBL:X59379

R:izumi, R.; Yamada, T.; Yoshikaki, S.; Sasaki, H.; Hatton, M.; Sasaki, Y.

Gene 112, 189-195, 1992

A:Title: Positive and negative regulatory elements for the expression of the Alzheimer's

A:Reference number: I49485; MUID:92209998

A:Accession: I49485

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-19 <RRS>

A:Cross-references: GB:J010603; NID:9220328; PIDN:BAA01456.1; PID:9220329

C:Genetics:

A:Map position: 16C3

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase I

C:Keywords: alternative splicing; amyloid; transmembrane protein

Query Match 100.0%; Score 48; DB 2; Length 695;

Best Local Similarity 100.0%; Pred. No. 0.048;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ISEVKMDAEF 10  
 |||||||||  
 Db 591 ISEVKMDAEF 600

## RESULT 4

S00550

Alzheimer's disease amyloid beta protein precursor - rat

N:Alternate names: beta-A4 amyloid protein

C:Species: Rattus norvegicus (Norway rat)

C:Date: 30-Jun-1989 #sequence revision 30-Jun-1989 #text change 13-Aug-1999

C:Accession: S00550; A1245; A39820; S46251

R:Shivers, B.D.; Hilbich, C.; Multhaup, G.; Salbaum, M.; Beyreuther, K.; Seeburg, P.H.

EMBO J. 7, 1365-1370, 1988

A:Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan co

A:Reference number: A1245; MUID:88264430

A:Accession: A1245

A:Molecule type: protein

A:Residues: 18-37, 'X', 39-40, 'X', 42-44 <SCH>

A:Note: evidence for heparan sulfate attachment

R:Hesse, L.; Behr, D.; Masters, C.L.; Multhaup, G.

FEBS Lett. 349, 109-116, 1994

A:Title: The beta-A4 amyloid precursor protein binding to copper.

A:Reference number: S46251; MUID:94320627

A:Contents: annotation; copper binding sites

A:Note: rat peptides were isolated but not sequenced

R:Tompa, A.; Styles, J.; Mehta, P.; Kim, K.S.; Miller, D.L.

J. Biol. Chem. 266, 8464-8469, 1991

A:Title: Purification and tissue level of the beta-amyloid peptide precursor of rat b

A:Reference number: A39820; MUID:91217087

A:Accession: A39820

A>Status: preliminary

A:Molecule type: protein

A:Residues: 18-32 <POT>

A:Experimental source: brain

C:Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques is

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase

C:Keywords: alternative splicing; amyloid; glycoprotein; transmembrane protein

F:625-648/Domain: transmembrane #status predicted <TM>

Query Match 100.0%; Score 48; DB 2; Length 695;

Best Local Similarity 100.0%; Pred. No. 0.048;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ISEVKMDAEF 10  
 |||||||||  
 Db 591 ISEVKMDAEF 600

## RESULT 5

ORNU4

Alzheimer's disease amyloid beta protein precursor [validated] - human

N:Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor Xla inh

N:Contains: amyloid beta protein long; plaque form; amyloid beta protein short; vascu

protein precursor splice form APP(770)

C:Species: Homo sapiens (man)

C:Date: 30-Jun-1987 #sequence revision 28-Jul-1995 #text change 15-Sep-2000

C:Accession: S02260; S05194; A32277; A33260; A35486; I39452; I39453; I39454;

4668; A28583; A29362; A60805; J10038; S06121; A60355; A5011; A38384; S29076; S38252;

R:Jemire, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.;

Nucleic Acids Res. 17, 517-522, 1989

A:Title: The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid is encode

A:Reference number: S02260; MUID:89128427

A:Accession: S02260

A:Molecule type: DNA

A:Residues: 1-288, 'V', 365-770 <LEM1>

A:Cross-references: EMBL:X13466

A:Note: alternative splice form APP(695)

R:Jemire, H.G.

submitted to the EMBL Data Library, November 1988

A:Reference number: S05194

A:Accession: S05194

A:Molecule type: DNA

A:Residues: 1-14, 'W', 17-288, 'V', 365-770 <LEM2>

A:Cross-references: GB:M24546; GB:M24547; NID:9341202; PIDN:AC13654.1; PID:9516074

A:Note: alternative splice form APP(695)

R:Jemire, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.;

Nucleic Acids Res. 17, 517-522, 1989

A:Title: Characterization of the 5'-end region and the first two exons of the beta-pr

A:Reference number: A32277; MUID:89165870

A:Accession: A32277

A:Molecule type: DNA

A:Residues: 1-75 <LAF>

A:Cross-references: GB:M24546; GB:M24547; NID:9341202; PIDN:AC13654.1; PID:9516074

A:Note: alternative splice form APP(695)

R:Jemire, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.;

Nucleic Acids Res. 17, 517-522, 1989

A:Title: Characterization of the 5'-end region and the first two exons of the beta-pr

A:Reference number: A32277; MUID:89165870

A:Accession: A32277

A:Molecule type: DNA

A:Residues: 1-75 <LAF>

A:Cross-references: GB:M24546; GB:M24547; NID:9341202; PIDN:AC13654.1; PID:9516074

A:Note: alternative splice form APP(695)

R:Jemire, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.;

Nucleic Acids Res. 17, 517-522, 1989

A:Title: Characterization of the 5'-end region and the first two exons of the beta-pr

A:Reference number: A32277; MUID:89165870

A:Accession: A32277

A:Molecule type: DNA

A:Residues: 1-75 <LAF>

A:Cross-references: GB:M24546; GB:M24547; NID:9341202; PIDN:AC13654.1; PID:9516074

A:Note: alternative splice form APP(695)

R:Jemire, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.;

Nucleic Acids Res. 17, 517-522, 1989

A:Title: Characterization of the 5'-end region and the first two exons of the beta-pr

A:Reference number: A32277; MUID:89165870

A:Accession: A32277

A:Molecule type: DNA

A:Residues: 1-75 <LAF>

A:Cross-references: GB:M24546; GB:M24547; NID:9341202; PIDN:AC13654.1; PID:9516074

A:Note: alternative splice form APP(695)

R:Jemire, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.;

Nucleic Acids Res. 17, 517-522, 1989

A:Title: Characterization of the 5'-end region and the first two exons of the beta-pr

A:Reference number: A32277; MUID:89165870

A:Accession: A32277

A:Molecule type: DNA

A:Residues: 1-75 <LAF>

A:Cross-references: GB:M24546; GB:M24547; NID:9341202; PIDN:AC13654.1; PID:9516074

A:Note: alternative splice form APP(695)

R:Jemire, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.;

Nucleic Acids Res. 17, 517-522, 1989

A:Title: Characterization of the 5'-end region and the first two exons of the beta-pr

A:Reference number: A32277; MUID:89165870

A:Accession: A32277

A:Molecule type: DNA

A:Residues: 1-75 <LAF>

A:Reference number: A33260; MUID:89392030  
 A:Accession: A33260  
 A:Molecule type: DNA  
 A:Residues: 656-737 <TOH>  
 A:Cross-references: GB:M29270; NID:q178663; PIDN:AAA51768.1; PID:q178665  
 R:Prelli, F.; Levy, E.; van Duren, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B.  
 Biochem. Biophys. Res. Commun. 170, 301-307, 1990  
 A:Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid of  
 A:Reference number: A35486; MUID:90321244  
 A:Accession: A35486  
 A:Molecule type: DNA  
 A:Residues: 672-710 <PRE1>  
 A:Note: 693-Gln was found in DNA isolated from HCHMA-D patients  
 R:Yoshikaki, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.  
 Gene 87, 257-263, 1990  
 A:Title: Genomic organization of the human amyloid beta-protein precursor gene.  
 A:Reference number: 139451; MUID:90236318  
 A:Accession: 139452  
 A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMH  
 A:Molecule type: DNA  
 A:Residues: 1-770 <YOS1>  
 A:Cross-references: GB:M33112; NID:q178613; PIDN:AA559502.1; PID:q178616  
 A:Accession: 139451  
 A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMH  
 A:Molecule type: DNA  
 A:Residues: 1-530, 'QMTMPVTPAPFEAKVGR' <YOS2>  
 A:Cross-references: GB:M34875; NID:q178608; PIDN:AA559501.1; PID:q178615  
 R:Yoshikaki, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.  
 Gene 102, 291-292, 1991  
 A:Reference number: A59020; MUID:91340168  
 A:Accession: 139453  
 A:Contents: annotation; extratum  
 A:Note: revised physical map for reference 139451  
 R:Levy, E.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van Dine  
 Science 248, 1124-1126, 1990  
 A:Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemorrh  
 A:Reference number: 139453; MUID:90260663  
 A:Accession: 139453  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 656-737 <LEV>  
 A:Cross-references: GB:M37896; NID:q178618; PIDN:AAA51727.1; PID:q178620  
 A:Note: a mutation with 693-Gln is presented  
 R:Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.  
 Science 254, 97-99, 1991  
 A:Title: A mutation in the amyloid precursor protein associated with hereditary Alzheim  
 A:Reference number: 159562; MUID:92022553  
 A:Accession: 159562  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 689-716, 'F', 718-737 <MUR>  
 A:Cross-references: GB:S57665; NID:q236720; PIDN:AA81991.1; PID:q236721  
 R:Ramano, K.; Orr, H.T.; Payami, H.; Wjisman, E.M.; Alonso, M.E.; Pulst, S.M.; Anderson,  
 arakis, S.E.; Korenberg, J.R.; Sharma, V.; Kukulski, W.; Larson, E.; Heston, L.L.; Martin,  
 Am. J. Hum. Genet. 51, 998-1014, 1992  
 A:Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for the  
 A:Reference number: AA4017; MUID:93035397  
 A:Accession: AA4017  
 A:Molecule type: DNA  
 A:Residues: 687-692, 'G', 694-718 <KAM1>  
 A:Cross-references: GB:S45136; NID:q257379; PIDN:AA23646.1; PID:q257380  
 A:Experimental source: familial Alzheimer disease family LT  
 A:Note: sequence extracted from NCBI backbone (NCBIF:115376)  
 R:Kang, J.; Lemire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grieschik, K.H.;  
 Nature 325, 733-736, 1987  
 A:Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surfac  
 A:Reference number: A05134; MUID:87144572

A:Accession: A03134  
 A:Molecule type: mRNA  
 A:Residues: 1-288, 'V', 365-770 <KAN>  
 A:Cross-references: GB:X00264; NID:q28525; PIDN:CAA68374.1; PID:q28526  
 A:Note: alternative splice form APP(695)  
 R:Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.  
 Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987  
 A:Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascula  
 A:Reference number: A29030; MUID:87231971  
 A:Accession: A29030  
 A:Molecule type: mRNA  
 A:Residues: 284-288, 'V', 365-646, 'E', 648-770 <ROB>  
 A:Cross-references: GB:M16765; NID:q178539; PIDN:AAA51722.1; PID:q178540  
 A:Note: the authors translated the codon GAG for residue 647 as Asp  
 R:Goldhaber, D.; Lemman, M.I.; McBride, O.W.; Saffioti, U.; Gajdusek, D.C.  
 Science 235, 877-880, 1987  
 A:Title: Characterization and chromosomal localization of a cDNA encoding brain amylo  
 A:Reference number: A47584; MUID:87120328  
 A:Accession: A47584  
 A:Molecule type: mRNA  
 A:Residues: 674-756, 'S', 758-770 <GOL>  
 A:Cross-references: GB:M15533; NID:q178706; PIDN:AAA5540.1; PID:q178707  
 A:Experimental source: Drlan  
 R:Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van  
 Science 235, 880-884, 1987  
 A:Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near  
 A:Reference number: A47585; MUID:87120329  
 A:Accession: A47585  
 A:Molecule type: mRNA  
 A:Residues: 674-703 <TANI>  
 A:Cross-references: GB:M15532; NID:q177957; PIDN:AAA51564.1; PID:q177958  
 R:Dyck, T.; Weldmann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Mue  
 EMBO J. 7, 949-957, 1988  
 A:Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 p  
 A:Reference number: S02638; MUID:8826437  
 A:Accession: S02638  
 A:Molecule type: mRNA  
 A:Residues: 672-678 <DYR>  
 R:Tanzi, R.E.; McClatchey, A.I.; Lampert, E.D.; Villa-Komaroff, L.; Gusella, J.F.; N  
 Nature 331, 528-529, 1988  
 A:Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA assoc  
 A:Reference number: S00707; MUID:88122640  
 A:Accession: S00707  
 A:Molecule type: mRNA  
 A:Residues: 286-344, 'I', 365-366 <TAN2>  
 A:Cross-references: EMBL:X06982; NID:q28817; PIDN:CAA30042.1; PID:q929612  
 A:Experimental source: EMBL:promyelocytic leukemia cell line HL60  
 A:Note: alternative splice form APP(751)  
 R:Ponte, P.; Gonzalez-Demhilt, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.;  
 Nature 331, 525-527, 1988  
 A:Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhi  
 A:Reference number: S00925; MUID:88122639  
 A:Accession: S00925  
 A:Molecule type: mRNA  
 A:Residues: 1-344, 'I', 365-770 <PO2>  
 A:Cross-references: GB:X06989; EMBL:X00297; NID:q28720; PIDN:CAA30050.1; PID:q28721  
 A:Note: alternative splice form APP(751)  
 R:Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.  
 Nature 331, 530-532, 1988  
 A:Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibi  
 A:Reference number: A38949; MUID:88122641  
 A:Accession: A38949  
 A:Molecule type: mRNA  
 A:Residues: 287-367 <KIT>  
 A:Cross-references: GB:X06981; NID:q28816; PIDN:CAA30041.1; PID:q929611  
 A:Experimental source: fibroblastoma cell line  
 A:Note: alternative splice form APP(770)  
 R:Vitek, M.P.; Rasooli, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ash  
 Brain Res. Mol. Brain Res. 4, 121-131, 1988  
 A:Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of thre  
 A:Reference number: A30320  
 A:Accession: A30320  
 A:Status: not compared with conceptual translation

Query Match	100.0%	Score 48	DB 1	Length 770
Best Local Similarity	100.0%	Pred. No. 0.054		
Matches	10	Conservative	0	Mismatches 0
				Indels 0
				Gaps 0
QY	1	ISEVKMDAEF	10	
db	666	ISEVKMDAEF	675	

```

Query March      91.7%: Score 44: DB 2: Length 33:
Best Local Similarity 100.0%: Pred. No. 0 011:
Matches      9: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY      2 SEVKMDAEF 10
          |||||||
Db      1 SEVKMDAEF 9

```

Query Match	91.7%;	Score 44;	DB 2;	Length 57;
Best Local Similarity	100.0%;	Pred. No. 0.021;		
Matches	9;	Conservative	0;	Mismatches 0;
Indels	0;	Gaps	0;	

QY 2 SEVKMDAEF 10  
|||||  
Db 1 SEVKMDAEF 9

RESULT 8  
F60045 Alzheimer's disease amyloid beta/A4 protein precursor - pig (fragment)  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 13-Aug-1999  
C:Accession: F60045  
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
Brain Res. Mol. Brain Res. 10, 299-305, 1991  
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d  
A:Reference number: A60045; MUID:92017079  
A:Accession: F60045  
A:Molecule type: mRNA  
A:Residues: 1-57 <JOH>  
A:Cross-references: EMBL:X56127; NID:91895; PIDN:CAA39592.1; PID:91896  
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase  
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 91.7%; | Score 44; | DB 2; | Length 57; || Best Local Similarity | 100.0%; | Pred. No. 0.021; |  |  |
| Matches | 9; | Conservative | 0; | Mismatches 0; |
| Indels | 0; | Gaps | 0; |  |

QY 2 SEVKMDAEF 10  
|||||  
Db 1 SEVKMDAEF 9

RESULT 9  
G60045 Alzheimer's disease amyloid beta/A4 protein precursor - guinea pig (fragment)  
C:Species: Cavia porcellus (guinea pig)  
C:Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 28-Jul-1995  
C:Accession: G60045  
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
Brain Res. Mol. Brain Res. 10, 299-305, 1991  
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d  
A:Reference number: A60045; MUID:92017079  
A:Accession: G60045  
A:Molecule type: mRNA  
A:Residues: 1-57 <JOH>  
A:Cross-references: EMBL:X56126  
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase  
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 91.7%; | Score 44; | DB 2; | Length 57; || Best Local Similarity | 100.0%; | Pred. No. 0.021; |  |  |
| Matches | 9; | Conservative | 0; | Mismatches 0; |
| Indels | 0; | Gaps | 0; |  |

QY 2 SEVKMDAEF 10  
|||||  
Db 1 SEVKMDAEF 9

RESULT 10  
D60045 Alzheimer's disease amyloid beta/A4 protein precursor - bovine (fragment)  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 28-Jul-1995  
C:Accession: D60045  
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
Brain Res. Mol. Brain Res. 10, 299-305, 1991  
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d  
A:Reference number: A60045; MUID:92017079  
A:Accession: D60045

A:Residues: 1-57 <JOH>  
 A:Cross-references: EMBL:X56124  
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase  
 C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match  
 Best Local Similarity 100.0%; Score 44; DB 2; Length 57;  
 Pred. No. 0.021; Mismatches 0; Indels 0; Gaps 0;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 SEVKMDAEF 10  
 |||||  
 Db 1 SEVKMDAEF 9

RESULT 11  
 A60045

Alzheimer's disease amyloid beta/M protein precursor - dog (fragment)

C:Species: Canis lupus familiaris (dog)  
 C>Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 28-Jul-1995

C:Accession: A60045  
 R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog;  
 A:Reference number: A60045; MUID:92017079

A:Accession: A60045  
 A:Molecule type: mRNA  
 A:Residues: 1-57 <JOH>

A:Cross-references: EMBL:X56125

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase  
 C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match  
 Best Local Similarity 100.0%; Score 44; DB 2; Length 57;  
 Pred. No. 0.021; Mismatches 0; Indels 0; Gaps 0;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 SEVKMDAEF 10  
 |||||  
 Db 1 SEVKMDAEF 9

RESULT 12  
 B60045

Alzheimer's disease amyloid beta/A4 protein precursor - polar bear (fragment)

C:Species: Ursus maritimus (polar bear)  
 C>Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 13-Aug-1999

C:Accession: B60045  
 R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog;  
 A:Reference number: A60045; MUID:92017079

A:Accession: B60045  
 A:Molecule type: mRNA  
 A:Residues: 1-57 <JOH>

A:Cross-references: EMBL:X56128; NID:92165; PIDN:CAA3593.1; PID:92166

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase  
 C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match  
 Best Local Similarity 100.0%; Score 44; DB 2; Length 57;  
 Pred. No. 0.021; Mismatches 0; Indels 0; Gaps 0;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 SEVKMDAEF 10  
 |||||  
 Db 1 SEVKMDAEF 9

RESULT 13  
 JH0773

Alzheimer's disease amyloid beta protein precursor - African clawed frog

C:Species: Xenopus laevis (African clawed frog)

C>Date: 10-Jun-1993 #sequence\_revision 10-Jun-1993 #text\_change 13-Aug-1999

C:Accession: JH0773  
 R:Okado, H.; Okamoto, H.

Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992  
 A:Title: A Xenopus homolog of the human beta-amyloid precursor protein: development  
 A:Reference number: JH0773; MUID:93129227

A:Accession: JH0773  
 A:Molecule type: mRNA  
 A:Residues: 1-747 <OKA>

A:Cross-references: GB:S52417; NID:9263150; PIDN:AA824853.1; PID:9263151

A:Experimental source: larva

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase  
 C:Keywords: alternative splicing; amyloid  
 F:287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match  
 Best Local Similarity 87.5%; Score 42; DB 2; Length 747;  
 Pred. No. 1; Mismatches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 ISEVKMDAEF 10  
 |||||  
 Db 643 ISEVKMDSEY 652

RESULT 14  
 E89026

protein F13A2.1 [imported] - Caenorhabditis elegans

C:Species: Caenorhabditis elegans  
 C>Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 10-May-2001

C:Accession: E89026  
 R:Anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998  
 A:Title: Genome sequence of the nematode C. elegans: a platform for investigating bio

A:Reference number: A75000; MUID:99066613; PMID:9851916  
 A:Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C\_

A:Accession: E89026  
 A:Status: preliminary  
 A:Molecule type: DNA

A:Residues: 1-142 <STO>

A:Cross-references: GB:chr\_V; PIDN:AA869895.1; PID:92384795; GSPDB:GN00023; CESP:F13A  
 A:Gene: F13A2.1  
 A:Map position: 5

Query Match  
 Best Local Similarity 70.8%; Score 34; DB 2; Length 142;  
 Pred. No. 8.1; Mismatches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 EVKMDAEF 10  
 |||||  
 Db 56 EIKQDAEF 63

RESULT 15  
 E69446

hypothetical protein AF1574 - Archaeoglobus fulgidus

C:Species: Archaeoglobus fulgidus  
 C>Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 24-Nov-1999

C:Accession: E69446  
 R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod

; Fleischmann, R.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E  
 Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.

Nature 390, 364-370, 1997  
 A:Authors: Overbeek, T.; Cotton, M.D.; Spriggs, T.; Artlich, P.; Kaine, B.P.; Skyes,

Smith, H.O.; Woese, C.R.; Venter, J.C.  
 A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch

A:Reference number: A69250; MUID:98049343  
 A:Accession: E69446  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA  
 A:Residues: 1-400 <KIB>

A:Cross-references: GB:AF000994; GB:AF000782; NID:92689317; PIDN:AA889681.1; PID:9264  
 C:Superfamily: Archaeoglobus fulgidus hypothetical protein AF1574

Query Match  
 70.8%; Score 34; DB 2; Length 400;

Tue Oct 29 11:23:30 2002

us-09-580-018-3.rpr

Page 6

Best Local Similarity 70.0%; Pred. No. 25;  
Matches 7; Conservative 2; Mismatches

1; Indels

0; Gaps 0;

QY 1 ISEVKMDAEF 10  
|:|:|:|  
Db 143 ITEVKVKAEP 152

Search completed: October 29, 2002, 10:31:00  
Job Time : 12.4286 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Comphen Ltd.

OK protein - protein search, using sw model

Run on: October 29, 2002, 10:22:36 ; Search time 5 Seconds  
(without alignments)  
77.439 Million cell updates/sec

Title: US-09-580-018-3  
Perfect score: 48  
Sequence: 1 ISEVKMDAEF 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 segs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	48	100.0	58 1 A4_CANFA	Q28380 canis faml
2	48	100.0	59 1 A4_BOVIN	Q28053 bos taurus
3	48	100.0	751 1 A4_SAISC	Q95241 salmili sci
4	48	100.0	770 1 A4_HUMAN	P05067 homo sapien
5	48	100.0	770 1 A4_MOUSE	P12023 mus musculi
6	48	100.0	770 1 A4_RAT	P08592 rattus norv
7	44	91.7	57 1 A4_PIG	Q29023 sus scrofa
8	44	91.7	57 1 A4_URSUMA	Q29149 ursus marit
9	44	91.7	58 1 A4_RABIT	Q28748 oryctolagus
10	44	91.7	58 1 A4_SHEEP	Q28757 ovis aries
11	34	70.8	400 1 YF74_ARCFU	Q28698 archaeoglob
12	34	70.8	3562 1 PGCV_CHICK	Q90953 gallus gall
13	32	66.7	269 1 T2S1_STREI	O52512 streptomyce
14	32	66.7	354 1 BCPIA_CHILT	Q46135 chlorobium
15	32	66.7	365 1 BCPIA_CHILT	Q46393 chlorobium
16	32	66.7	1456 1 RRPO_PVX	P09395 potato vitu
17	32	66.7	1456 1 RRPO_PVX3	P17779 potato vitu
18	32	66.7	4563 1 APB_HUMAN	P04114 homo sapien
19	31	64.6	178 1 YJGA_HAELI	P45076 haemophilus
20	31	64.6	183 1 YJGA_ECOLI	P26550 escherichia
21	31	64.6	363 1 R1BB_PHOPO	P51562 photobacter
22	31	64.6	419 1 P47K_PSECL	P31521 pseudomonas
23	31	64.6	1017 1 MCM6_YEAST	P53091 saccharomyc
24	31	64.6	1024 1 Y075_MYCGE	P47321 mycoplasma
25	30	62.5	112 1 RBFA_MYCGE	P47389 mycoplasma
26	30	62.5	127 1 ILBP_PIG	P10289 sus scrofa
27	30	62.5	187 1 TRE1_SALTI	P12057 salmoneila
28	30	62.5	261 1 YN10_ARCFU	O27974 archaeoglob
29	30	62.5	265 1 YGL7_YEAST	P53133 saccharomyc
30	30	62.5	304 1 PH85_KLILA	O92241 kluyveromyc
31	30	62.5	305 1 PH85_YEAST	P17157 saccharomyc
32	30	62.5	463 1 YD14_SCHPO	O92342 schizosacch
33	30	62.5	464 1 SPN5_SCHPO	P48010 schizosacch

34	30	62.5	656 1 V091_FOWPV	O72896 fowlpox vir
35	30	62.5	855 1 HAUS_YEAST	P38970 saccharomyc
36	30	62.5	863 1 PHSG_MYCTU	Q10639 mycobacteri
37	30	62.5	1514 1 NX1A_RAT	Q63372 rattus norv
38	30	62.5	4639 1 DYHC_DROME	P37272 drosophila
39	29	60.4	78 1 RL31_RICPR	O92447 rickettsia
40	29	60.4	185 1 RRF_ECOLI	P16174 escherichia
41	29	60.4	214 1 SC14_SCHCO	P35795 schizophyll
42	29	60.4	227 1 G786_HUMAN	O92520 homo sapien
43	29	60.4	274 1 YA99_SCHPO	Q09787 schizosacch
44	29	60.4	279 1 RPA2_SCHPO	O92373 schizosacch
45	29	60.4	326 1 CC14_CAEEL	P18834 ctenorhabdi

## ALIGNMENTS

```

RESULT 1
ID A4_CANFA STANDARD; PRT: 58 AA.
AC Q28280;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-APP) (A-beta)] (Fragment).
CN APP.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_Taxid=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis."
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC
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CC
CC EMBL: X56125; CAA39590.1; -.
CC HSSP: P05067; IBA4.
DR InterPro: IPR001868; A4_APP.
DR PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR PROSITE: PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.
FT NON_TER 1 49
FT CHAIN 7 49 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 34 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 35 58 POTENTIAL.
FT NON_TER 58 58
SQ SEQUENCE 58 AA; 6285 MW; 8469D48A2E12DFA CRC64;
Query Match 100.0%; Score 48; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.0024;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 ISEVKMDAEF 10
|||||||

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Db      1 ISEVKMDAEF 10

RESULT 2
ID      A4_BOVIN      STANDARD;      PRT;      59 AA.
AC      Q28053;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      30-MAY-2000 (Rel. 39, Last annotation update)
DE      Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE      protein (Beta-APP) (A-beta)] (fragment).
GN      APP.
OS      Bos taurus (Bovine).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC      Bovidae; Bovine; Bos.
OX      NCBI_TaxID=9913;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Brain;
RX      MEDLINE=92017079; Pubmed=1656157;
RA      Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT      "Conservation of the sequence of the Alzheimer's disease amyloid
RT      peptide in dog, polar bear and five other mammals by cross-species
RT      polymerase chain reaction analysis."
RL      Brain Res. Mol. Brain Res. 10:299-305(1991).
CC      -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC      INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC      G(O) (BY SIMILARITY).
CC      -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC      -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; X56124; CAA39589.1; -
DR      EMBL; X56126; CAA39591.1; -
DR      HSSP; P05067; 1BA4.
DR      InterPro; IPR001868; A4_APP.
DR      PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR      PROSITE; PS00320; A4_INTRA; PARTIAL.
KW      Glycoprotein; Amyloid; Neurone; Transmembrane.
FT      CHAIN 1 49
FT      DOMAIN <1 34 BETA-AMYLOID PROTEIN (POTENTIAL).
FT      TRAASMEM 35 58 POTENTIAL.
FT      DOMAIN 59 >59 CYTOPLASMIC (POTENTIAL).
FT      NON_TER 59 59
SO      SEQUENCE 59 AA; 6414 MW; F43469D48A2E12D CRC64;

Query Match 100.0%; Score 48; DB 1; Length 59;
Best Local Similarity 100.0%; Pred. No. 0.0024;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      1 ISEVKMDAEF 10
DB      1 ISEVKMDAEF 10

RESULT 3
ID      A4_SAISC      STANDARD;      PRT;      751 AA.
AC      Q95241;
DT      15-DEC-1998 (Rel. 37, Created)
DT      15-DEC-1998 (Rel. 37, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Alzheimer's disease amyloid A4 protein precursor [Contains: Beta-

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DE      amyloid protein (Beta-APP) (A-beta)].
GN      APP.
OS      Saimiri sciureus (Common squirrel monkey).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Saimiri.
OX      NCBI_TaxID=9521;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Liver, and Kidney;
RX      MEDLINE=96108492; Pubmed=8532114;
RA      Levy E., Amorim A., Frangione B., Walker L.C.;
RT      "Beta-amyloid precursor protein gene in squirrel monkeys with
RT      cerebral amyloid angiopathy."
RL      Neurobiol. Aging 16:805-808(1995).
CC      -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC      INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC      G(O).
CC      -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC      -1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
CC      WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
CC      RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
CC      NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
CC      PHOSPHORYLATION (BY SIMILARITY).
CC      -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC      -1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
CC      -----
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CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; S81024; AAD1347.1; -
DR      HSSP; P05067; 1AAP.
DR      InterPro; IPR001868; A4_APP.
DR      InterPro; IPR002223; Kunitz_BPTI.
DR      Pfam; PF02177; A4_EXTRA; 1.
DR      Pfam; PF00014; Kunitz_BPTI; 1.
DR      PRINTS; PR00203; AMYLOID4.
DR      PRINTS; PR00759; BASICPTASE.
DR      SMART; SM00006; A4_EXTRA; 1.
DR      SMART; SM00131; KU; 1.
DR      PROSITE; PS00319; A4_EXTRA; 1.
DR      PROSITE; PS00320; A4_INTRA; 1.
DR      PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR      PROSITE; PS0279; BPTI_KUNITZ_2; 1.
KW      Glycoprotein; Amyloid; Neurone; Transmembrane; Alternative splicing;
KW      signal; Serine protease inhibitor.
FT      SIGNAL 1 17
FT      CHAIN 18 751
FT      CHAIN 18 695
FT      DOMAIN 653 695
FT      DOMAIN 681 704
FT      TRANSMEM 705 751
FT      DOMAIN 287 345
FT      SITE 740 743
FT      ACT_SITE 301 302
FT      DISULFID 291 341
FT      DISULFID 300 324
FT      DISULFID 316 337
FT      CARBOHYD 523 523
FT      CARBOHYD 552 552
SO      SEQUENCE 751 AA; 84893 MW; 6C3E431089569049 CRC64;

Query Match 100.0%; Score 48; DB 1; Length 751;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      1 ISEVKMDAEF 10
DB      647 ISEVKMDAEF 656

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RESULT 4  
 ID A4\_HUMAN STANDARD: PRT: 770 AA.  
 AC P05067; P09000; Q16011;  
 DT 13-APR-1987 (Rel. 05, Created)  
 DT 01-NOV-1991 (Rel. 20, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Alzheimer's disease amyloid A4 protein precursor (Protease nexin-II)  
 DE (PN-II) (ABPI) [containing: Beta-amyloid protein (Beta.AP) (A-beta)].  
 GN APP OR A4 OR CVAP OR ADL.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OX NCBI\_TaxId=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=87144572; PubMed=2881207;  
 RA Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L.,  
 RA Grzeschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.;  
 RT "The precursor of Alzheimer's disease amyloid A4 protein resembles a  
 RT cell-surface receptor.";  
 RL Nature 325:733-736(1987).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=88122639; PubMed=2893289;  
 RA Ponte P., Gonzalez-Dewhitt P., Schilling J., Miller J., Hsu D.,  
 RA Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F.,  
 RA Cordell B.;  
 RT "A new A4 amyloid mRNA contains a domain homologous to serine  
 RT proteinase inhibitors.";  
 RL Nature 331:525-527(1988).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=89128427; PubMed=2783775;  
 RA Lemire H.G., Salbaum J.M., Multhaup G., Kang J., Bayney R.M.,  
 RA Unterbeck A., Beyreuther K., Mueller-Hill B.;  
 RT "The Pread(69) precursor protein of Alzheimer's disease A4 amyloid  
 RT is encoded by 16 exons.";  
 RL Nucleic Acids Res. 17:517-522(1989).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=97263807; PubMed=9108164;  
 RA Hatori M., Tsukahara F., Furuhata Y., Tanahashi H., Hirose M.,  
 RA Saito M., Tsukuni S., Sakaki Y.;  
 RT "A novel method for making nested deletions and its application for  
 RT sequencing of a 300 kb region of human APP locus.";  
 RL Nucleic Acids Res. 25:1802-1808(1997).  
 RN [5]  
 RP SEQUENCE OF 286-345 AND 365-366 FROM N.A.  
 RX MEDLINE=88122640; PubMed=2893290;  
 RA Tanzi R.E., McClatchey A.I., Lampert E.D., Villa-Komaroff L.,  
 RA Gusella J.F., Neve R.L.;  
 RT "Protease inhibitor domain encoded by an amyloid protein precursor  
 RT mRNA associated with Alzheimer's disease.";  
 RL Nature 331:528-530(1988).  
 RN [6]  
 RP SEQUENCE OF 287-367 FROM N.A.  
 RX MEDLINE=88122641; PubMed=2893291;  
 RA Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.;  
 RT "Novel precursor of Alzheimer's disease amyloid protein shows  
 RT protease inhibitory activity.";  
 RL Nature 331:530-532(1988).  
 RN [7]  
 RP SEQUENCE OF 284-289 AND 365-770 FROM N.A.  
 RX MEDLINE=87231971; PubMed=3035574;  
 RA Rokakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;  
 RT "Molecular cloning and characterization of a cDNA encoding the  
 RT cerebrovascular and the neuritic plaque amyloid peptides.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).  
 RN [8]

RP SEQUENCE OF 507-770 FROM N.A.  
 RX MEDLINE=88124954; PubMed=2893379;  
 RA Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,  
 RA Marotta C.A.;  
 RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer  
 RT disease brain: coding and noncoding regions of the fetal precursor  
 RT mRNA are expressed in the cortex.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).  
 RN [9]  
 RP SEQUENCE OF 672-681.  
 RX MEDLINE=88035004; PubMed=3312495;  
 RA Pardridge W.M., Winters H.V., Yang J., Eisenberg J., Choi T.B.,  
 RA Tourtellotte W.W., Huebner V., Shively J.E.;  
 RT "Amyloid angiopathy of Alzheimer's disease: amino acid composition  
 RT and partial sequence of a 4,200-dalton peptide isolated from cortical  
 RT microvessels.";  
 RL J. Neurochem. 49:1394-1401(1987).  
 RN [10]  
 RP SEQUENCE OF 739-770 FROM N.A.  
 RX MEDLINE=90236318; PubMed=2110105;  
 RA Yoshikai S.-I., Sasaki H., Doi-Ura K., Furuya H., Sasaki Y.;  
 RT "Genomic organization of the human amyloid beta-protein precursor  
 RT gene.";  
 RL Gene 87:257-263(1990).  
 RN [11]  
 RP SEQUENCE OF 1-10 FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=89016647; PubMed=3140222;  
 RA Schon E.A., Mita S., Sadlock J., Herbert J.;  
 RT "A cDNA specifying the human amyloid beta precursor protein (ABPP)  
 RT encodes a 95-kDa polypeptide.";  
 RL Nucleic Acids Res. 16:9351-9351(1988).  
 RN [12]  
 RP SEQUENCE OF 18-50.  
 RX MEDLINE=87250462; PubMed=3597385;  
 RA van Nostrand W.E., Cunningham D.D.;  
 RT "Purification of protease nexin II from human fibroblasts.";  
 RL J. Biol. Chem. 262:8508-8514(1987).  
 RN [13]  
 RP IDENTITY OF APP WITH NEXIN-II.  
 RX MEDLINE=89384866; PubMed=2506449;  
 RA Oltersdorf T., Fritz L.C., Schenk D.B., Lieberburg I.,  
 RA Johnson-Wood K.L., Beattie E.C., Ward P.J., Blacher R.W., Dovey H.F.,  
 RA Sinha S.;  
 RT "The secreted form of the Alzheimer's amyloid precursor protein with  
 RT the Kunitz domain is protease nexin-II.";  
 RL Nature 341:144-147(1989).  
 RN [14]  
 RP PROTEASE-SPECIFICITY OF INHIBITOR DOMAIN.  
 RX MEDLINE=90211252; PubMed=1969731;  
 RA Kido H., Fukutomi A., Schilling J., Wang Y., Cordell B., Katunuma N.;  
 RT "Protease-specificity of Kunitz inhibitor domain of Alzheimer's  
 RT disease amyloid protein precursor.";  
 RL Biochem. Biophys. Res. Commun. 167:716-721(1990).  
 RN [15]  
 RP COMPLEX WITH G(O).  
 RX MEDLINE=93188965; PubMed=8446172;  
 RA Nishimoto I., Okamoto T., Matsuura Y., Takahashi S., Okamoto T.,  
 RA Murayama Y., Ogata E.;  
 RT "Alzheimer amyloid protein precursor complexes with brain GTP-binding  
 RT protein G(O).";  
 RL Nature 362:75-79(1993).  
 RN [16]  
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 28-133.  
 RX MEDLINE=99215582; PubMed=10201399;  
 RA Rossjohn J., Cappai R., Fell S.C., Henry A., McKinstry W.J.,  
 RA Galatis D., Hesse L., Multhaup G., Beyreuther K., Masters C.L.,  
 RA Parker M.W.;  
 RT "Crystal structure of the N-terminal, growth factor-like domain of  
 RT Alzheimer amyloid precursor protein.";  
 RL Nat. Struct. Biol. 6:327-331(1999).  
 RN [17]  
 RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF 287-344.

```

RX MEDLINE-91104913; PubMed-2125487;
RA Hynes T.R., Randal M., Kennedy L.A., Eigenbrodt C., Kosiakof A.A.;
RT "X-ray crystal structure of the protease inhibitor domain of
RT Alzheimer's amyloid beta-protein precursor."
RL Biochemistry 29:10018-10022(1990).
[18]
RP STRUCTURE BY NMR OF 289-344.
RX MEDLINE-92031486; PubMed-1718421;
RA Heald S.L., Tilton R.F., Jr., Hammond L.S., Lee A., Bayney R.M.,
RA Kanaruck M.E., Ramabhadran T.V., Dreyer R.N., Davis G., Unterdeck A.,
RA Tamburini P.P.;
RT "Sequential NMR resonance assignment and structure determination of
RT the knitz-type inhibitor domain of the Alzheimer's beta-amyloid
RT precursor protein."
RL Biochemistry 30:10467-10478(1991).
[19]
RP STRUCTURE BY NMR OF 672-699.
RX MEDLINE-94281210; PubMed-7516706;
RA Talafoos J., Marchowski K.J., Klopman G., Zagorski M.G.;
RT "Solution structure of residues 1-28 of the amyloid beta-peptide."
RL Biochemistry 33:7786-7796(1994).
[20]
RP STRUCTURE BY NMR OF 696-706.
RX MEDLINE-97128622; PubMed-8973180;
RA Kohno T., Kobayashi K., Maeda T., Sato K., Takashima A.;
RT "Three-dimensional structures of the amyloid beta peptide (25-35) in
RT membrane-mimicking environment."
RL Biochemistry 35:16094-16104(1996).
[21]
RP STRUCTURE BY NMR OF 672-711.
RX MEDLINE-98359783; PubMed-9693002;
RA Coles M., Bicknell W., Watson A.A., Fairlie D.P., Craik D.J.;
RT "Solution structure of amyloid beta-peptide(1-40) in a water-micelle
RT environment. Is the membrane-spanning domain where we think it is?"
RL Biochemistry 37:11064-11077(1998).
[22]
RP STRUCTURE BY NMR OF 672-689.
RX MEDLINE-20400066; PubMed-10940222;
RA Poulsen S.-A., Watson A.A., Craik D.J.;
RT "Solution structures in aqueous SDS micelles of two amyloid beta
RT peptides of Abeta(1-28) mutated at the alpha-secretase cleavage
RT site."
RL J. Struct. Biol. 130:142-152(2000).
[23]
RP STRUCTURE BY NMR OF 681-706.
RX MEDLINE-20400065; PubMed-10940221;
RA Zhang S., Iwata K., Lachemann M.-J., Peng J.W., Li S., Stinson E.R.,
RA Lu Y., Felix A.M., Maggio J.E., Lee J.P.;
RT "The Alzheimer's peptide A beta adopts a collapsed coil structure in
RT water."
RL J. Struct. Biol. 130:130-141(2000).
[24]
RP SIGNAL SEQUENCE CLEAVAGE SITE, AND TOPOLOGY.
RX MEDLINE-88296437; PubMed-290137;
RA Dykx J., Wellmann A., Muthaap G., Salbaum J.M., Lemaire H.-G.,
RA Kang J., Weiller-Hill B., Masters C.L., Beyreuther K.;
RT "Identification, transmembrane orientation and biogenesis of the
RT amyloid A4 precursor of Alzheimer's disease."

```

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Query Match 100.0%; Score 48; DB 1; Length 770;
Best Local Similarity 100.0%; Pred. No. 0.036;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ISEVKMAEE 10
DB 666 ISEVKMAEE 675

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RESULT 5
ID A4_MOUSE STANDARD; PRT: 770 AA.
AC P12023;
DT 01-OCT-1989 (Rel. 12, Created)

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DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog precursor
DE (Amyloidogenic glycoprotein) (Ag).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.
RC STRAIN-BALB/C; TISSUE=Brain;
RX MEDLINE-92096458; PubMed-1756177;
RA de Strooper B., van Leuven F., van den Bergh H.;
RT "The amyloid beta protein precursor or protease nexin II from mouse
RT is closer related to its human homolog than previously reported."
RL Biochim. Biophys. Acta 1129:141-143(1991).
[2]
RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE-88106489; PubMed-3322280;
RA Yamada T., Sasaki H., Furuya H., Miyata T., Goto I., Sakaki Y.;
RT "Complementary DNA for the mouse homolog of the human amyloid beta
RT protein precursor."
RL Biochem. Biophys. Res. Commun. 149:665-671(1987).
[3]
RP REVISIONS.
RA Yamada T.;
RL Submitted (MAR-1988) to the EMBL/Genbank/DBJ databases.
[4]
RP SEQUENCE OF 289-364 FROM N.A.
RC STRAIN-CD-1; TISSUE=Placenta;
RX MEDLINE-89345111; PubMed-2569710;
RA Fukuchi K., Martin G.M., Deeb S.S.;
RT "Sequence of the protease inhibitor domain of the A4 amyloid protein
RT precursor of Mus domestics."
RL Nucleic Acids Res. 17:5396-5396(1989).
[5]
RP SEQUENCE OF 1-19 FROM N.A.
RX MEDLINE-92209998; PubMed-1555768;
RA Izumi R., Yamada T., Yoshikai S.I., Sasaki H., Hattori M.,
RA Sakai Y.;
RT "Positive and negative regulatory elements for the expression of the
RT Alzheimer's disease amyloid precursor-encoding gene in mouse."
RL Gene 112:189-195(1992).
[6]
RP SEQUENCE OF 281-380 FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE=Brain, and Kidney;
RX MEDLINE-89149813; PubMed-2493250;
RA Yamada T., Sasaki H., Donura K., Goto I., Sakaki Y.;
RT "Structure and expression of the alternatively-spliced forms of mRNA
RT for the mouse homolog of Alzheimer's disease amyloid beta protein
RT precursor."
RL Biochem. Biophys. Res. Commun. 158:906-912(1989).
[7]
RP SUBCELLULAR LOCATION: Type I membrane protein.
[8]
RP SUBCELLULAR PRODUCTS: 5 ISOFORMS; APP(395), APP(563), APP(695),
RP APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE
RP SPLICING.
[9]
RP TISSUE SPECIFICITY: AAA(770) IS EXPRESSED IN KIDNEY. AAA(751) IS
RP WIDELY EXPRESSED. AAA(695) IS EXPRESSED IN BRAIN, KIDNEY AND
RP LIVER.
[10]
RP DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
RP WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
RP RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
RP NEXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
RP PHOSPHORYLATION (BY SIMILARITY).
[11]
RP STIMULATORY: BELONGS TO THE APP FAMILY.
[12]
RP SIMILARITY: CONTAINS 1 BPT1/KUNITZ INHIBITOR DOMAIN.
[13]
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OY 1 SEVKMDAEF 10  
 DB 666 ISEVKMDAEF 675

## RESULT 7

A4\_PIG STANDARD: PRT: 57 AA.

ID A4\_PIG

AC 029023:

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Alzheimer's disease amyloid A4 protein homolog [contains: Beta-amyloid

protein (Beta-APP) (A-beta)] (Fragment).

GN APP.

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OX NCBI\_TaxID=9823;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RA MEDLINE=92017079; PubMed=1656157;

RX Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;

RT "Conservation of the sequence of the Alzheimer's disease amyloid

peptide in dog, polar bear and five other mammals by cross-species

polymerase chain reaction analysis.";

RT Brain Res. Mol. Brain Res. 10:299-305(1991).

CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO

INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN

G(O) (BY SIMILARITY).

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.

-----

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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC EMBL: X56127; CA39592.1; -.

DR HSSP: P05067; 1BA4.

DR InterPro: IPR001868; A4\_APP.

DR PROSITE: PS00319; A4\_EXTRA; PARTIAL.

DR PROSITE: PS00320; A4\_INTRA; PARTIAL.

KW Glycoprotein; Amyloid; Neurone; Transmembrane.

FT NON\_TER 1 48 BETA-AMYLOID PROTEIN (POTENTIAL).

FT CHAIN 6 48 EXTRACELLULAR (POTENTIAL).

FT DOMAIN <1 33 POTENTIAL.

FT TRANSMEM 34 57 POTENTIAL.

FT NON\_TER 57 57

SO SEQUENCE 57 AA; 6172 MW; 84209D88BBA82DFA CRC64;

Query Match 91.7%; Score 44; DB 1; Length 57;

Best Local Similarity 100.0%; Pred. No. 0.016;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 SEVKMDAEF 10

DB 1 SEVKMDAEF 9

RESULT 8

A4\_URSMA STANDARD: PRT: 57 AA.

ID A4\_URSMA

AC 029149:

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid

protein (Beta-APP) (A-beta)] (Fragment).

GN APP.

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

OX NCBI\_TaxID=9986;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RA MEDLINE=92017079; PubMed=1656157;

RX Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;

RT "Conservation of the sequence of the Alzheimer's disease amyloid

peptide in dog, polar bear and five other mammals by cross-species

polymerase chain reaction analysis.";

DE protein (Beta-APP) (A-beta)] (Fragment).

GN APP.

OS Ursus maritimus (Polar bear) (Thalarchos maritimus).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.

OX NCBI\_TaxID=29073;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RA MEDLINE=92017079; PubMed=1656157;

RX Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;

RT "Conservation of the sequence of the Alzheimer's disease amyloid

peptide in dog, polar bear and five other mammals by cross-species

polymerase chain reaction analysis.";

RT Brain Res. Mol. Brain Res. 10:299-305(1991).

CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO

INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN

G(O) (BY SIMILARITY).

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.

-----

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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC EMBL: X56128; CA39593.1; -.

DR HSSP: P05067; 1AML.

DR InterPro: IPR001868; A4\_APP.

DR PROSITE: PS00319; A4\_EXTRA; PARTIAL.

DR PROSITE: PS00320; A4\_INTRA; PARTIAL.

KW Glycoprotein; Amyloid; Neurone; Transmembrane.

FT NON\_TER 1 48 BETA-AMYLOID PROTEIN (POTENTIAL).

FT CHAIN 6 48 EXTRACELLULAR (POTENTIAL).

FT DOMAIN <1 33 POTENTIAL.

FT TRANSMEM 34 57 POTENTIAL.

FT NON\_TER 57 57

SO SEQUENCE 57 AA; 6172 MW; 84209D88BBA82DFA CRC64;

Query Match 91.7%; Score 44; DB 1; Length 57;

Best Local Similarity 100.0%; Pred. No. 0.016;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 SEVKMDAEF 10

DB 1 SEVKMDAEF 9

RESULT 9

A4\_RABIT STANDARD: PRT: 58 AA.

ID A4\_RABIT

AC 028748:

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid

protein (Beta-APP) (A-beta)] (Fragment).

GN APP.

OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

OX NCBI\_TaxID=9986;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RA MEDLINE=92017079; PubMed=1656157;

RX Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;

RT "Conservation of the sequence of the Alzheimer's disease amyloid

peptide in dog, polar bear and five other mammals by cross-species

polymerase chain reaction analysis.";

```
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -----
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -----
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
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CC -----
DR EMBL: X56130; CAA39595.1; -.
DR HSSP: P05067; 1AMT.
DR InterPro: IPR001868; A4_APP.
DR PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR PROSITE: PS00320; A4_INTRA; PARTIAL.
KM Glycoprotein; Amyloid; Neurone; Transmembrane.
FT CHAIN 1 48 BETA-AMYLOID PROTEIN (POTENTIAL).
FT NON_TER 1 1
FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 34 57 POTENTIAL.
FT DOMAIN 58 >58 CYTOPLASMIC (POTENTIAL).
FT NON_TER 58 58
SQ SEQUENCE 58 AA; 6300 MW; F434209D8EBA82D CRC64;

Query Match 91.7%; Score 44; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SEVKMDAEF 10
Db 1 SEVKMDAEF 9

RESULT 10
A4-SHEEP STANDARD; PRT; 58 AA.
AC Q28757;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-APP) (A-beta)] (Fragment).
GN APP.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RA MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RA "Conservation of the sequence of the Alzheimer's disease amyloid
RA peptide in dog, polar bear and five other mammals by cross-species
RA polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -----
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -----
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
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CC -----
DR EMBL: X56130; CAA39595.1; -.
DR HSSP: P05067; 1AMT.
DR InterPro: IPR001868; A4_APP.
DR PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR PROSITE: PS00320; A4_INTRA; PARTIAL.
KM Glycoprotein; Amyloid; Neurone; Transmembrane.
FT CHAIN 1 48 BETA-AMYLOID PROTEIN (POTENTIAL).
FT NON_TER 1 1
FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 34 57 POTENTIAL.
FT DOMAIN 58 >58 CYTOPLASMIC (POTENTIAL).
FT NON_TER 58 58
SQ SEQUENCE 58 AA; 6300 MW; F434209D8EBA82D CRC64;

Query Match 91.7%; Score 44; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SEVKMDAEF 10
Db 1 SEVKMDAEF 9

RESULT 11
YF74_ARCFU STANDARD; PRT; 400 AA.
AC Q28698;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein AF1574 precursor.
GN AF1574.
OS Archaeoglobus fulgidus.
OC Archaea; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;
OC Archaeoglobus.
OX NCBI_TaxID=2234;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RC MEDLINE=96049345; PubMed=9389475;
RX Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
RX Kechum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
RX Richardson D.L., Kierlavage A.R., Graham D.E., Kyriades N.C.,
RX Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
RX Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
RX Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
RX Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
RX Cotton M.D., Spriggs T., Artlich P., Kalne B.P., Sykes S.M.,
RX Sadow P.M., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
RX Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
RX Venter J.C.;
RT "The complete genome sequence of the hyperthermophilic, sulphate-
RT reducing archaeon Archaeoglobus fulgidus.";
RL Nature 390:364-370(1997).
CC -----
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CC -----
DR EMBL: AE000994; AAB89681.1; -.
DR TIGR: AF1574; -.
KW Hypothetical protein; Signal; Complete proteome.
FT SIGNAL 1 23
FT CHAIN 24 400 HYPOTHETICAL PROTEIN AF1574.
SQ SEQUENCE 400 AA; 44117 MW; 5C7BBA00505FD59 CRC64;
```

Query Match 70.8%; Score 34; DB 1; Length 400;  
Best Local Similarity 70.0%; Pred. No. 14;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ISEVKMDAEF 10  
1:111:111  
Db 143 ITEVKVKAEE 152

RESULT 12  
PGCV\_CHICK STANDARD; PRT; 3562 AA.  
ID PGCV\_CHICK 090953; 090945;  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE (chondroitin sulfate proteoglycan core protein 2) (PG-M).  
GN CP5G2.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-WHITE LEGHORN; TISSUE-Limb bud;  
RX MEDLINE=93300846; PubMed=8314802;  
RA Shinozuka T., Nishida Y., Ito K., Kimata K.,  
RT "cDNA cloning of PG-M, a large chondroitin sulfate proteoglycan  
RT spliced multiforms of PG-M and their relationships to versican.";  
J Biol. Chem. 268:14461-14469(1993).  
RL J Biol. Chem. 268:14461-14469(1993).  
CC -I- FUNCTION: May play a role in intercellular signaling and in  
CC connecting cells with the extracellular matrix. May take part in  
CC the regulation of cell motility, growth and differentiation. Binds  
CC hyaluronic acid.  
CC -I- SUBCELLULAR LOCATION: Secreted; extracellular matrix.  
CC -I- ALTERNATIVE PRODUCTS: At least 2 isoforms; V0 (shown here) and  
CC V1: are produced by alternative splicing.  
CC -I- TISSUE SPECIFICITY: Prechondrogenic condensation area of  
CC developing limb buds.  
CC -I- DEVELOPMENTAL STAGE: Disappears after the cartilage development  
CC (by similarity).  
CC -I- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.  
CC -I- SIMILARITY: CONTAINS 2 LINK DOMAINS.  
CC -I- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.  
CC -I- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.  
CC -I- SIMILARITY: CONTAINS 1 SUSHI (SCR) DOMAIN.  
CC -----  
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CC -----  
DR EMBL: X60226; CAA42787.1; -;  
DR EMBL: D13542; BAA02742.1; -;  
DR HSSP: P20693; 1HLJ.  
DR InterPro: IPR000152; Asx\_hydroxyl.  
DR InterPro: IPR000561; EGF-like.  
DR InterPro: IPR000742; EGF\_2.  
DR InterPro: IPR001881; EGF\_Ca.  
DR InterPro: IPR003599; Ig.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR000538; Link.  
DR InterPro: IPR000436; Sushi\_SCR\_CCP.  
DR InterPro: IPR001304; lectin\_c.  
DR Pfam: PF000008; EGF\_2.  
DR Pfam: PF00047; Ig\_1.  
DR Pfam: PF00059; lectin\_c; 1.

DR Pfam: PF000084; sushi; 1.  
DR Pfam: PF00193; link; 2.  
DR ProDom: PD000918; link; 2.  
DR SMART: SM00032; CCP; 1.  
DR SMART: SM00034; CLECT; 1.  
DR SMART: SM00179; EGF\_Ca; 1.  
DR SMART: SM00001; EGF\_Like; 1.  
DR SMART: SM00409; Ig; 1.  
DR SMART: SM00445; Link; 2.  
DR PROSITE: PS00010; ASX\_HYDROXYL; 1.  
DR PROSITE: PS00022; EGF\_1; 2.  
DR PROSITE: PS01186; EGF\_2; 1.  
DR PROSITE: PS01187; EGF\_Ca; 2.  
DR PROSITE: PS01241; LINK; 2.  
DR PROSITE: PS00615; C-TYPE LECTIN\_1; 1.  
DR PROSITE: PS50041; C-TYPE LECTIN\_2; 1.  
DR Glycoprotein: Proteoglycan; Lectin; Extracellular matrix; Sushi;  
KW Signal: Repeat: EGF-like domain; Calcium; Immunoglobulin domain;  
KW Hyaluronic acid; Alternative splicing.  
KW Hyaluronic acid; Alternative splicing.  
FT SIGNAL 1 26  
FT CHAIN 27 3562  
FT DOMAIN 37 136  
FT DOMAIN 166 243  
FT DOMAIN 264 345  
FT DOMAIN 3254 3290  
FT DOMAIN 3292 3328  
FT DOMAIN 3341 3455  
FT DOMAIN 3460 3518  
FT DISULFID 44 129  
FT DISULFID 171 242  
FT DISULFID 195 216  
FT DISULFID 269 344  
FT DISULFID 293 314  
FT DISULFID 3258 3269  
FT DISULFID 3263 3289  
FT DISULFID 3280 3307  
FT DISULFID 3301 3316  
FT DISULFID 3318 3327  
FT DISULFID 3334 3345  
FT DISULFID 3362 3454  
FT DISULFID 3430 3446  
FT DISULFID 3461 3504  
FT DISULFID 3490 3517  
FT CARBOHYD 163 163  
FT CARBOHYD 235 235  
FT CARBOHYD 329 329  
FT CARBOHYD 529 529  
FT CARBOHYD 709 709  
FT CARBOHYD 948 948  
FT CARBOHYD 1409 1409  
FT CARBOHYD 1479 1479  
FT CARBOHYD 1523 1523  
FT CARBOHYD 1530 1530  
FT CARBOHYD 1625 1625  
FT CARBOHYD 1751 1751  
FT CARBOHYD 1988 1988  
FT CARBOHYD 2088 2088  
FT CARBOHYD 2089 2089  
FT CARBOHYD 2507 2507  
FT CARBOHYD 2642 2642  
FT CARBOHYD 2679 2679  
FT CARBOHYD 2748 2748  
FT CARBOHYD 2762 2762  
FT CARBOHYD 3069 3069  
FT CARBOHYD 3194 3194  
FT CARBOHYD 3232 3232  
FT CARBOHYD 3545 3545  
FT VARSPLIC 485 1411  
SQ SEQUENCE 3562 AA; 388078 MW; 98C566B8C160222 CRC64;

Query Match 70.8%; Score 34; DB 1; Length 3562;  
Best Local Similarity 66.7%; Pred. No. 1,4e+02;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 SEVKMDAEF 10  
1:|||||

Db 1709 STIKLDAEF 1717

RESULT 13  
T2SL-STREPT  
ID T2SL-STREPT STANDARD: PRT; 269 AA.  
AC 052512;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Type II restriction enzyme SfiI (EC 3.1.21.4) (Endonuclease SfiI)  
DE (r.SfiI).  
CN SfiI.  
OS Streptomyces fimbriatus.  
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
OC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.  
NCBI\_TaxID=68197;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA van Cott E.M., Moran L.S., Slatko B.E., Wilson G.G.;  
RT "Characterization of the SfiI restriction and modification genes";  
RL Submitted (DEC-1997) to the EMBL/Genbank/DBJ databases.  
CC -1- FUNCTION: RECOGNIZES THE DOUBLE-STRANDED SEQUENCE GGCCNNNNNGGCC  
CC AND CLEAVES BEFORE N-9.  
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage of DNA to give  
CC specific double-stranded fragments with terminal 5'-phosphates.  
CC -----  
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CC -----  
DR EMBL; AF039750; AAB95365.1; -  
DR REBASE; 1655; SfiI.  
KM Hydrolyase: Endonuclease; Nuclease; Restriction system.  
SQ SEQUENCE 269 AA; 31044 MW; 3C48499BAA5055EA CRC64;

Query Match 66.7%; Score 32; DB 1; Length 269;  
Best Local Similarity 66.7%; Pred. No. 24;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 SEVKMDAEF 10  
1:|||||

Db 115 SOLPMDAEF 123

RESULT 14  
BCPA-CHLIT  
ID BCPA-CHLIT STANDARD: PRT; 354 AA.  
AC Q46135;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Bacteriochlorophyll A protein (Bchl a protein) (BCP) (Fenna-Matthews-  
DE Olson protein) (FMO-protein) (Fragment).  
GN FMOA.  
OS Chlorobium limicola f.sp. thiosulfatophilum.  
OC Bacteria; Green sulfur bacteria; Chlorobium.  
NCBI\_TaxID=115852;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE=95352646; PubMed=7626630;  
RA Hager-Braun C., Xie D.L., Jarosch U., Herold E., Butner M.,  
RA Zimmermann R., Deutzmann R., Hauska G., Nelson N.;  
RT "Stable photobleaching of P840 in Chlorobium reaction center  
RT preparations: presence of the 42-kDa bacteriochlorophyll a protein

RT and a 17-kDa polypeptide.";  
RL Biochemistry 34:9617-9624(1995).  
CC -1- FUNCTION: INTERMEDIARY IN THE TRANSFER OF EXCITATION ENERGY FROM  
CC THE CHLOROPHYLL TO THE REACTION CENTERS.  
CC -1- SUBUNIT: HOMOTRIMER. EACH SUBUNIT CONTAINS 7 MOLECULES OF  
CC BACTERIOCHLOROPHYLL A.  
CC -----  
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CC -----  
DR EMBL; X83529; CAA58510.1; -  
DR HSSP; Q46393; IKS.A.  
DR InterPro; IPR003426; Bchl\_A.  
DR Pfam; PF02327; Bchl\_A; 1.  
KM Electron transport; Photosynthesis; Reaction center; Magnesium;  
KW Bacteriochlorophyll.  
FT NON-TER 1 1  
FT BINDING 99 99 BACTERIOCHLOROPHYLL A, 1 (BY SIMILARITY).  
FT BINDING 134 134 BACTERIOCHLOROPHYLL A, 6 (BY SIMILARITY).  
FT BINDING 278 278 BACTERIOCHLOROPHYLL A, 4 (BY SIMILARITY).  
FT BINDING 285 285 BACTERIOCHLOROPHYLL A, 7 (BY SIMILARITY).  
FT BINDING 286 286 BACTERIOCHLOROPHYLL A, 3 (BY SIMILARITY).  
SQ SEQUENCE 354 AA; 39243 MW; F4D4D565BDCDB1B CRC64;

Query Match 66.7%; Score 32; DB 1; Length 354;  
Best Local Similarity 75.0%; Pred. No. 31;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 EVKMDAEF 10  
1:|||||

Db 254 EVKMDAEF 261

RESULT 15  
BCPA-CHLITE  
ID BCPA-CHLITE STANDARD: PRT; 365 AA.  
AC Q46393;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE Bacteriochlorophyll A protein (Bchl a protein) (BCP) (Fenna-Matthews-  
DE Olson protein) (FMO-protein).  
GN FMOA.  
OS Chlorobium tepidum.  
OC Bacteria; Green sulfur bacteria; Chlorobium.  
NCBI\_TaxID=1097;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Dracheva S., Williams J.A.C., Blankenship R.E.;  
RT "Cloning and sequencing of the FMO-protein gene from Chlorobium  
RT tepidum.";  
RL (in) Murata N. (eds.);  
RL Research in photosynthesis, pp.2:53-56, Kluwer Academic Publishers,  
RL Dordrecht (1992).  
RN [2]  
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).  
RX MEDLINE=97415773; PubMed=9268671.  
RA Li Y.F., Zhou W., Blankenship R.E., Allen J.P.;  
RT "Crystal structure of the bacteriochlorophyll a protein from  
RT Chlorobium tepidum.";  
RL J. Mol. Biol. 271:456-471(1997).  
CC -1- FUNCTION: INTERMEDIARY IN THE TRANSFER OF EXCITATION ENERGY FROM  
CC THE CHLOROPHYLL TO THE REACTION CENTERS.  
CC -1- SUBUNIT: HOMOTRIMER. EACH SUBUNIT CONTAINS 7 MOLECULES OF  
CC BACTERIOCHLOROPHYLL A.  
CC -----  
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-----  
DR EMBL: L13700: AAA23111.1; -.  
DR PDB: 1KSA: 25-FEB-98.  
DR InterPro: IPR003426; Bchl\_A.  
DR Pfam: PF02327; Bchl\_A: 1.  
KW Electron transport; Photosynthesis; Reaction center; Magnesium;  
KW 3D-structure; Bacteriochlorophyll.  
FT INIT\_MET 0 BY SIMILARITY.  
FT BINDING 110 110 BACTERIOCHLOROPHYLL A, 1.  
FT BINDING 145 145 BACTERIOCHLOROPHYLL A, 6.  
FT BINDING 289 289 BACTERIOCHLOROPHYLL A, 4.  
FT BINDING 296 296 BACTERIOCHLOROPHYLL A, 7.  
FT BINDING 297 297 BACTERIOCHLOROPHYLL A, 3.  
SQ SEQUENCE 365 AA; 40163 MW; BB48DFE24DF6A780 CRC64;

## Query Match

66.7%; Score 32; DB 1; Length 365;

Best Local Similarity 75.0%; Pred. No. 32;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 EYKMDAEF 10  
|||:|  
DB 265 EVKVDGEF 272

Search completed: October 29, 2002, 10:27:27  
Job time : 6 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 29, 2002, 10:23:11 ; Search time 18 Seconds  
(without alignments)  
96.108 Million cell updates/sec

Title: US-09-580-018-3  
Perfect score: 48  
Sequence: 1 ISEVKMDAER 10

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues  
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: SPREMBL\_19:\*  
2: sp\_archaea:\*  
3: sp\_bacteria:\*  
4: sp\_fungi:\*  
5: sp\_human:\*  
6: sp\_invertebrate:\*  
7: sp\_mammal:\*  
8: sp\_mmc:\*  
9: sp\_organelle:\*  
10: sp\_phage:\*  
11: sp\_plant:\*  
12: sp\_rodent:\*  
13: sp\_virus:\*  
14: sp\_vertebrate:\*  
15: sp\_unclassified:\*  
16: sp\_rvirus:\*  
17: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	100.0	79	11	035463
2	48	100.0	82	4	P78438
3	48	100.0	82	4	Q16014
4	48	100.0	82	4	Q16019
5	48	100.0	82	4	Q16020
6	48	100.0	607	11	099K32
7	48	100.0	695	6	Q95KN7
8	48	100.0	695	11	P97487
9	48	100.0	695	11	060496
10	48	100.0	770	6	Q9TU10
11	48	97.9	534	13	093296
12	47	97.9	569	13	Q9PVL1
13	47	97.9	695	13	Q9DCJ8
14	47	97.9	751	13	Q9DCJ7
15	42	87.5	693	13	Q98SG0
16	42	87.5	693	13	Q98SF9

17	42	87.5	747	13	Q91963	Q91963 xenopus. ap
18	37	77.1	423	2	052379	052379 raietonia s
19	37	77.1	423	2	045693	045693 burkholderi
20	36	75.0	630	2	Q93IK4	Q93IK4 vibrio sp.
21	34	70.8	142	5	016896	016896 caenorhabdi
22	34	70.8	317	17	Q962T2	Q962T2 sulfolobus
23	34	70.8	699	13	057394	057394 narke japon
24	34	70.8	700	16	Q9K679	Q9K679 bacillus ha
25	33	68.8	242	10	Q9C7X4	Q9C7X4 arabidopsis
26	33	68.8	389	17	Q9HR27	Q9HR27 halobacteri
27	33	68.8	626	2	Q56633	Q56633 vibrio chol
28	33	68.8	626	2	Q9AGW8	Q9AGW8 vibrio chol
29	33	68.8	626	16	Q9KTQ7	Q9KTQ7 vibrio chol
30	32	66.7	143	4	Q9H935	Q9H935 homo sapien
31	32	66.7	261	16	Q25173	Q25173 homo sapien
32	32	66.7	261	16	Q9ZKH1	Q9ZKH1 heliobacte
33	32	66.7	266	5	Q965M5	Q965M5 caenorhabdi
34	32	66.7	282	5	002335	002335 caenorhabdi
35	32	66.7	338	2	Q9AL67	Q9AL67 chlorobium
36	32	66.7	350	2	Q9AL73	Q9AL73 chlorobium
37	32	66.7	350	2	Q9AL69	Q9AL69 chlorobium
38	32	66.7	350	2	Q9AL72	Q9AL72 chlorobium
39	32	66.7	400	2	Q52295	Q52295 shigella fl
40	32	66.7	405	4	Q9BU21	Q9BU21 homo sapien
41	32	66.7	426	17	Q9V2P8	Q9V2P8 pyrococcus
42	32	66.7	470	16	Q9RYP8	Q9RYP8 delinococcus
43	32	66.7	539	4	Q9NWD6	Q9NWD6 homo sapien
44	32	66.7	539	4	Q9NWA5	Q9NWA5 homo sapien
45	32	66.7	614	4	Q965R8	Q965R8 homo sapien

## ALIGNMENTS

RESULT 1	ID	035463	PRELIMINARY:	PRT:	79	AA.
AC	035463:					
DT	01-JAN-1998 (TREMBLrel. 05, Created)					
DT	01-JAN-1998 (TREMBLrel. 05, Last sequence update)					
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)					
DE	ALZHEIMER'S AMYLOID BETA PROTEIN (FRAGMENT).					
GN	BETA APP.					
OS	Cricetulus griseus (Chinese hamster).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;					
OC	Cricetulus.					
OX	NCBI_TaxID=10029;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RA	Sambamurti K., Plinix I., Gandhi S.;					
RL	Submitted (OCT-1997) to the EMBL/Genbank/DBJ databases.					
DR	EMBL; AF030413; AAB86608.1; -.					
DR	HSSP; P05067; 1BA4.					
FT	NON_TER	1				
FT	NON_TER	79	79			
SO	SEQUENCE	79	AA;	8538	MM;	37F2C6C3BF3F597 CRC64;
QY	Query Match					100.0%; Score 48; DB 11; Length 79;
	Best local Similarity					100.0%; Pred. No. 0.02;
	Matches 10; Conservative					0; Mismatches 0; Indels 0; Gaps 0;
DB	1 ISEVKMDAER 10					
	15 ISEVKMDAER 24					
RESULT 2	ID	P78438	PRELIMINARY:	PRT:	82	AA.
AC	P78438:					
DT	01-MAY-1997 (TREMBLrel. 03, Created)					
DT	01-MAY-1997 (TREMBLrel. 03, Last sequence update)					

DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)  
 DE AMYLOID PROTEIN (BETA-AMYLOID PROTEIN) (FRAGMENT).  
 GN APP.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89392030; PubMed=2675837;  
 RA Johnstone E.M., Chaney M.O., Moore R.E., Ward K.E., Norris F.H.,  
 RA Little S.P.;  
 RT "Alzheimer's disease amyloid peptide is encoded by two exons and shows  
 RT similarity to soybean trypsin inhibitor.";  
 RL Biochem. Biophys. Res. Commun. 163:1248-1255(1989).  
 RN [2]  
 RP SEQUENCE OF 19-48 FROM N.A.  
 RX MEDLINE=87120329; PubMed=2949367;  
 RA Tanzi R.E., Gusella J.F., Watkins P.C., Bruns G.A., George-Hyslop P.,  
 RA Van Keuren M.L., Patterson D., Pagan S., Kurnit D.M., Neve R.L.;  
 RT "Amyloid beta protein gene: cDNA, mRNA distribution, and genetic  
 RT linkage near the Alzheimer locus.";  
 RL Science 235:880-884(1987).  
 RN [3]  
 RP SEQUENCE OF 32-63 FROM N.A.  
 RX MEDLINE=93035397; PubMed=1415269;  
 RA Kamino K., Orr H.T., Payami H., Wajsmann E.M., Alonso M.E., Pulst S.M.,  
 RA Anderson L., O'dahl S., Nemens E., White J.A.;  
 RT "Linkage and mutational analysis of familial Alzheimer disease  
 RT kindreds for the APP gene region.";  
 RL Am. J. Hum. Genet. 51:998-1014(1992).  
 DR EMBL: M29270; AAA51768.1; -;  
 DR EMBL: M29269; AAA51768.1; JOINED.  
 DR EMBL: M15532; AAA51764.1; -;  
 DR EMBL: S45136; AAB23646.1; -;  
 DR HSSP: P05067; 1BA4.  
 FT NON\_TER 1  
 SQ SEQUENCE 82 AA; 8994 MW; 8DA9E42B813A070E CRC64;

Query Match 100.0%; Score 48; DB 4; Length 82;  
 Best Local Similarity 100.0%; Pred. No. 0.02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ISEVKMDAEF 10  
 |||||  
 DB 11 ISEVKMDAEF 20

RESULT 3  
 ID Q16014 PRELIMINARY; PRT; 82 AA.  
 AC Q16014;  
 DT 01-NOV-1996 (TReMBLrel. 01, Created)  
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
 DE BETA-AMYLOID PEPTIDE (FRAGMENT).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93236601; PubMed=8476439;  
 RA Denman R.B., Rosenzwaig R., Miller D.L.;  
 RT "A system for studying the effect(s) of familial Alzheimer disease  
 RT mutations on the processing of the beta-amyloid peptide precursor.";  
 RL Biochem. Biophys. Res. Commun. 192:96-103(1993).  
 DR EMBL: S60721; AAB26263.2; -;  
 DR HSSP: P05067; 1BA4.  
 FT NON\_TER 1  
 FT NON\_TER 82  
 SQ SEQUENCE 82 AA; 8972 MW; F534AAB53EA9230A CRC64;

Query Match 100.0%; Score 48; DB 4; Length 82;  
 Best Local Similarity 100.0%; Pred. No. 0.02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ISEVKMDAEF 10  
 |||||  
 DB 12 ISEVKMDAEF 21

RESULT 4  
 ID Q16019 PRELIMINARY; PRT; 82 AA.  
 AC Q16019;  
 DT 01-NOV-1996 (TReMBLrel. 01, Created)  
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
 DE BETA-AMYLOID PEPTIDE (FRAGMENT).  
 GN BETA APP.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93236601; PubMed=8476439;  
 RA Denman R.B., Rosenzwaig R., Miller D.L.;  
 RT "A system for studying the effect(s) of familial Alzheimer disease  
 RT mutations on the processing of the beta-amyloid peptide precursor.";  
 RL Biochem. Biophys. Res. Commun. 192:96-103(1993).  
 DR EMBL: S61380; AAB26264.2; -;  
 DR HSSP: P05067; 1BA4.  
 FT NON\_TER 1  
 FT NON\_TER 82  
 SQ SEQUENCE 82 AA; 8938 MW; F534AA50E579230A CRC64;

Query Match 100.0%; Score 48; DB 4; Length 82;  
 Best Local Similarity 100.0%; Pred. No. 0.02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ISEVKMDAEF 10  
 |||||  
 DB 12 ISEVKMDAEF 21

RESULT 5  
 ID Q16020 PRELIMINARY; PRT; 82 AA.  
 AC Q16020;  
 DT 01-NOV-1996 (TReMBLrel. 01, Created)  
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
 DE BETA-AMYLOID PEPTIDE (FRAGMENT).  
 GN BETA APP.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93236601; PubMed=8476439;  
 RA Denman R.B., Rosenzwaig R., Miller D.L.;  
 RT "A system for studying the effect(s) of familial Alzheimer disease  
 RT mutations on the processing of the beta-amyloid peptide precursor.";  
 RL Biochem. Biophys. Res. Commun. 192:96-103(1993).  
 DR EMBL: S61383; AAB26265.2; -;  
 DR HSSP: P05067; 1BA4.  
 FT NON\_TER 1  
 FT NON\_TER 82  
 SQ SEQUENCE 82 AA; 8882 MW; F534AA5AE5D9230A CRC64;

Query Match 100.0%; Score 48; DB 4; Length 82;  
 Best Local Similarity 100.0%; Pred. No. 0.02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ISEVKMDAEF 10  
 |||||||  
 Db 12 ISEVKMDAEF 21

## RESULT 6

099K32 PRELIMINARY; PRT; 607 AA.  
 AC 099K32;  
 DT 01-JUN-2001 (TREMBlrel. 17, Created)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE HYPOThETICAL 68.4 KDA PROTEIN (FRAGMENT).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=MAMMARY TUMOR. WAP-TGF ALPHA MODEL. 7 MONTHS OLD, CROSS  
 RC TISSUE;  
 RA Strausberg R.;  
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC005490; AA05490.1; -;  
 DR HSSP; P05067; IAPP.  
 DR InterPro; IPR001868; A4\_APP.  
 DR InterPro; IPR002223; Kunitz\_BPTI.  
 DR Pfam; PF00014; Kunitz\_BPTI; 1.  
 DR PRINTS; PR00203; AMYLOIDA.  
 DR PRINTS; PR00759; BASICPTASE.  
 DR SMART; SM00131; KU; 1.  
 DR PROSITE; PS00319; A4\_EXTRA; 1.  
 DR PROSITE; PS00320; BPTI\_KUNITZ\_1; 1.  
 DR PROSITE; PS00280; BPTI\_KUNITZ\_2; 1.  
 DR PROSITE; PS0279; BPTI\_KUNITZ\_2; 1.  
 KW Hypothetical protein; Serine protease inhibitor.  
 FT NON\_TER  
 FT SEQUENCE 607 AA; 68391 MW; BF802214CBATD172 CRC64;  
 SQ  
 Query Match 100.0%; Score 48; DB 11; Length 607;  
 Best Local Similarity 100.0%; Pred. No. 0.15;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ISEVKMDAEF 10  
 |||||||  
 Db 503 ISEVKMDAEF 512

RESULT 7  
 095KN7 PRELIMINARY; PRT; 695 AA.  
 AC 095KN7;  
 DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE AMYLOID B-PROTEIN PRECURSOR.  
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecinae; Macaca.  
 NCBI\_TaxID=9541;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=CEREBELLUM;  
 RX MEDLINE-91273117; PubMed-1905108;  
 RX Podlasky M.B., Tolian D.R., Selkoe D.J.;  
 RT "Homology of the amyloid beta protein precursor in monkey and human  
 RT supports a primate model for beta amyloidosis in Alzheimer's  
 RT disease";  
 RL Am. J. Pathol. 138:1423-1435(1991).  
 DR EMBL; M58727; AAA36829.1; -;  
 FT SIGNAL 1 17 POTENTIAL.

FT CHAIN 597 636 POTENTIAL.  
 SQ SEQUENCE 695 AA; 78663 MW; 4F6EA0139F969D56 CRC64;

Query Match 100.0%; Score 48; DB 6; Length 695;  
 Best Local Similarity 100.0%; Pred. No. 0.17;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ISEVKMDAEF 10  
 |||||||  
 Db 591 ISEVKMDAEF 600

## RESULT 8

097487 PRELIMINARY; PRT; 695 AA.  
 AC 097487; P97942;  
 DT 01-MAY-1997 (TREMBlrel. 03, Created)  
 DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE HIPPOCAMPAL AMYLOID PROTEIN.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SAMP8; TISSUE=HIPPOCAMPUS;  
 RA Flood J.F., Kumar V.B., Sasser T., Morley J.E.;  
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE OF 581-662 FROM N.A.  
 RC STRAIN=129SV;  
 RA Wragg M.A., Busfield F., Duff K., Korenblatt K., Capechi M.,  
 RA Loring J.F., Goate A.M.;  
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U84012; AAB41502.1; -;  
 DR EMBL; U82624; AAB40919.1; -;  
 DR HSSP; P05067; IMMP.  
 DR MGD; MGI:88059; APP.  
 DR InterPro; IPR001868; A4\_APP.  
 DR Pfam; PF02177; A4\_EXTRA; 1.  
 DR PRINTS; PR00203; AMYLOIDA.  
 DR SMART; SM00006; A4\_EXTRA; 1.  
 DR PROSITE; PS00319; A4\_EXTRA; 1.  
 DR PROSITE; PS00320; A4\_EXTRA; 1.  
 SQ SEQUENCE 695 AA; 78414 MW; 9A5FBE2ED261236E CRC64;  
 Query Match 100.0%; Score 48; DB 11; Length 695;  
 Best Local Similarity 100.0%; Pred. No. 0.17;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ISEVKMDAEF 10  
 |||||||  
 Db 591 ISEVKMDAEF 600

RESULT 9  
 060496 PRELIMINARY; PRT; 695 AA.  
 AC 060496;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE PUTATIVE AMYLOID PRECURSOR PROTEIN.  
 OS Cavia sp.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.  
 NCBI\_TaxID=10143;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=BRAIN;  
 RX MEDLINE=97236426; PubMed-9116031;

```

RA Beck M., Mueller D., Bigl V.;
RT "Amyloid precursor protein in Guinea pigs - complete cDNA sequence and
RL Biochim. Biophys. Acta 1351:17-21(1997).
DR EMBL; X97631; CA66230.1; -.
DR HSSP; P05067; 1BA4.
DR InterPro; IPR001868; A4_APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
SQ SEQUENCE 695 AA; 78701 MW; 5196A0C4017F16AB CRC64;

Query Match 100.0%; Score 48; DB 11; Length 695;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISEVKMDAEF 10
Db 591 ISEVKMDAEF 600

RESULT 10
Q9TUI0 PRELIMINARY; PRT; 770 AA.
AC Q9TUI0;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE AMYLOID PRECURSOR PROTEIN.
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Kimura A., Takahashi T.;
RT "Amyloid Precursor Protein 770."
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB032550; BAB84580.1; -.
DR HSSP; P05067; 1AAP.
DR InterPro; IPR001868; A4_APP.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICTPASE.
DR SMART; SM00006; A4_EXTRA; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor.
SQ SEQUENCE 770 AA; 86961 MW; 5F7A1DCB28CC583E CRC64;

Query Match 100.0%; Score 48; DB 6; Length 770;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISEVKMDAEF 10
Db 666 ISEVKMDAEF 675

RESULT 11
Q93296 PRELIMINARY; PRT; 534 AA.
AC Q93296;
DT 01-NOV-1998 (TREMblrel. 08, Created)
DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)

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DE AMYLOID PROTEIN (FRAGMENT).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 98337885; PubMed=9671674;
RA Barnes N.Y., Li L., Yoshikawa K., Schwartz L.M., Oppenheim R.W.,
RA Milligan C.E.;
RT "Increased production of amyloid precursor protein provides a
RT substrate for caspase-3 in dying motoneurons."
RL J. Neurosci. 18:5869-5880(1998).
DR EMBL; AF042098; AAC25052.1; -.
DR HSSP; P05067; 1BA4.
DR InterPro; IPR001868; A4_APP.
DR PRINTS; PR00203; AMYLOIDA4.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
FT NON_TER 1
SQ SEQUENCE 534 AA; 60597 MW; FB53ECC2E6D4C92 CRC64;

Query Match 97.9%; Score 47; DB 13; Length 534;
Best Local Similarity 90.0%; Pred. No. 0.22;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISEVKMDAEF 10
Db 430 VSEVKMDAEF 439

RESULT 12
Q9PVL1 PRELIMINARY; PRT; 569 AA.
AC Q9PVL1;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE AMYLOID PROTEIN (FRAGMENT).
GN App.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA Coulson E.J., Paliaga K., Beyreuther K., Masters C.L.;
RT "What the evolution of the amyloid protein precursor supergene family
RT tells us about its function."
RL Neurochem. Int. 0:0-0(2000).
DR EMBL; AF030341; AAF12698.1; -.
DR HSSP; P05067; 1BA4.
DR InterPro; IPR001868; A4_APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
FT NON_TER 1
SQ SEQUENCE 569 AA; 64753 MW; 0AB8B851863A19D CRC64;

Query Match 97.9%; Score 47; DB 13; Length 569;
Best Local Similarity 90.0%; Pred. No. 0.23;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISEVKMDAEF 10
Db 466 VSEVKMDAEF 475

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RESULT 13
Q9DGCJ8      PRELIMINARY;      PRT;      695 AA.
ID   Q9DGCJ8
AC   Q9DGCJ8;
DT   01-MAR-2001 (TREMBLrel. 16, Created)
DT   01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE   BETA-AMYLROID PRECURSOR PROTEIN 695 ISOFORM.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Sarasa M., Rodolasse A., Sorribas V.;
RT   "Cloning of full-length chicken beta-amyloid precursor protein
RT   isoforms."
RL   Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR   EMBL; AF289218; AAG00593.1;
DR   HSSP; P05067; IBA4.
DR   InterPro; IPR001868; A4_APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
SQ   SEQUENCE 695 AA; 78565 MW; F201ED02AEC86D95 CRC64;

Query Match
Best Local Similarity 97.9%; Score 47; DB 13; Length 695;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISEVKMDAEF 10
DB 591 VSEVKMDAEF 600

RESULT 14
Q9DGCJ7      PRELIMINARY;      PRT;      751 AA.
ID   Q9DGCJ7;
AC   Q9DGCJ7;
DT   01-MAR-2001 (TREMBLrel. 16, Created)
DT   01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE   BETA-AMYLROID PRECURSOR PROTEIN 751 ISOFORM.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Sarasa M., Rodolasse A., Sorribas V.;
RT   "Cloning of full-length chicken beta-amyloid precursor protein
RT   isoforms."
RL   Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR   EMBL; AF289219; AAG00594.1;
DR   HSSP; P05067; IBA4.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00311; KU_1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1;
DR   PROSITE; PS0279; BPTI_KUNITZ_2; 1.
SQ   SEQUENCE 751 AA; 84705 MW; E78B9413A8033D84 CRC64;

Query Match
Best Local Similarity 97.9%; Score 47; DB 13; Length 751;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISEVKMDAEF 10
DB 647 VSEVKMDAEF 656

RESULT 15
Q98SG0      PRELIMINARY;      PRT;      693 AA.
ID   Q98SG0;
AC   Q98SG0;
DT   01-JUN-2001 (TREMBLrel. 17, Created)
DT   01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE   BETA-AMYLROID PRECURSOR PROTEIN A.
OS   APP.
GN   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Van den Hurk W.H.;
RL   Thesis (2001) Department of Biological Sciences,
RL   University of Nijmegen/Nijmegen, Netherlands.
DR   EMBL; AJ296150; CAC37193.1;
DR   HSSP; P05067; IH23.
DR   InterPro; IPR001868; A4_APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
KW   Signal.
FT   SIGNAL.
SQ   SEQUENCE 693 AA; 78568 MW; CAF1DF655C1A853 CRC64;

Query Match
Best Local Similarity 87.5%; Score 42; DB 13; Length 693;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISEVKMDAEF 10
DB 589 ISEVKMDSEY 598

Search completed: October 29, 2002, 10:29:40
Job time : 20.1429 secs

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OM protein - protein search, using sw model

Run on: October 29, 2002, 10:23:56 : Search time 9 seconds  
(without alignments)  
27.140 Million cell updates/sec

Title: US-09-580-018-3

Perfect score: 48

Sequence: 1 ISEVKMDAEF 10

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA: \*  
1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep: \*  
2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep: \*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep: \*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep: \*  
5: /cgn2\_6/ptodata/1/1aa/PCYUS.COMB.pep: \*  
6: /cgn2\_6/ptodata/1/1aa/Backfile1.pep: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	48	100.0	11	5	PCT-US94-07043A-7
2	48	100.0	12	5	PCT-US94-07043A-2
3	48	100.0	16	5	PCT-US94-07043A-1
4	48	100.0	27	1	US-08-141-3324-11
5	48	100.0	27	1	US-08-541-902-11
6	48	100.0	45	1	US-08-462-859A-5
7	48	100.0	45	1	US-08-123-659A-5
8	48	100.0	45	1	US-08-464-247A-5
9	48	100.0	45	1	US-08-464-248A-5
10	48	100.0	58	1	US-08-371-930-25
11	48	100.0	58	5	PCT-US94-01712-25
12	48	100.0	63	1	US-08-462-859A-3
13	48	100.0	63	1	US-08-462-859A-4
14	48	100.0	63	1	US-08-123-659A-3
15	48	100.0	63	1	US-08-123-659A-4
16	48	100.0	63	1	US-08-464-247A-3
17	48	100.0	63	1	US-08-464-247A-4
18	48	100.0	63	1	US-08-464-248A-3
19	48	100.0	63	1	US-08-464-248A-4
20	48	100.0	105	2	US-08-729-345-1
21	48	100.0	117	2	US-08-729-345-3
22	48	100.0	152	6	5187153-4
23	48	100.0	162	6	5220013-4
24	48	100.0	162	6	5223482-4
25	48	100.0	264	1	US-07-990-893-5
26	48	100.0	487	1	US-08-462-859A-9
27	48	100.0	487	1	US-08-123-659A-9

28	48	100.0	487	1	US-08-464-247A-9	Sequence 9, Appli
29	48	100.0	487	1	US-08-464-248A-9	Sequence 9, Appli
30	48	100.0	492	1	US-08-462-859A-7	Sequence 7, Appli
31	48	100.0	492	1	US-08-123-659A-7	Sequence 7, Appli
32	48	100.0	492	1	US-08-464-247A-7	Sequence 7, Appli
33	48	100.0	492	1	US-08-464-248A-7	Sequence 7, Appli
34	48	100.0	537	2	US-08-453-552-4	Sequence 4, Appli
35	48	100.0	537	2	US-08-710-637-4	Sequence 4, Appli
36	48	100.0	537	5	PCT-US93-00907-4	Sequence 4, Appli
37	48	100.0	656	1	US-08-371-930-23	Sequence 23, Appli
38	48	100.0	656	5	PCT-US94-01712-23	Sequence 23, Appli
39	48	100.0	676	1	US-08-371-930-24	Sequence 24, Appli
40	48	100.0	676	5	PCT-US94-01712-24	Sequence 24, Appli
41	48	100.0	694	1	US-08-339-152A-18	Sequence 18, Appli
42	48	100.0	694	2	US-08-007-999B-5	Sequence 5, Appli
43	48	100.0	694	2	US-08-689-276A-5	Sequence 5, Appli
44	48	100.0	695	1	US-08-371-930-27	Sequence 27, Appli
45	48	100.0	695	1	US-08-123-702-2	Sequence 2, Appli

#### ALIGNMENTS

RESULT 1  
PCT-US94-07043A-7  
Sequence 7, Application PC/TUS9407043A  
GENERAL INFORMATION:  
APPLICANT: Tamburini, Paul P.; Benz, G nter; H blich,  
APPLICANT: Dieter; Dreyer, Robert N.; Koenig, Gerhard  
TITLE OF INVENTION: CATHEPSIN D IS AN AMYLOIDGENIC  
TITLE OF INVENTION: PROTEASE IN ALZHEIMER S DISEASE  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Miles Inc.  
STREET: 400 Morgan Lane  
CITY: West Haven  
STATE: Connecticut  
COUNTRY: USA  
ZIP: 06516  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 800 kb storage  
COMPUTER: Sharp PC 4600  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/07043A  
FILING DATE: June 21, 1994  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/10889  
FILING DATE: November 12, 1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/995,660  
FILING DATE: December 16, 1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/880,914  
FILING DATE: May 11, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Pamela A. Simonton  
REGISTRATION NUMBER: 31,060  
REFERENCE/DOCKET NUMBER: MTI 224.3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (203) 937-2340  
TELEFAX: (203) 937-2795  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
PCT-US94-07043A-7  
Query Match 100.0%; Score 48; DB 5; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.00057;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ISEVKMDAEF 10  
|||||

Db 1 ISEVKMDAEF 10

RESULT 2  
PCT-US94-07043A-2  
Sequence 2, Application PC/TUS9407043A  
GENERAL INFORMATION:  
APPLICANT: Tamburini, Paul P.; Benz, G nter; H bich,  
APPLICANT: Dieter; Dreyer, Robert N.; Koenig, Gerhard  
TITLE OF INVENTION: CATHEPSIN D IS AN AMYLOIDGENIC  
TITLE OF INVENTION: PROTEASE IN ALZHEIMER S DISEASE  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Miles Inc.  
STREET: 400 Morgan Lane  
CITY: West Haven  
STATE: Connecticut  
COUNTRY: USA  
ZIP: 06516  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 800 kb storage  
COMPUTER: Sharp PC 4600  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/07043A  
FILING DATE: June 21, 1994  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/10889  
FILING DATE: November 12, 1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/995,660  
FILING DATE: December 16, 1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/880,914  
FILING DATE: May 11, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Pamela A. Simonton  
REGISTRATION NUMBER: 31,060  
REFERENCE/DOCKET NUMBER: MTI 224.3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (203) 937-2340  
TELEFAX: (203) 937-2795  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
PCT-US94-07043A-2

Query Match 100.0%; Score 48; DB 5; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0.00063;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ISEVKMDAEF 10  
|||||

Db 1 ISEVKMDAEF 10

RESULT 3  
PCT-US94-07043A-1  
Sequence 1, Application PC/TUS9407043A  
GENERAL INFORMATION:  
APPLICANT: Tamburini, Paul P.; Benz, G nter; H bich,  
APPLICANT: Dieter; Dreyer, Robert N.; Koenig, Gerhard  
TITLE OF INVENTION: CATHEPSIN D IS AN AMYLOIDGENIC  
TITLE OF INVENTION: PROTEASE IN ALZHEIMER S DISEASE  
NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Miles Inc.  
STREET: 400 Morgan Lane  
CITY: West Haven  
STATE: Connecticut  
COUNTRY: USA  
ZIP: 06516  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 800 kb storage  
COMPUTER: Sharp PC 4600  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/07043A  
FILING DATE: June 21, 1994  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/10889  
FILING DATE: November 12, 1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/995,660  
FILING DATE: December 16, 1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/880,914  
FILING DATE: May 11, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Pamela A. Simonton  
REGISTRATION NUMBER: 31,060  
REFERENCE/DOCKET NUMBER: MTI 224.3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (203) 937-2340  
TELEFAX: (203) 937-2795  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
PCT-US94-07043A-1

Query Match 100.0%; Score 48; DB 5; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0.00086;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ISEVKMDAEF 10  
|||||

Db 1 ISEVKMDAEF 10

RESULT 4  
US-08-141-324-11  
Sequence 11, Application US/08141324  
Patent No. 5475097  
GENERAL INFORMATION:  
APPLICANT: Travis, James  
APPLICANT: Potempa, Jan S.  
APPLICANT: Barr, Philip J.  
APPLICANT: Pavloff, Nadine  
APPLICANT: Pike, Robert N.  
TITLE OF INVENTION: Lysine-specific Porphyromonas gingivalis  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Greenlee and Winner, P.C.  
STREET: 5370 Manhattan Circle, Suite 201  
CITY: Boulder  
STATE: CO  
COUNTRY: US  
ZIP: 80303  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25



CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/141,324  
FILING DATE: 21-OCT-1993  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Ferber, Donna M.  
REGISTRATION NUMBER: 33,878  
REFERENCE/DOCKET NUMBER: 44-93  
TELEPHONE: 303-499-8080  
TELEFAX: 303-499-8080  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-141-324-11

Query Match 100.0%; Score 48; DB 1; Length 27;  
Best Local Similarity 100.0%; Pred. No. 0.0015;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ISEVKMDAEF 10  
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Db 3 ISEVKMDAEF 12

RESULT 5  
US-08-541-902-11  
Sequence 11, Application US/08541902  
Patent No. 5707620  
GENERAL INFORMATION:  
APPLICANT: Travis, James  
APPLICANT: Potempa, Jan S.  
APPLICANT: Barr, Philip J.  
APPLICANT: Pavloff, Nadine  
APPLICANT: Pike, Robert N.  
TITLE OF INVENTION: Lysine-specific Porphyromonas gingivalis  
TITLE OF INVENTION: Protease  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Greenlee and Winner, P.C.  
STREET: 5370 Manhattan Circle, Suite 201  
CITY: Boulder  
STATE: CO  
COUNTRY: US  
ZIP: 80303  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/541,902  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/141,324  
FILING DATE: 21-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Ferber, Donna M.  
REGISTRATION NUMBER: 33,878  
REFERENCE/DOCKET NUMBER: 44-93  
TELEPHONE: 303-499-8080  
TELEFAX: 303-499-8080  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27 amino acids

TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-541-902-11

Query Match 100.0%; Score 48; DB 1; Length 27;  
Best Local Similarity 100.0%; Pred. No. 0.0015;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ISEVKMDAEF 10  
|||  
Db 3 ISEVKMDAEF 12

RESULT 6  
US-08-462-859A-5  
Sequence 5, Application US/08462859A  
Patent No. 5652092  
GENERAL INFORMATION:  
APPLICANT: Jacobsen, J. S.  
APPLICANT: Vittek, M. P.  
TITLE OF INVENTION: No. 5652092el Amyloid Precursor and Method of  
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation  
TITLE OF INVENTION: of B-Amyloid Peptide  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: American Cyanamid Company  
STREET: One Cyanamid Plaza  
CITY: Wayne  
STATE: New Jersey  
COUNTRY: United States  
ZIP: 07470-8426  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/462,859A  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Barnhard, Elizabeth M.  
REGISTRATION NUMBER: 31,088  
REFERENCE/DOCKET NUMBER: 31,844-04  
TELEPHONE: (201)831-3305  
TELEFAX: (201)831-3305  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 45 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-462-859A-5

Query Match 100.0%; Score 48; DB 1; Length 45;  
Best Local Similarity 100.0%; Pred. No. 0.0026;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ISEVKMDAEF 10  
|||  
Db 4 ISEVKMDAEF 13

RESULT 7  
US-08-123-659A-5  
Sequence 5, Application US/08123659A  
Patent No. 5656477

GENERAL INFORMATION:  
APPLICANT: Jacobsen, J. S.  
APPLICANT: Vittek, M. P.  
TITLE OF INVENTION: No. 5656477e1 Amyloid Precursor and Method of  
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation  
TITLE OF INVENTION: of B-Amyloid Peptide  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Anne Rosenblum  
STREET: 163 Delaware Avenue, Suite 212  
CITY: Delmar  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 12054  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA: US/08/123,659A  
APPLICATION NUMBER: US/08/123,659A  
FILING DATE: 20-SEP-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Rosenblum, Anne M.  
REGISTRATION NUMBER: 30,419  
REFERENCE/DOCKET NUMBER: 31,844-01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (518)475-0611  
TELEFAX: (518)475-0619  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 45 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-123-659A-5

Query Match 100.0%; Score 48; DB 1; Length 45;  
Best Local Similarity 100.0%; Pred. No. 0.0026;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISEVKMDAEF 10  
|||||  
DB 4 ISEVKMDAEF 13

RESULT 8  
US-08-464-247A-5  
Sequence 5, Application US/08464247A  
Patent No. 5693478  
GENERAL INFORMATION:  
APPLICANT: Jacobsen, J. S.  
APPLICANT: Vittek, M. P.  
TITLE OF INVENTION: No. 5693478e1 Amyloid Precursor and Method of  
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation  
TITLE OF INVENTION: of B-Amyloid Peptide  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: American Cyanamid Company  
STREET: One Campus Drive  
CITY: Parsippany  
STATE: New Jersey  
COUNTRY: United States  
ZIP: 07054  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: US/08/464,247A  
APPLICATION NUMBER: US/08/464,247A  
FILING DATE: 05-JUN-1995

CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Barnhard, Elizabeth M.  
REGISTRATION NUMBER: 31,088  
REFERENCE/DOCKET NUMBER: 31,844-03  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-683-2158  
TELEFAX: 201-683-4117  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 45 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-464-247A-5

Query Match 100.0%; Score 48; DB 1; Length 45;  
Best Local Similarity 100.0%; Pred. No. 0.0026;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISEVKMDAEF 10  
|||||  
DB 4 ISEVKMDAEF 13

RESULT 9  
US-08-464-248A-5  
Sequence 5, Application US/08464248A  
Patent No. 5703209  
GENERAL INFORMATION:  
APPLICANT: Jacobsen, J. S.  
APPLICANT: Vittek, M. P.  
TITLE OF INVENTION: No. 5703209e1 Amyloid Precursor and Method of  
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation  
TITLE OF INVENTION: of B-Amyloid Peptide  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: American Cyanamid Company  
STREET: One Cyanamid Plaza  
CITY: Wayne  
STATE: New Jersey  
COUNTRY: United States  
ZIP: 07470-8426  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: US/08/464,248A  
APPLICATION NUMBER: US/08/464,248A  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Barnhard, Elizabeth M.  
REGISTRATION NUMBER: 31,088  
REFERENCE/DOCKET NUMBER: 31,844-02  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (201)831-3246  
TELEFAX: (201)831-3305  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 45 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-464-248A-5

Query Match 100.0%; Score 48; DB 1; Length 45;  
Best Local Similarity 100.0%; Pred. No. 0.0026;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISEVKMDAEF 10  
|||||  
Db 4 ISEVKMDAEF 13

## RESULT 10

US-08-371-930-25  
Sequence 25, Application US/08371930  
Patent No. 5578451  
GENERAL INFORMATION:  
APPLICANT: Nishimoto, Ikuo  
TITLE OF INVENTION: ALZHEIMER'S DISEASE THERAPEUTICS  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" diskette, 1.44 Mb  
COMPUTER: IBM PS/2 Model 502 or 55SX  
OPERATING SYSTEM: MS-DOS (Version 5.0)  
SOFTWARE: Wordperfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/371,930  
FILING DATE:  
CLASSIFICATION: 436  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/019,208  
FILING DATE: February 18, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 00786/154001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 58  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-371-930-25

Query Match 100.0%; Score 48; DB 1; Length 58;  
Best Local Similarity 100.0%; Pred. No. 0.0034;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISEVKMDAEF 10  
|||||  
Db 41 ISEVKMDAEF 50

## RESULT 11

PCT-US94-01712-25  
Sequence 25, Application PC/TUS9401712  
GENERAL INFORMATION:  
APPLICANT: Nishimoto, Ikuo  
TITLE OF INVENTION: ALZHEIMER'S DISEASE THERAPEUTICS  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM PS/2 Model 502 or 55SX  
OPERATING SYSTEM: MS-DOS (Version 5.0)  
SOFTWARE: Wordperfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/01712  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/019,208  
FILING DATE: February 18, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 00786/154001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 58  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
PCT-US94-01712-25

Query Match 100.0%; Score 48; DB 5; Length 58;  
Best Local Similarity 100.0%; Pred. No. 0.0034;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISEVKMDAEF 10  
|||||  
Db 41 ISEVKMDAEF 50

## RESULT 12

US-08-462-859A-3  
Sequence 3, Application US/08462859A  
Patent No. 5652092  
GENERAL INFORMATION:  
APPLICANT: Jacobsen, J. S.  
TITLE OF INVENTION: No. 5652092el Amyloid Precursor and Method of  
TITLE OF INVENTION: Using Same to Access Agents which Down-Regulate Formation  
TITLE OF INVENTION: of B-Amyloid Peptide  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: American Cyanamid Company  
STREET: One Cyanamid Plaza  
CITY: Wayne  
STATE: New Jersey  
COUNTRY: United States  
ZIP: 07470-8426  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/462,859A  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Barnhard, Elizabeth M.  
REGISTRATION NUMBER: 31,088  
REFERENCE/DOCKET NUMBER: 31,844-04  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (201)831-3246  
TELEFAX: (201)831-3305  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 63 amino acids  
TYPE: amino acid

STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-462-859A-3

Query Match 100.0%; Score 48; DB 1; Length 63;  
Best Local Similarity 100.0%; Pred. No. 0.0038;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISEVKMDAEF 10  
|||||  
DB 4 ISEVKMDAEF 13

RESULT 13  
US-08-462-859A-4  
Sequence 4, Application US/08462859A  
Patent No. 5652092  
GENERAL INFORMATION:  
APPLICANT: Jacobsen, J. S.  
TITLE OF INVENTION: No. 5652092el Amyloid Precursor and Method of  
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: American Cyanamid Company  
STREET: One Cyanamid Plaza  
CITY: Wayne  
STATE: New Jersey  
COUNTRY: United States  
ZIP: 07470-8426  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/462,859A  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Barnhard, Elizabeth M.  
REGISTRATION NUMBER: 31,088  
REFERENCE/DOCKET NUMBER: 31,844-04  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (201)831-3246  
TELEFAX: (201)831-3305  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 63 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-462-859A-4

Query Match 100.0%; Score 48; DB 1; Length 63;  
Best Local Similarity 100.0%; Pred. No. 0.0038;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISEVKMDAEF 10  
|||||  
DB 4 ISEVKMDAEF 13

RESULT 14  
US-08-123-659A-3  
Sequence 3, Application US/08123659A  
Patent No. 5656477  
GENERAL INFORMATION:  
APPLICANT: Jacobsen, J. S.  
APPLICANT: Vitek, M. P.

TITLE OF INVENTION: No. 5656477el Amyloid Precursor and Method of  
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Anne Rosenblum  
STREET: 163 Delaware Avenue, Suite 212  
CITY: Delmar  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 12054  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/123,659A  
FILING DATE: 20-SEP-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Rosenblum, Anne M.  
REGISTRATION NUMBER: 30,419  
REFERENCE/DOCKET NUMBER: 31,844-01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (518)475-0611  
TELEFAX: (518)475-0619  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 63 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-123-659A-3

Query Match 100.0%; Score 48; DB 1; Length 63;  
Best Local Similarity 100.0%; Pred. No. 0.0038;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISEVKMDAEF 10  
|||||  
DB 4 ISEVKMDAEF 13

RESULT 15  
US-08-123-659A-4  
Sequence 4, Application US/08123659A  
Patent No. 5656477  
GENERAL INFORMATION:  
APPLICANT: Jacobsen, J. S.  
APPLICANT: Vitek, M. P.  
TITLE OF INVENTION: No. 5656477el Amyloid Precursor and Method of  
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Anne Rosenblum  
STREET: 163 Delaware Avenue, Suite 212  
CITY: Delmar  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 12054  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/123,659A  
FILING DATE: 20-SEP-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Rosenblum, Anne M.

REGISTRATION NUMBER: 30,419  
REFERENCE/DOCKET NUMBER: 31,844-01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (518)475-0611  
TELEFAX: (518)475-0619  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 63 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-123-659A-4

Query Match 100.0%; Score 48; DB 1; Length 63;  
Best Local Similarity 100.0%; Pred. No. 0.0038;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ISEVKMDAEF 10  
| | | | | | | | | |  
Db 4 ISEVKMDAEF 13

Search completed: October 29, 2002, 10:32:07  
Job time : 10 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 29, 2002, 10:22:21 ; Search time 23.1429 Seconds  
(without alignments)  
47.995 Million cell updates/sec

Title: US-09-580-018-4

Perfect score: 49

Sequence: 1 SEVKMDAEPK 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A.Geneseq\_032802.\*

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22:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	49	100.0	10	13	AA24261	Human amyloidin pr
2	49	100.0	10	21	AA69703	Beta-APP alpha-sec
3	49	100.0	10	22	AAE10654	Human wild-type AP
4	49	100.0	10	22	AAE06899	Human amyloid prec
5	49	100.0	10	22	AAU06628	Asp2 recognition s
6	49	100.0	10	22	AAU07227	Human beta-amyloid
7	49	100.0	10	22	AAE02606	Human wild-type AP
8	49	100.0	10	22	AAE66574	Synthetic peptide
9	49	100.0	10	22	AAH46208	Human APP derived
10	49	100.0	10	22	AAE61336	Synthetic peptide f
11	49	100.0	11	22	AAE5143	APP beta-secretase

12	49	100.0	11	22	AAE75144	ASP 1 substrate se
13	49	100.0	11	22	AAE97468	ASP2 substrate w11
14	49	100.0	13	19	AAW70869	Beta-amyloid pepti
15	49	100.0	16	21	AAE06315	Human beta-amyloid
16	49	100.0	16	21	AAE06317	Human beta-amyloid
17	49	100.0	18	22	AAE00608	Beta-amyloid precu
18	49	100.0	20	21	AAE69713	Beta-APP alpha-sec
19	49	100.0	23	22	AAE75147	ASP 1 substrate se
20	49	100.0	23	22	AAE97473	ASP2 substrate w11
21	49	100.0	33	20	AAE98002	Amyloid precursor
22	49	100.0	39	21	AAE69717	Beta-APP alpha-sec
23	49	100.0	45	18	AAE26512	Amyloid precursor
24	49	100.0	45	18	AAE26392	Amyloid precursor
25	49	100.0	45	19	AAW44748	APP-REP 751 (BAP d
26	49	100.0	45	19	AAW42977	Deletion beta-amy
27	49	100.0	53	16	AAE64168	Variant beta-amylo
28	49	100.0	54	21	AAE32126	Amyloid-beta precu
29	49	100.0	57	21	AAE10910	Human amyloid prec
30	49	100.0	58	15	AAE58937	Amyloid precursor
31	49	100.0	63	18	AAE26511	Amyloid precursor
32	49	100.0	63	18	AAE26391	Amyloid precursor
33	49	100.0	63	19	AAW44747	APP-REP 751 BAP pe
34	49	100.0	63	19	AAW44746	APP-REP 751 (BAP E
35	49	100.0	63	19	AAW42975	Beta-amyloid pepti
36	49	100.0	63	19	AAW42976	Beta-amyloid pepti
37	49	100.0	67	19	AAW71377	Peptide derived fr
38	49	100.0	93	22	AAE19083	Novel human diagno
39	49	100.0	104	19	AAW51100	Amino acid sequenc
40	49	100.0	112	17	AAE93556	Familial Alzheimer
41	49	100.0	115	20	AAW97999	London-PAD APP pol
42	49	100.0	117	19	AAW51102	Flag-amyloid prote
43	49	100.0	162	9	AAE83151	Deduced sequence 1
44	49	100.0	162	12	AAE10023	Beta-amyloid-relat
45	49	100.0	162	14	AAE37863	Deduced from clone

## ALIGNMENTS

RESULT 1	AAE24261	standard; Protein: 10 AA.
ID	AAE24261	
AC	AAE24261	
DT	09-NOV-1992	(first entry)
XX	Human amyloidin protease substrate sequence #1.	
DE		
XX		
KW	Alzheimer's disease; beta amyloid precursor protein; APP; zinc;	
KW	metalloprotease; hAP; protease inhibitor; APP592-601	
XX		
OS	Synthetic.	
XX		
FT	Key	Location/Qualifiers
FT	Modified-site	1
FT		/note="Acetylated-Ser"
XX		
XX	W09207068-A.	
XX		
XX	30-APR-1992.	
XX		
XX	04-OCT-1991;	91WO-US07290.
XX		
XX	05-OCT-1990;	90US-0594122.
XX	30-SEP-1991;	91US-0766351.
XX		
XX	(ATHE-) ATHENA NEUROSCIENCES INC.	
XX	(ELIL) LILLY & CO ELI.	
XX		
XX	Dorey HF, Johnstone EM, Little SP, McConlogue L, Seubert PA;	
XX	Sinha S;	

DR WPI: 1992-167148/20.  
XX Human amyloidin protease - used for cleaving Met-Asp bond in  
PT amyloid-like substrate for identifying protease inhibitors  
XX  
PS Claim 1; Page 52; 62pp; English.  
XX  
CC Claimed human amyloidin protease is defined by its ability to  
CC cleave the Met-Asp bond of this synthetic substrate. The substrate,  
CC which corresponds to residues 592 to 601 of the 695 amino acid APP,  
CC can be used in an assay for identifying inhibitors of proteases  
CC which cleave Met-Asp bonds, e.g. amyloidin, human skin chymase or  
CC rat mast cell protease I or II.  
CC See AAR24260-3, AAR24266-7 and AAQ24875-Q24887.  
CC  
XX  
SQ Sequence 10 AA:  
  
Query Match 100.0%; Score 49; DB 13; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.00042;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 SEVKMDAEFR 10  
| | | | | | | | | |  
Db 1 SEVKMDAEFR 10  
  
RESULT 2  
AA69703  
ID AAY69703 standard; peptide: 10 AA.  
XX  
AC AAY69703;  
XX  
DT 11-APR-2000 (first entry)  
XX  
XX Beta-APP alpha-secretase substrate [KMD]-APP(-5,+5).  
DE  
XX Nootropic; neuroprotective; beta-amyloid precursor protein; metabolism;  
KM cleavage site; beta-secretase; neurodegenerative disease;  
KM Alzheimer's disease.  
XX  
OS Homo sapiens.  
XX  
PN MO9964587-A1.  
XX  
PD 16-DEC-1999.  
XX  
PF 04-JUN-1999; 99WO-FR01326.  
XX  
PR 05-JUN-1998; 98FR-0007068.  
PR 31-MAR-1999; 99US-0122599.  
XX  
PA (RHON ) RHONE-POULENC RORER SA.  
PA (UYPA ) UNIV CURIE PARIS VI P & M.  
XX  
XX Rholam M, Munoz-Glamez N, Moutaouakil M, Cohen P, Bertrand P;  
XX WPI: 2000-097537/08.  
DR  
XX Polypeptide with beta-secretase activity, specific for wild-type  
PT amyloid precursor protein, useful in treating Alzheimer's disease -  
XX  
PS Example 3; Page 24; 44pp; French.  
XX  
CC Peptides AAY69702-Y69718 represent synthetic peptide substrates for a  
CC novel polypeptide with beta-secretase activity that can cleave  
CC specifically the natural beta-amyloid precursor protein (bAPP). Normal  
CC cleavage of the protein occurs between amino acids Met596-Asp597 and  
CC Val36-Ile637 (positions 4-5 and 44-45 of AAY69701). The novel  
CC polypeptide is used to identify agents that interact specifically with  
CC it. These agents regulate metabolism of APP, particularly they slow down  
CC or reduce production of beta-amyloid, so can be used to treat  
CC neurodegenerative diseases, particularly Alzheimer's disease.  
CC  
XX

SQ Sequence 10 AA:  
  
Query Match 100.0%; Score 49; DB 21; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.00042;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 SEVKMDAEFR 10  
| | | | | | | | | |  
Db 1 SEVKMDAEFR 10  
  
RESULT 3  
AAE10654  
ID AAE10654 standard; peptide: 10 AA.  
XX  
AC AAE10654;  
XX  
DT 10-DEC-2001 (first entry)  
XX  
DE Human wild-type APP beta-secretase peptide, PHA-95812E.  
XX  
XX Human; aspartyl protease 1; Aspl; amyloid precursor protein;  
KW Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;  
KW amyloid plaque; neuronal loss; proteolytic; nootropic; neuroprotective;  
KW APP beta-secretase peptide.  
XX  
OS Homo sapiens.  
XX  
XX  
FH Key Location/Qualifiers  
FT Cleavage-site 5..6  
XX  
XX GB2357767-A.  
XX  
PD 04-JUL-2001.  
XX  
XX 22-SEP-2000; 2000GB-0023315.  
XX  
PR 23-SEP-1999; 99US-0155493.  
PR 23-SEP-1999; 99US-0404133.  
PR 23-SEP-1999; 99WO-US20881.  
PR 13-OCT-1999; 99US-0416901.  
PR 06-DEC-1999; 99US-0169232.  
XX  
XX (PHAA ) PHARMACIA & UPJOHN CO.  
XX  
PA Bienkowski MJ, Gurney M;  
XX  
PI WPI: 2001-444208/48.  
DR  
XX Polypeptide comprising fragments of human aspartyl protease with  
PT amyloid precursor protein processing activity and alpha-secretase  
PT activity, for identifying modulators useful in treating Alzheimer's  
PT disease -  
XX  
XX Example 12; Page 84; 187pp; English.  
XX  
XX The patent discloses human aspartyl protease 1 (hu-Aspl) or modified  
CC Aspl proteins which lack transmembrane domain or amino terminal  
CC domain or cytoplasmic domain and retains alpha-secretase activity  
CC and amyloid protein precursor (APP) processing activity. The proteins  
CC of the invention are useful for assaying hu-Aspl alpha-secretase  
CC activity, which in turn is useful for identifying modulators of  
CC hu-Aspl alpha-secretase activity, where modulators that increase  
CC hu-Aspl alpha-secretase activity are useful for treating Alzheimer's  
CC disease (AD) which causes progressive dementia with consequent  
CC formation of amyloid plaques, neurofibrillary tangles, gliosis and  
CC neuronal loss. Hu-Aspl protease substrate is useful for assaying  
CC hu-Aspl proteolytic activity, by contacting hu-Aspl protein with  
CC the substrate under acidic conditions and determining the level of  
CC hu-Aspl proteolytic activity. The present sequence is wild-type  
CC human amyloid precursor protein (APP) beta-secretase specific  
CC substrate peptide, PHA-95812E. This peptide is used for assaying  
CC the beta-secretase activity of human Aspartyl protease 2a (Asp2a)  
CC



CC protein. The peptide is also used for determining the relationship  
CC between Aspartyl protease 1 (Asp1) and APP protein.

SO Sequence 10 AA;

Query Match 100.0%; Score 49; DB 22; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.00042;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SEVKMDAEFR 10  
| | | | | | | | | |  
Db 1 SEVKMDAEFR 10

#### RESULT 4

AAE06899 standard; peptide; 10 AA.

AAE06899;

23-OCT-2001 (first entry)

Human amyloid precursor protein wild-type beta-secretase peptide.

Human; aspartyl protease 2; Asp 2; beta-amyloid precursor protein; APP;  
beta-secretase; Alzheimer's disease; dementia; amyloid plaque; gliosis;  
neurofibrillary tangle; neuronal loss; amyloid-beta peptide; neurotropic;  
neuroprotective; antisense therapy; gene therapy.

Homo sapiens.

Key Location/Qualifiers  
Cleavage-site 5.6

MO200150829-A2.

19-JUL-2001.

09-MAY-2001; 2001WO-1B00799.

09-MAY-2001; 2001WO-1B00799.

(BIEN/) BIENKOWSKI M J.  
(GURN/) GURNEY M E.  
(HEIN/) HEINRIKSON R L.  
(PARO/) PARODI L A.  
(YANR/) YAN R.

Bienkowski MJ, Gurney ME, Heinrichson RL, Parodi LA, Yan R;

WPI: 2001-483072/52.

Novel purified polypeptide comprising fragment of mammalian aspartyl  
protease 2, lacking Asp2 transmembrane domain and retaining beta  
secretase activity of Asp2 useful for identifying inhibitors of Asp2  
activity

Claim 127; Page 80; 185pp; English.

The invention relates to human aspartyl proteases (Hu-Asp), beta-amyloid  
precursor protein (APP) isoforms and their corresponding DNA molecules.  
Human aspartyl proteases can act as beta-secretase proteases useful for  
treating Alzheimer's disease. APP isoforms are useful for identifying  
modulators of amyloid-beta peptide production, for use in designing  
therapeutics for the treatment and prevention of Alzheimer's disease,  
dementia, formation of amyloid plaques, neurofibrillary tangles, gliosis  
and neuronal loss. APP isoforms are also used in methods for identifying  
inhibitors and modulators of human Asp2 activity. The invention relates  
to a method for identifying agents that modulate the activity of human  
aspartyl protease Asp2. Amyloid-beta peptides obtained from APP are used  
as a means to screen in cellular assays for the inhibitors of beta and  
gamma-secretase. Hu-Asp DNA fragments are useful as probes or primers in  
polymerase chain reactions (PCR). The probes are useful for detecting

CC Hu-Asp nucleic acids in in vitro assays and in Northern and Southern  
CC blots. The present sequence is human amyloid precursor protein (APP)  
CC wild type beta-secretase peptide used in beta-secretase assay.

SO Sequence 10 AA;

Query Match 100.0%; Score 49; DB 22; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.00042;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SEVKMDAEFR 10  
| | | | | | | | | |  
Db 1 SEVKMDAEFR 10

#### RESULT 5

AAU06628 standard; Peptide; 10 AA.

AAU06628;

24-OCT-2001 (first entry)

Asp2 recognition site from wild-type APP.

Aspartyl protease; Asp2; beta-secretase; neurotropic;  
KW neuroprotective; amyloid protein precursor; APP; Alzheimer's disease;  
KW amyloid-beta; Abeta.

Homo sapiens.

Key Location/Qualifiers  
Cleavage-site 5  
/label= Asp2-protease\_cleavage\_site

WO200149098-A2.

12-JUL-2001.

09-MAY-2001; 2001WO-1B00798.

09-MAY-2001; 2001WO-1B00798.

(BIEN/) BIENKOWSKI M J.  
(GURN/) GURNEY M E.  
(HEIN/) HEINRIKSON R L.  
(PARO/) PARODI L A.  
(YANR/) YAN R.

Bienkowski MJ, Gurney ME, Heinrichson RL, Parodi LA, Yan R;

WPI: 2001-502549/55.

Novel purified polypeptide comprising fragment of mammalian aspartyl  
protease 2, lacking Asp2 transmembrane domain and retaining beta  
secretase activity of Asp2 useful for identifying inhibitors of Asp2  
activity

Claim 127; Page 101; 185pp; English.

The invention relates to a purified polypeptide comprising a fragment of  
mammalian aspartyl protease (Asp2) protein which lacks the Asp2  
transmembrane domain and the Asp2 protein, and where the polypeptide and  
the fragment retain the beta-secretase activity of the mammalian Asp2  
protein. The invention also details polynucleotides for the Asp  
proteins and vectors expressing them, and a polypeptide (isoform of  
amyloid protein precursor (APP)) comprising the amino acid sequence of an  
APP or its fragment containing an APP cleavage site recognizable by a  
mammalian beta-secretase, and further comprising two lysine residues at  
the carboxyl terminus of the amino acid sequence of the mammalian APP or  
APP fragment. Also included in the invention are methods of identifying  
modulators or inhibitors of Asp2. Modulators and inhibitors of Asp2 are  
useful for treating Alzheimer's disease. APP is useful in methods for

CC identifying inhibitors or modulators of human Asp2 activity and  
CC amyloid-beta (Aβeta) peptide production. APP is also useful in designing  
CC therapeutics for the treatment or prevention of Alzheimer's disease.  
CC APP comprising the APP-Sw-beta-secretase peptide sequence (NDA), which  
CC is associated with increased levels of Aβeta processing is useful in  
CC assays relating the Alzheimer's research. The expression vector is useful  
CC for recombinantly expressing APP. Nucleic acids that hybridise to  
CC Asp oligonucleotides are useful as probes or primers. The probes are  
CC useful for detecting Hu-Asp nucleic acids in *in vitro* assays and in  
CC Northern and Southern blots. The present sequence is a peptide substrate  
CC for Asp2 corresponding to the wild-type APP beta-secretase site.

Query Match	100.0%	Score 49	DB 22	Length 10
Best Local Similarity	100.0%	Pred. NO.	0.00042	
Matches 10; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

```
Qy 1 SEVKMDAEFR 10
    | | | | | | | |
Db 1 SEVKMDAEFR 10
```

RESULT 6  
AAU07227  
ID AAU07227 standard; Peptide; 10 AA

AC AAU07227;

DT 24-OCT-2001 (first entry)

DE Human beta-amyloid protein precursor, APP-beta40 and 42 secretase site.

KW Human; aspartyl protease 1; Asp-1; nootropic; neuroprotective;  
 KW aspartyl protease 2; Asp2; amyloid protein precursor; APP;  
 KW beta-secretase; Alzheimer's disease; APP-beta40; APP-beta42.

OS Homo sapiens.

PN WO200149097-A2.

PD 12-JUL-2001

PF 09-MAY-2001; 2001WO-IB00797.

PR 09-MAY-2001; 2001WO-IB00797.

PA (BIEN/) BIENKOWSKI M J.

PA (HEIN/) HEINRIKSON R L.

PA (YANR/) YAN R.

PI Bienkowski MJ, Gurney ME, Heinrichson RL, Parodi LA, Yan R, ...

DR WPI; 2001-502548/55.

PT Novel purified polypeptide comprising fragment of mammalian aspartyl  
PT protease 2, lacking Asp2 transmembrane domain and retaining beta  
PT serinease activity of Asp2 useful for identifying inhibitors of Asp2  
PT activity

PS Claim 127; Page 101; 185pp; English.

CC The invention relates to a novel purified polypeptide comprising a  
CC fragment of mammalian asparlyl protease 2 (Asp2) protein which lacks the  
CC Asp2 transmembrane domain and the Asp2 protein, and where the polypeptide  
CC and the fragment retain the beta-secretase activity of the mammalian Asp2  
CC protein. Also included is an isoform of amyloid protein precursor (APP)  
CC comprising the amino acid sequence of a APP or its fragment containing  
CC an APP cleavage site recognizable by a mammalian beta-secretase, and  
CC further comprising two lysine residues at the carboxyl terminus of the  
CC amino acid sequence of the mammalian APP or APP fragment. The

polypeptides are used for assaying for modulators of beta-secretase activity; identifying agents that inhibit the APP processing activity of human Asp2 aspartyl protease (Hu-Asp2); identifying agents that modulate the activity of Asp2; and for reducing cellular production of amyloid beta (beta) from APP. Agents identified by the above methods are useful for treating Alzheimer's disease; and for identifying modulators of amyloid-beta (Abeta) peptide production, for use in designing therapeutics for the treatment or prevention of Alzheimer's disease. Probes and primers derived from Asp nucleic acid sequences are useful for detecting Hu-Asp nucleic acids in *in vitro* assays and in Northern and Southern blots. The present sequence represents the amino acid sequence of human amyloid protein precursor, APP-beta40 and APP-beta42 secretase sites.

SO	Sequence	10 AA;
	Query Match	100.0%; Score 49; DB 22; Length 10;
	Best Local Similarity	100.0%; Pred. No. 0.00042;
Matches	10; Conservative	0; Mismatches 0; Indels 0; Gaps 0

Qy	1	SEVKMDAEFR	10
Db	1	SEVKMDAEFR	10

RESULT 7  
AAE02606  
ID AAE02606 standard; peptide; 10 AA

AC AAE02606;

DT 10-AUG-2001 (first entry)

DE Human wild-type APP beta-secretase substrate peptide, PHA-95812E

KW Human; alpha-secretase; amyloid precursor protein; APP; therapy;  
KW Alzheimer's disease; antialzheimer's; aspartyl protease 2a; Asp2a  
KW beta-secretase.

OS Homo sapiens

FH	Key	Location/Qualifiers
1	1	1
2	2	2
3	3	3
4	4	4
5	5	5
6	6	6
7	7	7
8	8	8
9	9	9
10	10	10
11	11	11
12	12	12
13	13	13
14	14	14
15	15	15
16	16	16
17	17	17
18	18	18
19	19	19
20	20	20
21	21	21
22	22	22
23	23	23
24	24	24
25	25	25
26	26	26
27	27	27
28	28	28
29	29	29
30	30	30
31	31	31
32	32	32
33	33	33
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38	38	38
39	39	39
40	40	40
41	41	41
42	42	42
43	43	43
44	44	44
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90	90	90
91	91	91
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94	94	94
95	95	95
96	96	96
97	97	97
98	98	98
99	99	99
100	100	100

XX

XX

XX

XX

PR 23-SEP-1999; 99WO-US20881.

PR 06-DEC-1999; 99US-0169232.

PA ( PHAA ) PHARMACIA &amp; UPJOHN CO.

PI Gurney M, Bienkowski MJ;

DR WPI; 2001-290516/30

PT Enzymes that cleave the alpha-secretase site of the amyloid precursor

PS Example 12; Page 85; 189pp; English

CC The present invention relates to enzymes for cleaving the alpha-  
CC secretase site of the amyloid precursor protein (APP) and methods of  
CC identifying those enzymes. The methods may be used to identify enzymes  
CC that may be used to cleave the alpha-secretase cleavage site of the APP  
CC protein. The enzymes may be used to treat or modulate the progress of  
CC Alzheimer's disease. The present sequence is human wild-type amyloid  
CC precursor protein (APP) beta-secretase specific substrate peptide,



```

XX Synthetic peptide from beta amyloid precursor protein.
PA Memapsin 2; catalyst; Alzheimer's.
XX
XX Unidentified.
XX
XX WO200100663-A2.
XX
XX 04-JAN-2001.
XX
XX 27-JUN-2000; 2000WO-US17661.
XX
XX 28-JUN-1999; 99US-0141363.
XX 30-NOV-1999; 99US-0168060.
XX 25-JAN-2000; 2000US-0177836.
XX 27-JAN-2000; 2000US-0178368.
XX 08-JUN-2000; 2000US-0210292.
XX
XX (OKLA-) OKLAHOMA MEDICAL RES FOUND.
XX
XX Tang JUN, Lin X, Koelsch G;
XX
XX WPI; 2001-102885/11.
XX
XX Purified recombinant catalytically active memapsin 2, used to screen
XX inhibitors of it, which are used to treat and prevent Alzheimer's
XX disease.
XX
XX Claim 6; Page 11; 86pp; English.
XX
XX The present invention relates to a purified recombinant
XX catalytically active memapsin 2. The invention may be used for
XX isolating inhibitors which are used to treat or prevent
XX Alzheimer's disease. The invention may also be used to screen
XX for individuals more genetically prone to develop Alzheimer's
XX disease.
XX
XX Sequence 10 AA:
SQ
Query Match 100.0%; Score 49; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00042;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 SEVKMDAEFR 10
DB 1 SEVKMDAEFR 10
RESULT 11
AAB75143
ID AAB75143 standard; peptide; 11 AA.
XX
XX AAB75143;
XX
XX 08-AUG-2001 (first entry)
XX
XX APP beta-secretase cleavage site spanning peptide SEQ ID NO:1.
XX
XX Amyloid precursor protein; APP; Asp 1; endocrepisin 1; inhibition;
XX Transmembrane aspartyl proteinase; APP Swedish variant; neurotrophic;
XX neuroprotective; beta-secretase cleavage site; Alzheimer's disease;
XX beta amyloid protein-related disease; antialzheimer.
XX
XX Homo sapiens.
XX
XX WO200131054-A1.
XX
XX 03-MAY-2001.
XX
XX 19-OCT-2000; 2000WO-GB04028.
XX
XX 22-OCT-1999; 99GB-0025136.

```

```

XX (SMK ) SMITHKLINE BEECHAM PLC.
XX (SMK ) SMITHKLINE BEECHAM CORP.
XX
XX Christie G, Hussain I, Powell DJ;
XX
XX WPI; 2001-328654/34.
XX
XX Identifying inhibitors of Asp 1-mediated cleavage, for treating or
XX preventing beta-amyloid protein-related disease, comprising measuring
XX the extent of substrate cleavage in a reaction system containing Asp 1
XX and a substrate.
XX
XX Disclosure; Page 3; 31pp; English.
XX
XX The present invention describes a method of screening for compounds
XX which inhibit Asp 1-mediated cleavage of a polypeptide or protein
XX substrate. The method comprises providing a reaction system comprising
XX Asp 1 and substrate, and measuring the extent of cleavage of the
XX substrate in the presence of test compound compared with that in the
XX presence of the test compound. Also described are: (1) a method of
XX screening for compounds which inhibit Asp 1 mediated cleavage of a
XX polypeptide or protein substrate comprising providing a reaction system
XX comprising Asp 1 and a labeled active site ligand, and measuring the
XX extent of binding of the labeled ligand in the presence of test compound
XX compared with that in the presence of the test compound; (2) a compound
XX identified by the method; (3) a pharmaceutical composition comprising the
XX compound of (2) and a carrier; (4) a method of inhibiting Asp 1 modulated
XX amyloid precursor protein (APP) cleavage, or treating or prophylaxis of
XX beta-amyloid protein-related disease, comprising administering to a
XX patient a compound of (2); (5) a compound which is an inhibitor of Asp 1
XX modulated APP cleavage; and (6) a method for treating or prophylaxis of
XX beta-amyloid protein-related disease comprising administering a compound
XX of (2) or (5). The compound which inhibits Asp 1 mediated cleavage of a
XX polypeptide or protein is useful in therapy, in the preparation of a
XX medicament for inhibiting Asp 1-modulated APP cleavage and for the
XX treatment or prophylaxis of beta-amyloid protein-related disease.
XX including Alzheimer's disease. The present sequence represents an APP
XX beta-secretase cleavage site spanning peptide which can be used as a
XX substrate in the method of the invention.
XX
XX Sequence 11 AA:
SQ
Query Match 100.0%; Score 49; DB 22; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00046;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 SEVKMDAEFR 10
DB 2 SEVKMDAEFR 11
RESULT 12
AAB75144
ID AAB75144 standard; peptide; 11 AA.
XX
XX AAB75144;
XX
XX 08-AUG-2001 (first entry)
XX
XX Asp 1 substrate sequence SEQ ID NO:3.
XX
XX Amyloid precursor protein; APP; Asp 1; endocrepisin 1; inhibition;
XX Transmembrane aspartyl proteinase; APP Swedish variant; neurotrophic;
XX neuroprotective; beta-secretase cleavage site; Alzheimer's disease;
XX beta amyloid protein-related disease; antialzheimer.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Modified-site 1
XX /note="N-terminally attached to maltose binding protein
XX (MBP)"
FT

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XX WO200131054-A1.
XX
XX 03-MAY-2001.
XX
XX 19-OCT-2000; 2000WO-GB04028.
XX
XX 22-OCT-1999; 99GB-0025136.
XX
XX (SMIK ) SMITHKLINE BEECHAM PLC.
XX (SMIK ) SMITHKLINE BEECHAM CORP.
XX
XX Christie G, Hussain I, Powell DJ;
XX WPI; 2001-328654/34.
XX
XX Identifying inhibitors of Asp 1-mediated cleavage, for treating or
XX preventing beta-amyloid protein-related disease, comprises measuring
XX the extent of substrate cleavage in a reaction system containing Asp 1
XX and a substrate -
XX
XX Disclosure; Page 3; 31pp; English.
XX
XX The present invention describes a method of screening for compounds
XX which inhibit Asp 1-mediated cleavage of a polypeptide or protein
XX substrate. The method comprises providing a reaction system comprising
XX Asp 1 and substrate, and measuring the extent of cleavage of the
XX substrate in the presence of test compound compared with that in the
XX presence of the test compound. Also described are: (1) a method of
XX screening for compounds which inhibit Asp 1 mediated cleavage of a
XX polypeptide or protein substrate comprising providing a reaction system
XX comprising Asp 1 and a labeled active site ligand, and measuring the
XX extent of binding of the labeled ligand in the presence of test compound
XX compared with that in the presence of the test compound; (2) a compound
XX identified by the method; (3) a pharmaceutical composition comprising the
XX compound of (2) and a carrier; (4) a method of inhibiting Asp 1 mediated
XX amyloid precursor protein (APP) cleavage, or treating or prophylaxis of
XX beta-amyloid protein-related disease, comprising administering to a
XX patient a compound of (2); (5) a compound which is an inhibitor of Asp 1
XX mediated APP cleavage; and (6) a method for treating or prophylaxis of
XX beta-amyloid protein-related disease comprising administering a compound
XX of (2) or (5). The compound which inhibits Asp 1 mediated cleavage of a
XX polypeptide or protein is useful in therapy, in the preparation of a
XX medicament for inhibiting Asp 1-mediated APP cleavage and for the
XX treatment or prophylaxis of beta-amyloid protein-related disease,
XX including Alzheimer's disease. The present sequence represents an Asp 1
XX substrate sequence which is given in the exemplification of the present
XX invention.
XX
XX Sequence 11 AA;
XX
XX Query Match 100.0%; Score 49; DB 22; Length 11;
XX Best Local Similarity 100.0%; Pred. No. 0.00046;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 SEVKMDAEFR 10
XX |
XX |
XX |
XX |
XX |
XX |
XX |
XX |
XX |
XX |
XX |
XX
XX Db 2 SEVKMDAEFR 11
XX
XX RESULT 13
XX AAB97468
XX ID AAB97468 standard; Protein; 11 AA.
XX
XX AC AAB97468;
XX
XX DT 03-AUG-2001 (first entry)
XX
XX DE Asp2 substrate wild-type beta-site peptide sequence.
XX
XX KW Asp2; endocrepain 2; memapsin 2; beta-amyloid protein;
XX Alzheimer's disease; cortical Lewy body disease; Parkinson's disease;
XX Asp2 inhibitor.
XX

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```

XX OS Unidentified.
XX
XX Key Location/Qualifiers
XX FH Modified-site 1
XX FT /Label= OTHER
XX FT /note= "optionally bound to maltose binding protein"
XX
XX WO200129563-A1.
XX
XX 26-APR-2001.
XX
XX 19-OCT-2000; 2000WO-GB04039.
XX
XX 21-OCT-1999; 99GB-0024957.
XX
XX (SMIK ) SMITHKLINE BEECHAM PLC.
XX (SMIK ) SMITHKLINE BEECHAM CORP.
XX
XX Christie G, Hussain I, Powell DJ;
XX WPI; 2001-300381/31.
XX
XX Screening for inhibitors of Asp 2 mediated polypeptide cleavage
XX comprises measuring substrate cleavage or ligand binding with a system
XX comprising Asp 2 and a substrate or labelled ligand in the presence or
XX absence of a test compound -
XX
XX Disclosure; Page 3; 34pp; English.
XX
XX The present invention describes a method of screening for compounds which
XX inhibit Asp2 (also known as memapsin 2 and endocrepain 2) mediated
XX cleavage of a protein substrate, involving measuring the extent of
XX cleavage of the substrate in the presence and absence of the test
XX compound. Asp2 is thought to be involved in the cleavage of amyloid
XX precursor protein which is excised to produce beta-amyloid. Beta-amyloid
XX is involved in the pathogenesis of Alzheimer's disease, Parkinson's
XX disease, cortical Lewy body disease and vascular and cerebrovascular
XX diseases, and Asp2 inhibitors could be useful in their treatment. The
XX present sequence is an example of an Asp2 substrate.
XX
XX Sequence 11 AA;
XX
XX Query Match 100.0%; Score 49; DB 22; Length 11;
XX Best Local Similarity 100.0%; Pred. No. 0.00046;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 SEVKMDAEFR 10
XX |
XX |
XX |
XX |
XX |
XX |
XX |
XX |
XX |
XX |
XX |
XX
XX Db 2 SEVKMDAEFR 11
XX
XX RESULT 14
XX AAW70869
XX ID AAW70869 standard; peptide; 13 AA.
XX
XX AC AAW70869;
XX
XX DT 04-FEB-1999 (first entry)
XX
XX DE Beta-amyloid peptide to create a monoclonal antibody.
XX
XX KW Beta-amyloid precursor protein; beta-APP; beta-amyloid peptide;
XX antibody; amyloid deposit; Alzheimer's disease.
XX
XX OS Synthetic.
XX OS Homo sapiens.
XX
XX PN WO9844955-A1.
XX
XX PD 15-OCT-1998.
XX
XX PF 09-APR-1998; 98WO-US06900.
XX

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XX 09-APR-1997; 97US-0041850.
PR (MCIN/) MCINNIS P A.
PA (MIND-) MINDSET LTD.
XX Chain DG;
XX WPI: 1998-594476/50.
XX Preventing or inhibiting progression of Alzheimer's Disease -
PT comprises use of recombinant DNA encoding an antibody specific for
PT the N- or C-terminus of an amyloid-beta peptide
XX
XX Example 1; Page 47; 58pp; English.
XX The present sequence represents a peptide derived from beta-amyloid
CC precursor protein (beta-Ap). The peptide is a beta-amyloid
CC peptide and is used to produce a monoclonal antibody. The specification
CC describes a method for prevention or inhibition of progression of
CC Alzheimer's disease. The method comprises administering a composition
CC comprising a recombinant DNA molecule containing a gene encoding a
CC recombinant antibody end-specific for the N-terminus or the C-terminus
CC of an amyloid-beta peptide, operably linked to a promoter which is
CC expressed in the central nervous system. The recombinant antibody
CC molecules prevent the accumulation of beta-amyloid peptides in the
CC extracellular space, interstitial fluid and cerebrospinal fluid and the
CC aggregation of such peptides into amyloid deposits in the brain. They
CC also inhibit the progression of Alzheimer's disease by inhibiting the
CC interaction of beta-amyloid peptides mediating Alzheimer's disease
CC induced neurotoxicity and inhibiting the Alzheimer's disease induced
CC complement activation and cytokine release involved in the inflammatory
CC process.
XX
XX Sequence 13 AA:
SQ
XX
XX Query Match 100.0%; Score 49; DB 19; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00056;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SEVKMDAEPF 10
Db 3 SEVKMDAEPF 12
XXXXXXXXXXXX
RESULT 15
AAB06315
ID AAB06315 standard; peptide; 16 AA.
XX
XX AAB06315;
AC
XX
XX 03-OCT-2000 (first entry)
DT
XX
XX Human beta-amyloid precursor protein beta-secretase cleavage site.
DE
XX
XX Human: beta-amyloid precursor protein; beta-Ap; beta-secretase;
KM subtilisin-kexin isoenzyme 1; SKI-1;
KM pro-brain-derived neurotrophic factor; PROBDNF; antiplaemic;
KM cytostatic; vasotropic; SKI-1 inhibitor; hypercholesterolaemia;
KM liver steatosis; Ras-dependent cancer; restenosis;
KM amyloid protein formation.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Cleavage-site 8..9
XX
XX WO200026348-A2.
XX
XX 11-MAY-2000.
XX
XX 04-NOV-1999; 99WO-CA01058.
XX
```

```
PR 04-NOV-1998; 98CA-2249648.
XX
XX (RECL-) INST RECH CLINIQUES MONTREAL.
XX
XX Seidah N, Chretien M, Marcinkiewicz M, Laaksonen R, Davignon J;
PI WPI: 2000-365601/31.
XX
XX Novel soluble proteic fragment of subtilisin-kexin isoenzyme for
PT producing a polypeptide useful for treating hypercholesterolemia, liver
PT steatosis and amyloidosis, comprises a specific amino acid sequence -
XX
XX Example 4; Page 51; 119pp; English.
XX The present sequence is the beta-secretase site of human beta-amyloid
CC precursor protein (beta-Ap). The sequence may be cleaved
CC by a mammalian subtilase, specifically subtilisin-kexin isoenzyme 1
CC (SKI-1), a type-I membrane-bound proteinase. Peptides which bind to and
CC are cleaved by SKI-1 may be used for monitoring SKI-1 activity, for
CC screening inhibitors of SKI-1 activity, or for screening enhancers of
CC SKI-1 activity. Proteic fragments of SKI-1 which bind to the SKI-1
CC catalytic site may be used as inhibitors of SKI-1 activity. They may be
CC used to treat diseases involving overexpression of SKI-1 or SKI-1
CC substrate. Such diseases include hypercholesterolaemia, high levels of
CC fatty acids, lipids or farnesyl pyrophosphate, liver steatosis,
CC Ras-dependent cancer, restenosis and amyloid protein formation.
XX
XX Sequence 16 AA:
SQ
XX
XX Query Match 100.0%; Score 49; DB 21; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.00071;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SEVKMDAEPF 10
Db 4 SEVKMDAEPF 13
XXXXXXXXXXXX
Search completed: October 29, 2002, 10:26:43
Job time : 23.1429 secs
```

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 29, 2002, 10:23:36 : Search time 10.4286 Seconds  
(without alignments)  
92.140 Million cell updates/sec

Title: US-09-580-018-4  
Perfect score: 49  
Sequence: 1 SEVKMDAEFR 10

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues  
Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : PIR-71:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	100.0	57	2 E60045	Alzheimer's disease
2	49	100.0	57	2 F60045	Alzheimer's disease
3	49	100.0	57	2 G60045	Alzheimer's disease
4	49	100.0	57	2 D60045	Alzheimer's disease
5	49	100.0	57	2 A60045	Alzheimer's disease
6	49	100.0	57	2 B60045	Alzheimer's disease
7	49	100.0	82	2 P00438	Alzheimer's disease
8	49	100.0	695	2 A9795	Alzheimer's disease
9	49	100.0	770	1 Q8H0A4	Alzheimer's disease
10	44	89.8	33	2 S23094	beta-amyloid prote
11	44	89.8	695	2 A27485	Alzheimer's disease
12	44	89.8	695	2 S00550	Alzheimer's disease
13	43	87.8	747	2 JH0773	Alzheimer's disease
14	39	79.6	142	2 E89026	Protein F13A2.1 [I
15	35	71.4	774	2 A61565	autolysin (amidase
16	34	69.4	626	2 A61565	conserved hypochet
17	34	69.4	3562	2 A47171	chondroitin sulfat
18	34	69.4	4563	1 LPHUB	apolipoprotein B-1
19	33	67.3	927	2 T38127	phosphoprotein - f
20	33	67.3	1245	2 G86404	probable P-glycop
21	32	65.3	263	2 D84226	hypothetical prote
22	32	65.3	354	2 S51143	FWO-protein - Chlo
23	32	65.3	392	2 T49471	mucin (muc3) relat
24	32	65.3	426	2 G75187	probable trehalose
25	32	65.3	625	2 D86244	protein Ser/Thr pr
26	32	65.3	700	2 E84131	transcription anti
27	32	65.3	929	2 T52517	hypothetical prote
28	32	65.3	1044	2 H97166	glycosyltransferas
29	32	65.3	1265	2 T51498	hypothetical prote

30	32	65.3	1906	2 AD2443	hypothetical prote
31	32	65.3	2514	2 T37320	ataxia telangiecta
32	32	65.3	2619	2 T24588	hypothetical prote
33	31	63.3	87	2 A97842	hypothetical prote
34	31	63.3	155	2 F75040	hypothetical prote
35	31	63.3	178	2 C64168	hypothetical prote
36	31	63.3	182	2 AC0449	conserved hypochet
37	31	63.3	37	2 S56460	probable alpha hel
38	31	63.3	183	2 C91280	probable alpha hel
39	31	63.3	183	2 C86121	conserved alpha hel
40	31	63.3	183	2 AD1056	conserved hypochet
41	31	63.3	188	2 S48290	OX40 ligand - mus
42	31	63.3	199	2 F72060	conserved hypochet
43	31	63.3	199	2 C86564	C1471 hypothetical
44	31	63.3	226	2 G69129	hypothetical prote
45	31	63.3	279	2 T41124	single-stranded DN

## ALIGNMENTS

## RESULT 1

E60045  
Alzheimer's disease amyloid beta/A4 protein precursor - sheep (fragment)  
C:Species: Ovis sp. (sheep)  
C:Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 28-Jul-1995  
C:Accession: E60045  
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
Brain Res. Mol. Brain Res. 10, 299-305, 1991  
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d  
A:Reference number: A60045; MUID:92017079  
A:Accession: E60045  
A:Molecule type: mRNA  
A:Residues: 1-57 <JOH>  
A:Cross-references: EMBL:X56130  
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas  
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

## Query Match

Best Local Similarity 100.0%; Score 49; DB 2; Length 57;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SEVKMDAEFR 10  
DB 1 SEVKMDAEFR 10

## RESULT 2

F60045  
Alzheimer's disease amyloid beta/A4 protein precursor - pig (fragment)  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 13-Aug-1999  
C:Accession: F60045  
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
Brain Res. Mol. Brain Res. 10, 299-305, 1991  
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d  
A:Reference number: A60045; MUID:92017079  
A:Accession: F60045  
A:Molecule type: mRNA  
A:Residues: 1-57 <JOH>  
A:Cross-references: EMBL:X56127; NID:91895; PIDN:CAA39592.1; PID:91896  
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas  
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

## Query Match

Best Local Similarity 100.0%; Score 49; DB 2; Length 57;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SEVKMDAEFR 10  
DB 1 SEVKMDAEFR 10

```

RESULT 3
G60045
Alzheimer's disease amyloid beta/A4 protein precursor - guinea pig (fragment)
C:Species: Cavia porcellus (guinea pig)
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: G60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079
A:Accession: G60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56126
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match      100.0%; Score 49; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEVKMDAER 10
DB 1 SEVKMDAER 10

RESULT 4
D60045
Alzheimer's disease amyloid beta/A4 protein precursor - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: D60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079
A:Accession: D60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56124
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match      100.0%; Score 49; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEVKMDAER 10
DB 1 SEVKMDAER 10

RESULT 5
A60045
Alzheimer's disease amyloid beta/A4 protein precursor - dog (fragment)
C:Species: Canis lupus familiaris (dog)
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: A60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079
A:Accession: A60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56125
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match      100.0%; Score 49; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 1 SEVKMDAER 10
DB 1 SEVKMDAER 10

RESULT 6
B60045
Alzheimer's disease amyloid beta/A4 protein precursor - polar bear (fragment)
C:Species: Ursus maritimus (polar bear)
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
C:Accession: B60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d
A:Reference number: A60045; MUID:92017079
A:Accession: B60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56128; NID:92165; PIDN:CA9593.1; PID:92166
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match      100.0%; Score 49; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEVKMDAER 10
DB 1 SEVKMDAER 10

RESULT 7
P00438
Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995
C:Accession: P00438; C60045
R:Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.E.
Biochem. Biophys. Res. Commun. 186, 905-911, 1992
A:Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precurs
A:Reference number: P00438; MUID:93075180
A:Accession: P00438
A:Molecule type: DNA
A:Residues: 1-82 <DAV>
A:Cross-references: GB:M83558; GB:M83657
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d
A:Reference number: A60045; MUID:92017079
A:Accession: C60045
A:Molecule type: mRNA
A:Residues: 12-68 <JOH>
A:Cross-references: EMBL:X56129
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match      100.0%; Score 49; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 0.0026;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEVKMDAER 10
DB 12 SEVKMDAER 21

RESULT 8
A49795
Alzheimer's disease amyloid beta protein precursor - crab-eating macaque
C:Species: Macaca fascicularis (crab-eating macaque)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A49795
R:Podlisky, M.B.; Tolan, D.R.; Selkoe, D.J.
Am. J. Pathol. 138, 1423-1435, 1991

```



A>Title: Homology of the amyloid beta protein precursor in monkey and human supports a p  
 A:Reference number: A49795; MUID:91273117  
 A:Accession: A49795  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-695 <POD>  
 A:Cross-references: GB:M58727; NID:9342062; PIDN:AAA36829.1; PID:9342063  
 C:Keywords: Alzheimer's disease amyloid beta protein; animal knnltz-type proteinase 1  
 C:Keywords: alternative splicing

Query Match 100.0%; Score 49; DB 1; Length 695;  
 Best Local Similarity 100.0%; Pred. No. 0.028;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SEVKDAEER 10  
 DB 592 SEVKDAEER 601

# RESULT 9

ORH04

Alzheimer's disease amyloid beta protein precursor [validated] - human  
 N:Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor XIA inhibi  
 N:Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vascular  
 protein precursor splice form APP(770)

C:Species: Homo sapiens (man)

C:Date: 30-Jun-1987 #sequence, revision 28-Jul-1995 #text change 15-Sep-2000

C:Accession: S02260; S05194; A32277; A33260; A35486; I39452; I39451; I39453; I59562; A44

4688; A28583; A29302; A60809; JLU0038; S06121; A60311; A38344; S20076; S38252; S3

R:Lemaitre, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.; Bey

Nucleic Acids Res. 17, 517-522, 1989

A>Title: The Pread(695) precursor protein of Alzheimer's disease A4 amyloid is encoded b

A:Reference number: S02260; MUID:89128427

A:Accession: S02260

A:Molecule type: DNA

A:Residues: 1-288, 'V', 365-770 <LEM1>

A:Cross-references: EMBL:X13466

A>Note: alternative splice form APP(695)

R:Lemaitre, H.G.

submitted to the EMBL Data Library, November 1988

A:Reference number: S05194

A:Accession: S05194

A:Molecule type: DNA

A:Residues: 1-14, 'VW', 17-288, 'V', 365-770 <LEM2>

A:Cross-references: EMBL:X13466; NID:935598; PIDN:CAA1830.1; PID:9871360

A>Note: alternative splice form APP(695)

R:La Pauci, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.

Biochem. Biophys. Res. Commun. 159, 297-304, 1989

A>Title: Characterization of the 5'-end region and the first two exons of the beta-prote

A:Reference number: A32277; MUID:89165870

A:Accession: A32277

A:Molecule type: DNA

A:Residues: 1-75 <LAR>

A:Cross-references: GB:M24546; GB:M24547; NID:9341202; PIDN:AA013654.1; PID:9516074

R:Johnston, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.

Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989

A>Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows similarit

A:Reference number: A33260; MUID:89392030

A:Accession: A33260

A:Molecule type: DNA

A:Residues: 656-737 <LOH>

A:Cross-references: GB:M29270; NID:9178863; PIDN:AAA51768.1; PID:9178865

R:Prelli, F.; Levy, E.; van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B.

Biochem. Biophys. Res. Commun. 170, 301-307, 1990

A>Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid of

A:Reference number: A35486; MUID:90321244

A:Accession: A35486

A:Molecule type: DNA

A:Residues: 672-710 <PRE1>

A>Note: 693-Gln was found in DNA isolated from HCMA-D patients

R:Yoshikaki, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.

Gene 87, 257-263, 1990

A>Title: Genomic organization of the human amyloid beta-protein precursor gene.

A:Reference number: I39451; MUID:90236318

A:Accession: I39452

A>Status: nucleic acid sequence not shown; translation not shown; translated from GB/

A:Molecule type: DNA

A:Residues: 1-770 <YOS1>

A:Cross-references: GB:M33112; NID:9178613; PIDN:AA859502.1; PID:9178616

A:Accession: I39451

A>Status: nucleic acid sequence not shown; translation not shown; translated from GB/

A:Molecule type: DNA

A:Residues: 1-530, 'QWIMPIVPAFWKAYGR' <YOS2>

A:Cross-references: GB:M34875; NID:9178608; PIDN:AA859501.1; PID:9178615

R:Yoshikaki, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.

Gene 102, 291-292, 1991

A:Reference number: A59020; MUID:91340168

A:Accession: A59020

A:Contents: annotation; erratum

A:Note: revised physical map for reference I39451

R:Levy, E.; Garman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van Du

Science 248, 1124-1126, 1990

A>Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemo

A:Reference number: I39453; MUID:90260663

A:Accession: I39453

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 656-737 <LEV>

A:Cross-references: GB:M37896; NID:9178618; PIDN:AAA51727.1; PID:9178620

A>Note: a mutation with 693-Gln is presented

R:Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.

Science 254, 97-99, 1991

A>Title: A mutation in the amyloid precursor protein associated with hereditary Alzhe

A:Reference number: I59562; MUID:9202553

A:Accession: I59562

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 688-716, 'F', 718-737 <MUR>

A:Cross-references: GB:S57655; NID:9236720; PIDN:AA819991.1; PID:9236721

R:Kamano, K.; Orr, H.T.; Payami, H.; Wisneman, E.M.; Alonso, M.E.; Puls, S.M.; Anders

arakis, S.E.; Korenberg, J.R.; Sharma, V.; Kukull, W.; Larson, E.; Heslon, L.L.; Mart

Am. J. Hum. Genet. 51, 998-1014, 1992

A>Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for t

A:Reference number: A44017; MUID:93035397

A:Accession: A44017

A:Molecule type: DNA

A:Residues: 687-692, 'G', 694-718 <RAM1>

A:Cross-references: GB:S45135; NID:9257377; PIDN:AA823645.1; PID:9257378

A:Experimental source: Familial Alzheimer disease family SB

A>Note: sequence extracted from NCBI backbone (NCBI:115374)

A:Accession: B44017

A:Molecule type: DNA

A:Residues: 687-718 <RAM2>

A:Cross-references: GB:S45136; NID:9257379; PIDN:AA823646.1; PID:9257380

A:Experimental source: Familial Alzheimer disease family LIT

A>Note: sequence extracted from NCBI backbone (NCBI:115376)

R:Kang, J.; Lemaitre, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.

Nature 335, 733-736, 1987

A>Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-sur

A:Reference number: A03134; MUID:87144572

A:Accession: A03134

A:Molecule type: mRNA

A:Residues: 1-288, 'V', 365-770 <KAN>

A:Cross-references: GB:Y00264; NID:928525; PIDN:CAA6374.1; PID:928526

A>Note: alternative splice form APP(695)

R:Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.

Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987

A>Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascula

A:Reference number: A29030; MUID:87231971

A:Accession: A29030

A:Molecule type: mRNA

A:Residues: 284-288, 'V', 365-646, 'E', 648-770 <ROB>

A:Cross-references: GB:M6765; NID:9178539; PIDN:AAA51722.1; PID:9178540

A>Note: the authors translated the codon GAG for residue 647 as Asp

R:Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Saffioti, U.; Gajdusek, D.C.

Science 235, 877-880, 1987

A:Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid  
 A:Reference number: A47584; MUID:87120328  
 A:Accession: A47584  
 A:Molecule type: mRNA  
 A:Residues: 674-756, 'S', '758-770' <GOL>  
 A:Cross-references: GB:M15533; NID:q178706; PIDN:AAA5540.1; PID:q178707  
 A:Note: Experimental source: brain  
 R:Tanzil, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van Ke  
 Science 235, 880-884, 1987  
 A:Title: Amyloid beta protein gene: CDNA, mRNA distribution, and genetic linkage near th  
 A:Reference number: A47585; MUID:87120329  
 A:Accession: A47585  
 A:Molecule type: mRNA  
 A:Residues: 674-703 <TANI>  
 A:Cross-references: GB:M15532; NID:q177957; PIDN:AAA51564.1; PID:q177958  
 R:Dykes, T.; Weidemann, A.; Muthaupa, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Mueller  
 EMBO J. 7, 949-957, 1988  
 A:Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 prec  
 A:Reference number: 502638; MUID:88296437  
 A:Accession: 502638  
 A:Molecule type: mRNA  
 A:Residues: 672-678 <DYR>  
 R:Tanzil, R.E.; McClatchey, A.I.; Lamperti, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Neve  
 Nature 331, 528-530, 1988  
 A:Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associat  
 A:Reference number: 500707; MUID:88122640  
 A:Accession: 500707  
 A:Molecule type: mRNA  
 A:Residues: 286-344, 'I', '365-366' <TAN2>  
 A:Cross-references: EMBL:X06982; NID:q28817; PIDN:CAA30042.1; PID:q929612  
 A:Note: Experimental source: promyelocytic leukemia cell line HL60  
 R:Porte, P.; Gonzalez-Demhitt, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.; Da  
 Nature 331, 523-527, 1988  
 A:Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibit  
 A:Reference number: 500925; MUID:88122639  
 A:Accession: 500925  
 A:Molecule type: mRNA  
 A:Residues: 1-344, 'I', '365-770' <PO2>  
 A:Cross-references: GB:X06989; EMBL:Y00297; NID:q28720; PIDN:CAA30050.1; PID:q28721  
 A:Note: Alternative splice form APP(751)  
 R:Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.  
 Nature 331, 530-532, 1988  
 A:Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibitor  
 A:Reference number: A38949; MUID:88122641  
 A:Accession: A38949  
 A:Molecule type: mRNA  
 A:Residues: 287-367 <KIT>  
 A:Cross-references: GB:X06981; NID:q28816; PIDN:CAA30041.1; PID:q929611  
 A:Note: Experimental source: glioblastoma cell line  
 A:Note: alternative splice form APP(770)  
 R:Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ashton  
 Brain Res. Mol. Brain Res. 4, 121-131, 1988  
 A:Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of three F  
 A:Reference number: A30320  
 A:Accession: A30320  
 A:Molecule type: mRNA  
 A:Status: not compared with conceptual translation  
 A:Residues: 284-288, 'V', '365-770' <VIT1>  
 A:Accession: B30320  
 A:Status: not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 122-288, 'V', '365-770' <VIT2>  
 A:Accession: C30320  
 A:Status: not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 606-770 <VIT3>  
 R:Zaini, S.B.; Sallim, M.; Chou, W.G.; Sajdel-Sulowska, E.M.; Majocha, R.E.; Marotta, C.A  
 Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988  
 A:Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease br  
 A:Reference number: A31087; MUID:88124954  
 A:Accession: A31087  
 A:Molecule type: mRNA

A:Residues: 507-770 <ZAT>  
 A:Cross-references: GB:M18734; NID:q178572; PIDN:AAA51726.1; PID:q178573  
 A:Note: the authors translated the codon GAA for residue 599 as Gly, ACC for residue  
 8 as Val, GCG for residue 609 as Asn, AAT for residue 610 as Gly, and GGT for residue  
 A:Note: the cited Genbank accession number, J03594, is not in release 101.0  
 R:Masters, C.L.; Muthaupa, G.; Simms, G.; Potgiesser, J.; Martins, R.N.; Beyreuther,  
 Query Match 100.0%; Score 49; DB 1; Length 770;  
 Best Local Similarity 100.0%; Pred. No. 0.031;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SEVKMDAEFR 10  
 |||||  
 DB 667 SEVKMDAEFR 676  
 RESULT 10  
 S23094  
 beta-amyloid protein precursor - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 03-May-1996  
 C:Accession: S23094  
 R:Kojima, S.; Omori, M.  
 FEBS Lett. 304, 57-60, 1992  
 A:Title: Two-way cleavage of beta-amyloid protein precursor by multicatalytic protein  
 A:Reference number: S23094; MUID:92316198  
 A:Accession: S23094  
 A:Molecule type: protein  
 A:Residues: 1-33 <KOJ>  
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinases  
 Query Match 89.8%; Score 44; DB 2; Length 33;  
 Best Local Similarity 100.0%; Pred. No. 0.011;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SEVKMDAEF 9  
 |||||  
 DB 1 SEVKMDAEF 9  
 RESULT 11  
 A27485  
 Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse  
 N:Alternate names: proteinase nexin II  
 C:Species: Mus musculus (house mouse)  
 C>Date: 31-Mar-1989 #sequence\_revision 31-Mar-1989 #text\_change 13-Aug-1999  
 C:Accession: A27485; S19727; I49485  
 R:Yamada, T.; Sasaki, H.; Furuya, H.; Miyata, T.; Goto, I.; Sakaki, Y.  
 Biochem. Biophys. Res. Commun. 149, 665-671, 1987  
 A:Title: Complementary DNA for the mouse homolog of the human amyloid beta protein pr  
 A:Reference number: A27485; MUID:88106489  
 A:Accession: A27485  
 A:Molecule type: mRNA  
 A:Residues: 1-695 <YAM>  
 A:Cross-references: GB:M18373; NID:q191568; PIDN:AAA37139.1; PID:q309085  
 A:Note: Experimental source: brain  
 R:de Strooper, B.; van Leuven, F.; van den Berghe, H.  
 Biochim. Biophys. Acta 1129, 141-143, 1991  
 A:Title: The amyloid beta protein precursor or proteinase nexin II from mouse is clos  
 A:Reference number: S19727; MUID:92096458  
 A:Accession: S19727  
 A:Molecule type: mRNA  
 A:Residues: 1-210, 'G', '212-220', 'S', '222-396', 'A', '398-402', 'T', '404-448', 'A', '450-695' <STR>  
 A:Cross-references: EMBL:X59379  
 R:Izumii, R.; Yamada, T.; Yoshikawa, S.; Sasaki, H.; Hattori, M.; Sakaki, Y.  
 Gene 112, 189-195, 1992  
 A:Title: Positive and negative regulatory elements for the expression of the Alzheim  
 A:Reference number: I49485; MUID:92209998  
 A:Accession: I49485  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-19 <RES>  
 A:Cross-references: GB:D10603; NID:q220328; PIDN:BA01456.1; PID:q220329

C:Genetics:  
A:Map position: 16C3  
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase A  
C:Keywords: alternative splicing; amyloid; transmembrane protein

Query Match 89.8%; Score 44; DB 2; Length 695;  
Best Local Similarity 100.0%; Pred. No. 0.33;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SEVKMDAEF 9  
|||||  
Db 592 SEVKMDAEF 600

## RESULT 12

Alzheimer's disease amyloid beta protein precursor - rat  
N:Alternate names: beta-A4 amyloid protein

C:Species: Rattus norvegicus (Norway rat)

C>Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 13-Aug-1999

C:Accession: S00550; A41245; A39820; S46251

R:Shivers, B.D.; Hilbich, C.; Multhaup, G.; Salbaum, M.; Beyreuther, K.; Seeburg, P.H.  
EMBO J. 7, 1365-1370, 1988

A:Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brain  
A:Reference number: S00550; MUID:88312583

A:Accession: S00550

A:Molecule type: mRNA

A:Residues: 1-695 <SH1>

A:Cross-references: EMBL:X07648; NID:955616; PIDN:CA030488.1; PID:955617

R:Schubert, D.; Schroeder, R.; Lacorbiere, M.; Salton, T.; Cole, G.

A:Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan core  
A:Reference number: A41245; MUID:88264430

A:Accession: A41245

A:Molecule type: protein

A:Residues: 18-37, 'X', 39-40, 'X', 42-44 <SCH>

A:Note: evidence for heparan sulfate attachment

R:Hesse, L.; Behner, D.; Masters, C.L.; Multhaup, G.

FEBS Lett. 349, 109-116, 1994

A:Title: The beta-A4 amyloid precursor protein binding to copper.

A:Reference number: S46251; MUID:94320627

A:Contents: annotation: copper binding sites

A:Note: rat peptides were isolated but not sequenced

R:Potempa, A.; Styles, J.; Mehra, P.; Kim, K.S.; Miller, D.L.

J. Biol. Chem. 266, 8464-8469, 1991

A:Title: Purification and tissue level of the beta-amyloid peptide precursor of rat brain

A:Reference number: A39820; MUID:91217087

A:Accession: A39820

A>Status: preliminary

A:Molecule type: protein

A:Residues: 18-32 <POT>

A:Experimental source: brain

C:Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques is characteristic of Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase A

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase A

C:Keywords: alternative splicing; amyloid; glycoprotein; transmembrane protein

F:625-648/Domain: transmembrane #status predicted <TM>

Query Match 89.8%; Score 44; DB 2; Length 695;  
Best Local Similarity 100.0%; Pred. No. 0.33;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SEVKMDAEF 9  
|||||  
Db 592 SEVKMDAEF 600

## RESULT 13

JH0773

Alzheimer's disease amyloid beta protein precursor - African clawed frog

C:Species: Xenopus laevis (African clawed frog)

C>Date: 10-Jun-1993 #sequence\_revision 10-Jun-1993 #text\_change 13-Aug-1999

C:Accession: JH0773

R:Okado, H.; Okamoto, H.

Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992

A:Title: A Xenopus homologue of the human beta-amyloid precursor protein: development

A:Reference number: JH0773; MUID:93129227

A:Accession: JH0773

A:Molecule type: mRNA

A:Residues: 1-747 <OKA>

A:Cross-references: GB:S52417; NID:9263150; PIDN:AAB24853.1; PID:9263151

A:Experimental source: larva

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase A

C:Keywords: alternative splicing; amyloid

F:287-337/Domain: animal Kunitz-type proteinase inhibitor homology <RP1>

Query Match 87.8%; Score 43; DB 2; Length 747;  
Best Local Similarity 80.0%; Pred. No. 0.58;  
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 SEVKMDAEF 10  
|||||  
Db 644 SEVKMDSEYR 653

## RESULT 14

protein F13A2.1 [imported] - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 10-May-2001

C:Accession: E89026

R:anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A:Title: Genome sequence of the nematode C. elegans: a platform for investigating blo

A:Reference number: A75000; MUID:99069613; PMID:9851916

A:Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C-

A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999;

A:Accession: E89026

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-142 <STO>

A:Cross-references: GB:chr\_V; PIDN:AAB69895.1; PID:92384795; GSPDB:GN00023; CESP:F13A

C:Genetics:

A:Gene: F13A2.1

A:Map position: 5

Query Match 79.6%; Score 39; DB 2; Length 142;  
Best Local Similarity 77.8%; Pred. No. 0.66;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 EVKMDAEFR 10  
|||  
Db 56 EVKMDAEFR 64

## RESULT 15

AG1565  
autolysin (amidase) homolog lin1064 [imported] - Listeria innocua (strain C11p11262)

C:Species: Listeria innocua

C>Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 27-Nov-2001

C:Accession: AG1565

R:Dominguez-Bernal, G.; Buchrieser, C.; Amend, A.; Baguerio, F.; Berche, P.; Bioec

D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi,

Science 294, 849-852, 2001

A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maltournam, A.;

ok, C.; Schlutener, T.; Simoes, N.; Tjereez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla

A:Title: Comparative genomics of Listeria species.

A:Reference number: AB1077; MUID:21537279; PMID:11679669

A:Accession: AG1565

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-774 <GLA>

A:Cross-references: GB:AL592022; PIDN:CA096295.1; PID:916413523; GSPDB:GN00178

A:Experimental source: strain C11p11262

C:Genetics:

A:Gene: lin1064

Query Match 71.4%; Score 35; DB 2; Length 774;  
Best Local Similarity 75.0%; Pred. No. 31;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 VKMDAEFR 10  
: : : : :  
Db 123 IKIDAEFR 130

Search completed: October 29, 2002, 10:31:01  
Job time : 11.4286 secs

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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 29, 2002, 10:22:36 ; Search time 5 Seconds

(without alignments)  
77.439 Million cell updates/sec

Title: US-09-580-018-4  
Perfect score: 49  
Sequence: 1 SEVKMDAEPF 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	100.0	57	1 A4_PIG	Q29023 sus scrofa
2	49	100.0	57	1 A4_URSM	Q29149 ursus marit
3	49	100.0	58	1 A4_CANRA	Q28280 canis famill
4	49	100.0	58	1 A4_RABIT	Q28746 oryctolagus
5	49	100.0	58	1 A4_SHEEP	Q28757 ovis aries
6	49	100.0	59	1 A4_BOVIN	Q28053 bos taurus
7	49	100.0	751	1 A4_SAISC	Q95241 salmistr sci
8	49	100.0	770	1 A4_HUMAN	P05067 homo sapien
9	44	89.8	770	1 A4_MOUSE	P12023 mus musculu
10	44	89.8	770	1 A4_RAT	P08592 rattus norv
11	37	75.5	269	1 T2S1_STRFI	O52512 streptomyc
12	34	69.4	3562	1 PGCV_CHICK	Q09053 gallus gall
13	34	69.4	4563	1 APB_HUMAN	P04114 homo sapien
14	33	67.3	927	1 CC15_SCHPO	Q09822 schizosacch
15	32	65.3	263	1 Y683_HALNI	O9hr12 halobacteri
16	32	65.3	354	1 BCPA_CHLIT	Q46135 chlorobium
17	32	65.3	365	1 BCPA_CHUTE	Q46393 chlorobium
18	31	63.3	178	1 YUGA_HAENI	P45076 haemophilus
19	31	63.3	183	1 YUGA_ECOLI	P26550 escherichia
20	31	63.3	198	1 TNF4_MOUSE	P43488 mus musculu
21	31	63.3	279	1 RFA2_SCHPO	O92373 schizosacch
22	31	63.3	479	1 Y098_MYCPN	P75535 mycoplasma
23	31	63.3	1024	1 Y075_MYCGE	P47321 mycoplasma
24	30	61.2	78	1 RL31_RICCN	O921d0 rickettsia
25	30	61.2	78	1 RL31_RICPR	O92427 rickettsia
26	30	61.2	197	1 OM26_HAENI	O57483 haemophilus
27	30	61.2	356	1 RFI_BACSU	P45782 bacillus su
28	30	61.2	394	1 EFTO_BOCAL	O31297 buchnera su
29	30	61.2	400	1 YF74_ARCFU	O28698 archaeoglob
30	30	61.2	419	1 P47K_PSECL	P31221 pseudomonas
31	30	61.2	463	1 YD14_SCHPO	O92342 schizosacch
32	30	61.2	464	1 SPN5_SCHPO	P48010 schizosacch
33	30	61.2	656	1 V091_FOMPV	O72896 fowlpox vlr

## ALIGNMENTS

RESULT 1	STANDARD:	PRT:	57 AA.
AD_PIG			
AC Q29023;			
DT 01-NOV-1997 (Rel. 35, Created)			
DT 01-NOV-1997 (Rel. 35, Last sequence update)			
DT 16-OCT-2001 (Rel. 40, Last annotation update)			
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid			
DE protein (Beta-Ap) (A-beta)] (Fragment).			
GN APP			
OS Sus scrofa (Pig).			
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.			
OX NCBI_TaxID=9823;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC TISSUE=Brain;			
RC MEDLINE=92017079; PubMed=1656157;			
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;			
RT "Conservation of the sequence of the Alzheimer's disease amyloid			
RT peptide in dog, polar bear and five other mammals by cross-species			
RT polymerase chain reaction analysis."			
RL Brain Res. Mol. Brain Res. 10:299-305(1991).			
-1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO			
INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN			
GTO) (BY SIMILARITY).			
-1- SUBCELLULAR LOCATION: Type I membrane protein.			
-1- SIMILARITY: BELONGS TO THE APP FAMILY.			
CC This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).			
DR EMBL: X56127; CA39592.1; -			
DR HSSP: P05067; 1BA4.			
DR InterPro: IPR001868; A4_APP.			
DR PROSITE: PS00319; A4_EXTRA; PARTIAL.			
DR PROSITE: PS00320; A4_INTRA; PARTIAL.			
RW Glycoprotein; Amyloid; Neutone; Transmembrane.			
FT NON_TER 1			
FT CHAIN 6			
FT DOMAIN <1 33			
FT TRANSMEM 34 57			
FT NON_TER 57			
SO SEQUENCE 57 AA; 6172 MW; 8420988BBA82DFA CRC64;			
Query Match	100.0%;	Score 49;	DB 1;
Best Local Similarity	100.0%;	Pred. No. 0.0014;	Length 57;
Matches 10;	Conservative 0;	Mismatches 0;	Indels 0;
Gaps 0;			
QY 1 SEVKMDAEPF 10			

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Db      1 SEVKMDAEPF 10

RESULT 2
ID      A4_URSMA      STANDARD:      PRT:      57 AA.
AC      029149;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      30-MAY-2000 (Rel. 39, Last annotation update)
DE      Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE      protein (Beta-Ap) (A-beta)] (Fragment).
GN      APP.
OS      Ursus maritimus (Polar bear) (Thalarcos maritimus).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.
OX      NCBI_TaxID=9615;

[1]
RN      SEQUENCE FROM N.A.
RP      TISSUE=Brain;
RX      MEDLINE=92017079; PubMed=1656157;
RA      Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT      "Conservation of the sequence of the Alzheimer's disease amyloid
RT      peptide in dog, polar bear and five other mammals by cross-species
RT      polymerase chain reaction analysis.";
RL      Brain Res. Mol. Brain Res. 10:299-305(1991).
CC      -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC      INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC      G(O) (BY SIMILARITY).
CC      -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC      -1- SIMILARITY: BELONGS TO THE APP FAMILY.
-----
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CC      or send an email to license@isb-sib.ch).
-----
CC      EMBL; X56128; CAA39593.1; -.
CC      HSSP; P05067; 1AM4.
DR      InterPro; IPR001868; A4_APP.
DR      PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR      PROSITE; PS00320; A4_INTRA; PARTIAL.
KW      Glycoprotein; Amyloid; Neurone; Transmembrane.
FT      NON_TER      1
FT      CHAIN      6 48      BETA-AMYLOID PROTEIN (POTENTIAL).
FT      DOMAIN      <1 33      EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM      34 57      POTENTIAL.
FT      NON_TER      57 57
SQ      SEQUENCE      57 AA: 6172 MW: 84209D88BA82DFA CRC64;

Query Match      100.0%; Score 49; DB 1; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 SEVKMDAEPF 10
Db      1 SEVKMDAEPF 10

RESULT 3
ID      A4_CANFA      STANDARD:      PRT:      58 AA.
AC      028280;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      30-MAY-2000 (Rel. 39, Last annotation update)
DE      Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE      protein (Beta-Ap) (A-beta)] (Fragment).
GN      APP.
OS      Canis familiaris (Dog).

```

```

CC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC      Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX      NCBI_TaxID=9615;

[1]
RN      SEQUENCE FROM N.A.
RP      TISSUE=Kidney;
RX      MEDLINE=92017079; PubMed=1656157;
RA      Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT      "Conservation of the sequence of the Alzheimer's disease amyloid
RT      peptide in dog, polar bear and five other mammals by cross-species
RT      polymerase chain reaction analysis.";
RL      Brain Res. Mol. Brain Res. 10:299-305(1991).
CC      -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC      INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC      G(O) (BY SIMILARITY).
CC      -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC      -1- SIMILARITY: BELONGS TO THE APP FAMILY.
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CC      EMBL; X56125; CAA39590.1; -.
CC      HSSP; P05067; 1BA4.
DR      InterPro; IPR001868; A4_APP.
DR      PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR      PROSITE; PS00320; A4_INTRA; PARTIAL.
KW      Glycoprotein; Amyloid; Neurone; Transmembrane.
FT      NON_TER      1
FT      CHAIN      7 49      BETA-AMYLOID PROTEIN (POTENTIAL).
FT      DOMAIN      <1 34      EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM      35 58      POTENTIAL.
FT      NON_TER      58 58
SQ      SEQUENCE      58 AA: 6285 MW: 8469D488A2E12DFA CRC64;

Query Match      100.0%; Score 49; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 SEVKMDAEPF 10
Db      2 SEVKMDAEPF 11

RESULT 4
ID      A4_RABIT      STANDARD:      PRT:      58 AA.
AC      028748;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE      protein (Beta-Ap) (A-beta)] (Fragment).
GN      APP.
OS      Oryctolagus cuniculus (Rabbit).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX      NCBI_TaxID=9986;

[1]
RN      SEQUENCE FROM N.A.
RP      TISSUE=Brain;
RX      MEDLINE=92017079; PubMed=1656157;
RA      Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT      "Conservation of the sequence of the Alzheimer's disease amyloid
RT      peptide in dog, polar bear and five other mammals by cross-species
RT      polymerase chain reaction analysis.";
RL      Brain Res. Mol. Brain Res. 10:299-305(1991).
CC      -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC      INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN

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CC G(O) (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
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CC -----
DR EMBL: X56129; CAA39594.1; -.
DR HSSP: P05067; 1BA4.
DR InterPro: IPR001868; A4_APP.
DR PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR PROSITE: PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.
FT NON_TER 1 1
FT CHAIN 1 48 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 34 57 POTENTIAL.
FT DOMAIN 58 >58 CYTOPLASMIC (POTENTIAL).
FT NON_TER 58 58
SQ SEQUENCE 58 AA; 6300 MW; FA34209D8EBA82D CRC64;

Query Match 100.0%; Score 49; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEVKMDAEFR 10
Db 1 SEVKMDAEFR 10

RESULT 5
A4_SHEEP STANDARD; PRT; 58 AA.
ID A4_SHEEP
AC 028757;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-APP) (A-beta)] (Fragment).
GN APP.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Cranata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RM SEQUENCE FROM N.A.
RC TISSUE=Heart;
RA MEDLINE-92017079; PubMed-1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
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DR EMBL: X56130; CAA39595.1; -.
DR HSSP: P05067; 1AML.
DR InterPro: IPR001868; A4_APP.
DR PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR PROSITE: PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.
FT NON_TER 1 1
FT CHAIN 1 48 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 34 57 POTENTIAL.
FT DOMAIN 58 >58 CYTOPLASMIC (POTENTIAL).
FT NON_TER 58 58
SQ SEQUENCE 58 AA; 6300 MW; FA34209D8EBA82D CRC64;

Query Match 100.0%; Score 49; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEVKMDAEFR 10
Db 1 SEVKMDAEFR 10

RESULT 6
A4_BOVIN STANDARD; PRT; 59 AA.
ID A4_BOVIN
AC 028053;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-APP) (A-beta)] (Fragment).
GN APP.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Cranata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RM SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA MEDLINE-92017079; PubMed-1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
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CC -----
DR EMBL: X56124; CAA39589.1; -.
DR EMBL: X56126; CAA39591.1; -.
DR HSSP: P05067; 1BA4.
DR InterPro: IPR001868; A4_APP.
DR PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR PROSITE: PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.
FT NON_TER 1 1
FT CHAIN 1 49 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 34 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 35 58 POTENTIAL.
FT DOMAIN 59 >59 CYTOPLASMIC (POTENTIAL).

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FT NON\_TER 59 59  
SQ SEQUENCE 59 AA; 6414 MW; F43469D488A2E12D CRC64;  
Query Match 100.0%; Score 49; DB 1; Length 59;  
Best Local Similarity 100.0%; Pred. No. 0.0014;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 SEVKMDAEFR 10  
|  
Db 2 SEVKMDAEFR 11  
RESULT 7  
A4\_SAIISC STANDARD; PRT; 751 AA.  
ID A4\_SAIISC  
AC G95241;  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Alzheimer's disease amyloid A4 protein precursor [contains: Beta-amyloid protein (Beta-ApP) (A-beta)].  
GN APP.  
OS Saimiri sciureus (Common squirrel monkey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.  
OX NCBI\_TaxID=9521;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver, and Kidney;  
RX MEDLINE=96108492; PubMed=8532114;  
RA Levy E., Amorim A., Franzone B., Walker L.C.;  
RT "Beta-amyloid precursor protein gene in squirrel monkeys with cerebral amyloid angiopathy."  
RL Neurobiol. Aging 16:805-808(1995).  
CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN G(O).  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE NXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF PHOSPHORYLATION (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.  
CC -1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.  
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CC -----  
DR EMBL; S81024; AAD14347.1; -  
DR HSSP; P05067; IAP.  
DR InterPro; IPR001868; A4\_APP.  
DR InterPro; IPR002223; Kunitz\_BPTI.  
DR Pfam; PF02177; A4\_EXTRA; 1.  
DR Pfam; PF00014; Kunitz\_BPTI; 1.  
DR PRINTS; PR00203; AMYLOIDA.  
DR PRINTS; PR00759; BASICPTASE.  
DR SMART; SM00006; A4\_EXTRA; 1.  
DR SMART; SM00131; KU; 1.  
DR PROSITE; PS00319; A4\_EXTRA; 1.  
DR PROSITE; PS00320; A4\_INTRA; 1.  
DR PROSITE; PS00280; BPTI\_KUNITZ\_1; 1.  
DR PROSITE; PS0279; BPTI\_KUNITZ\_2; 1.  
KW Glycoprotein; Amyloid; Neurope; Transmembrane; Alternative splicing;  
KW Signal; Serine protease inhibitor.  
FT SIGNAL 1 17 BY SIMILARITY.  
FT CHAIN 18 751 A4 PROTEIN.  
FT CHAIN 653 695 BETA-AMYLOID PROTEIN (POTENTIAL).  
FT

FT DOMAIN 18 680 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 681 704 POTENTIAL.  
FT DOMAIN 705 751 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 287 345 BPTI/KUNITZ INHIBITOR.  
FT SITE 740 743 CLATHRIN-BINDING (BY SIMILARITY).  
FT ACT\_SITE 301 302 REACTIVE BOND.  
FT DISULFID 291 341 BY SIMILARITY.  
FT DISULFID 300 324 BY SIMILARITY.  
FT DISULFID 316 337 BY SIMILARITY.  
FT CARBOHYD 523 523 N-LINKED (GLCNAC... ) (PROBABLE).  
FT CARBOHYD 552 552 N-LINKED (GLCNAC... ) (PROBABLE).  
SQ SEQUENCE 751 AA; 84893 MW; 6C3E43108569049 CRC64;  
Query Match 100.0%; Score 49; DB 1; Length 751;  
Best Local Similarity 100.0%; Pred. No. 0.02;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 SEVKMDAEFR 10  
|  
Db 648 SEVKMDAEFR 657  
RESULT 8  
A4\_HUMAN STANDARD; PRT; 770 AA.  
ID A4\_HUMAN  
AC P05067; P09000; Q16011;  
DT 13-AUG-1987 (Rel. 05, Created)  
DT 01-NOV-1991 (Rel. 20, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Alzheimer's disease amyloid A4 protein precursor (Protease nexin-II) (PN-II) (APPI) [contains: Beta-amyloid protein (beta-ApP) (A-beta)].  
GN APP OR A4 OR CVAP OR APL.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=87144572; PubMed=2881207;  
RA Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L., Grzeschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.;  
RT "The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surface receptor."  
RL Nature 325:733-736(1987).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=86122639; PubMed=2893289;  
RA Ponte P., Gonzalez-Dewhitt P., Schilling J., Miller J., Hsu D., Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F., Cordell B.;  
RT "A new A4 amyloid mRNA contains a domain homologous to serine protease inhibitors."  
RL Nature 331:525-527(1988).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89128427; PubMed=2783775;  
RA Lemaire H.-G., Salbaum J.M., Multhaup G., Kang J., Bayney R.M., Unterbeck A., Beyreuther K., Mueller-Hill B.;  
RT "The PrEA4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded by 16 exons."  
RL Nucleic Acids Res. 17:517-522(1989).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97263807; PubMed=9108164;  
RA Hattori M., Tsukahara F., Furuhata Y., Tanahashi H., Hirose M., Saito M., Tsukuni S., Sakaki Y.;  
RT "A novel method for making nested deletions and its application for sequencing of a 300 kb region of human APP locus."  
RL Nucleic Acids Res. 25:1802-1808(1997).  
RN [5]  
RP SEQUENCE OF 286-345 AND 365-366 FROM N.A.  
RX MEDLINE=88122640; PubMed=2893290;  
RX



RA Tanzi J.E., McClatchey A.I., Lamperti E.D., Villa-Komaroff L.,  
 RA Gusella J.F., Neve R.L.;  
 RT "Protease inhibitor domain encoded by an amyloid protein precursor  
 RT mRNA associated with Alzheimer's disease.";  
 RL Nature 331:528-530(1988).  
 RN [6]  
 RP SEQUENCE OF 287-367 FROM N.A.  
 RX MEDLINE=88122641; PubMed=2893291;  
 RA Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.;  
 RT "Novel precursor of Alzheimer's disease amyloid protein shows  
 RT protease inhibitory activity.";  
 RL Nature 331:530-532(1988).  
 RN [7]  
 RP SEQUENCE OF 284-289 AND 365-770 FROM N.A.  
 RX MEDLINE=87231971; PubMed=3035574;  
 RA Robakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;  
 RT "Molecular cloning and characterization of a cDNA encoding the  
 RT cerebrovascular and the neuritic plaque amyloid peptides.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).  
 RN [8]  
 RP SEQUENCE OF 507-770 FROM N.A.  
 RX MEDLINE=88124954; PubMed=2893379;  
 RA Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,  
 RA Marotta C.A.;  
 RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer  
 RT disease brain: coding and noncoding regions of the fetal precursor  
 RT mRNA are expressed in the cortex.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).  
 RN [9]  
 RP SEQUENCE OF 672-681.  
 RX MEDLINE=88035004; PubMed=3312495;  
 RA Padridge W.M., Vinters H.V., Yang J., Eisenberg J., Choi T.B.,  
 RA Tourtelotte W.W., Huebner V., Shively J.E.;  
 RT "Amyloid angiopathy of Alzheimer's disease: amino acid composition  
 RT and partial sequence of a 4,200-dalton peptide isolated from cortical  
 RT microvessels.";  
 RL J. Neurochem. 49:1394-1401(1987).  
 RN [10]  
 RP SEQUENCE OF 739-770 FROM N.A.  
 RX MEDLINE=90236318; PubMed=2110105;  
 RA Yoshikai S.-I., Sasaki H., Doh-Ura K., Furuya H., Sakaki Y.;  
 RT "Genomic organization of the human amyloid beta-protein precursor  
 RT gene.";  
 RL Gene 87:257-263(1990).  
 RN [11]  
 RP SEQUENCE OF 1-10 FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=89016647; PubMed=3140222;  
 RA Schon E.A., Mita S., Sadlock J., Herbert J.;  
 RT "A cDNA specifying the human amyloid beta precursor protein (ABPP)  
 RT encodes a 95-kDa polypeptide.";  
 RL Nucleic Acids Res. 16:9351-9351(1988).  
 RN [12]  
 RP SEQUENCE OF 18-50.  
 RX MEDLINE=87250462; PubMed=3597385;  
 RA van Nostrand W.E., Cunningham D.D.;  
 RT "Purification of protease nexin II from human fibroblasts.";  
 RL J. Biol. Chem. 262:8508-8514(1987).  
 RN [13]  
 RP IDENTITY OF APP WITH NEXIN-II.  
 RX MEDLINE=89384866; PubMed=2506449;  
 RA Oltersdorf T., Fritz L.C., Schenk D.B., Lieberburg I.,  
 RA Johnson-Wood K.L., Beattie E.C., Ward P.J., Blacher R.W., Dovey H.F.,  
 RA Sinha S.;  
 RT "The secreted form of the Alzheimer's amyloid precursor protein with  
 RT the Kunitz domain is protease nexin-II.";  
 RL Nature 341:144-147(1989).  
 RN [14]  
 RP PROTEASE-SPECIFICITY OF INHIBITOR DOMAIN.  
 RX MEDLINE=90211252; PubMed=1969731;  
 RA Kido H., Fukutomi A., Schilling J., Wang Y., Cordell B., Katunuma N.;  
 RT "Protease-specificity of kunitz inhibitor domain of Alzheimer's  
 RT disease amyloid protein precursor.";

RL Biochem. Biophys. Res. Commun. 167:716-721(1990).  
 RN [15]  
 RP COMPLEX WITH G(O).  
 RX MEDLINE=93186965; PubMed=8446172;  
 RA Nishimoto I., Okamoto T., Matsura Y., Takahashi S., Okamoto T.,  
 RA Murayama Y., Ogata E.;  
 RT "Alzheimer amyloid protein precursor complexes with brain GTP-binding  
 RT protein G(O).";  
 RL Nature 362:75-79(1993).  
 RN [16]  
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 28-133.  
 RX MEDLINE=99215582; PubMed=10201399;  
 RA Rossjohn J., Cappai R., Fell S.C., Henry A., McKinstry M.J.,  
 RA Galatis D., Hesse L., Multhaup G., Beyreuther K., Masters C.L.,  
 RA Parker M.W.;  
 RT "Crystal structure of the N-terminal, growth factor-like domain of  
 RT Alzheimer amyloid precursor protein.";  
 RL Nat. Struct. Biol. 6:327-331(1999).  
 RN [17]  
 RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF 287-344.  
 RX MEDLINE=91104913; PubMed=2125487;  
 RA Hynes T.R., Randal M., Kennedy L.A., Eigenbrodt C., Kosiakof A.A.;  
 RT "X-ray crystal structure of the protease inhibitor domain of  
 RT Alzheimer's amyloid beta-protein precursor.";  
 RL Biochemistry 29:10018-10022(1990).  
 RN [18]  
 RP STRUCTURE BY NMR OF 289-344.  
 RX MEDLINE=92031488; PubMed=1718421;  
 RA Heald S.L., Tilton R.F., Jr., Hammond L.S., Lee A., Bayney R.M.,  
 RA Kamarc M.E., Ramabhadran T.V., Dreyer R.N., Davis G., Unterbeck A.,  
 RA Tamburlini P.P.;  
 RT "Sequential NMR resonance assignment and structure determination of  
 RT the kunitz-type inhibitor domain of the Alzheimer's beta-amyloid  
 RT precursor protein.";  
 RL Biochemistry 30:10467-10478(1991).  
 RN [19]  
 RP STRUCTURE BY NMR OF 672-699.  
 RX MEDLINE=94281210; PubMed=7516706;  
 RA Talafous J., Marchowski K.J., Klopman G., Zagorski M.G.;  
 RT "Solution structure of residues 1-28 of the amyloid beta-peptide.";  
 RL Biochemistry 33:7788-7796(1994).  
 RN [20]  
 RP STRUCTURE BY NMR OF 696-706.  
 RX MEDLINE=97128622; PubMed=8973180;  
 RA Kohno T., Kobayashi K., Maeda T., Sato K., Takashima A.;  
 RT "Three-dimensional structures of the amyloid beta peptide (25-35) in  
 RT membrane-mimicking environment.";  
 RL Biochemistry 35:16094-16104(1996).  
 RN [21]  
 RP STRUCTURE BY NMR OF 672-711.  
 RX MEDLINE=98359783; PubMed=9693002;  
 RA Coles M., Bicknell W., Watson A.A., Fairlie D.P., Craik D.J.;  
 RT "Solution structure of amyloid beta-peptide(1-40) in a water-miscelle  
 RT environment. Is the membrane-spanning domain where we think it is?";  
 RL Biochemistry 37:11064-11077(1998).  
 RN [22]  
 RP STRUCTURE BY NMR OF 672-699.  
 RX MEDLINE=20400066; PubMed=10940222;  
 RA Poulsen S.A., Watson A.A., Craik D.J.;  
 RT "Solution structures in aqueous SDS micelles of two amyloid beta  
 RT peptides of Abeta(1-28) mutated at the alpha-secretase cleavage  
 RT site.";  
 RL J. Struct. Biol. 130:142-152(2000).  
 RN [23]  
 RP STRUCTURE BY NMR OF 681-706.  
 RX MEDLINE=20400065; PubMed=10940221;  
 RA Zhang S., Iwata K., Lachemann M.J., Peng J.W., Li S., Stimson E.R.,  
 RA Lu Y., Felix A.M., Maggio J.E., Lee J.P.;  
 RT "The Alzheimer's peptide a beta adopts a collapsed coil structure in  
 RT water.";  
 RL J. Struct. Biol. 130:130-141(2000).  
 RN [24]  
 RP SIGNAL SEQUENCE CLEAVAGE SITE, AND TOPOLOGY.

RX MEDLINE-88296437; PubMed-2900137;  
 RA Dykx T., Wellmann A., Muthaup G., Salbaum J.M., Lemaire H.-G.,  
 RA Kang J., Wellner-Hill B., Masters C.L., Beyreuther K.;  
 RT Identification, transmembrane orientation and biogenesis of the  
 RT amyloid A4 precursor of Alzheimer's disease.";

Query Match 100.0%; Score 49; DB 1; Length 770;  
 Best Local Similarity 100.0%; Pred. No. 0.02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SEVKMDAEFR 10  
 Db 667 SEVKMDAEFR 676

RESULT 9  
 ID A4\_MOUSE STANDARD; PRT; 770 AA.  
 AC P12023;  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Alzheimer's disease amyloid A4 protein homolog precursor  
 DE (Amyloidogenic glycoprotein) (Ag).  
 OS APP.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.  
 RC STRAIN-BALB/C; TISSUE-Brain;  
 RX MEDLINE-92096458; PubMed-1756177;  
 RA de Strooper B., Van Leuven F., Van den Berghe H.;  
 RT "The amyloid beta protein precursor or proteolase nexin II from mouse  
 RT is closer related to its human homolog than previously reported.";  
 RL Biochim. Biophys. Acta 1129:141-143(1991).  
 RN [2]  
 RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.  
 RC TISSUE-Brain;  
 RX MEDLINE-88106489; PubMed-3322280;  
 RA Yamada T., Sasaki H., Furuya H., Miyata T., Goto I., Sasaki Y.;  
 RT "Complementary DNA for the mouse homolog of the human amyloid beta  
 RT protein precursor.";  
 RL Biochem. Biophys. Res. Commun. 149:665-671(1987).  
 RN [3]  
 RP REVISIONS.  
 RA Yamada T.;  
 RL Submitted (MAR-1988) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE OF 289-364 FROM N.A.  
 RC STRAIN-CD-1; TISSUE-Placenta;  
 RX MEDLINE-89345111; PubMed-2569710;  
 RA Fukuchi K., Martin G.M., Deeb S.S.;  
 RT "Sequence of the protease inhibitor domain of the A4 amyloid protein  
 RT precursor of Mus domesticus.";  
 RL Nucleic Acids Res. 17:5396-5396(1989).  
 RN [5]  
 RP SEQUENCE OF 1-19 FROM N.A.  
 RX MEDLINE-92209998; PubMed-1555768;  
 RA Izumi R., Yamada T., Yoshikai S.I., Sasaki H., Hattori M.,  
 RA Sakai Y.;  
 RT "Positive and negative regulatory elements for the expression of the  
 RT Alzheimer's disease amyloid precursor-encoding gene in mouse.";  
 RL Gene 112:189-195(1992).  
 RN [6]  
 RP SEQUENCE OF 281-380 FROM N.A. AND ALTERNATIVE SPLICING.  
 RC TISSUE-Brain and Kidney;  
 RX MEDLINE-89149613; PubMed-2493250;  
 RA Yamada T., Sasaki H., Dohura K., Goto I., Sasaki Y.;  
 RT "Structure and expression of the alternatively-spliced forms of mRNA  
 RT for the mouse homolog of Alzheimer's disease amyloid beta protein  
 RT precursor.";

RL Biochem. Biophys. Res. Commun. 158:906-912(1989).  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS: APP(695), APP(563),  
 CC APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE  
 CC SPLICING.  
 CC -1- TISSUE SPECIFICITY: AAA(770) IS EXPRESSED IN KIDNEY. AAA(751) IS  
 CC WIDELY EXPRESSED. AAA(695) IS EXPRESSED IN BRAIN, KIDNEY AND  
 CC LIVER.  
 CC -1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION  
 CC WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC  
 CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE  
 CC NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF  
 CC PHOSPHORYLATION (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.  
 CC -1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.  
 CC -----  
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 CC -----  
 DR EMBL: X59379; -; NOT ANNOTATED\_CDS.  
 DR EMBL: M8373; AAA37139.1; -;  
 DR EMBL: X15210; CAA3280.1; -;  
 DR EMBL: D10603; BAA01456.1; -;  
 DR EMBL: M24397; BAA39929.1; -;  
 DR PIR: A27485; A27485.  
 DR PIR: S04855; S04855.  
 DR PIR: S19727; S19727.  
 DR HSSP: P05067; 1QCM.  
 DR MGD: MGI:86059; APP.  
 DR InterPro: IPR001868; A4\_APP.  
 DR InterPro: IPR002223; Kunitz\_BPTI.  
 DR Pfam: PF02177; A4\_EXTRTA; 1.  
 DR Pfam: PF00014; Kunitz\_BPTI; 1.  
 DR PRINTS: PR00759; BASICPRASE.  
 DR PRINTS: PR00759; BASICPRASE.  
 DR SMART: SM00006; A4\_EXTRTA; 1.  
 DR SMART: SM00131; KU; 1.  
 DR PROSITE: PS00319; A4\_EXTRTA; 1.  
 DR PROSITE: PS00320; A4\_INTRTA; 1.  
 DR PROSITE: PS00280; BPTI\_KUNITZ\_1; 1.  
 DR PROSITE: PS00279; BPTI\_KUNITZ\_2; 1.  
 DR GlycoProtein; Amyloid; Neurone; Transmembrane; Signal;  
 KW Alternative splicing; Serine protease inhibitor.  
 FT SIGNAL 1 17  
 FT CHAIN 1 770  
 FT FT  
 FT DOMAIN 18 699  
 FT TRANSMEM 700 723  
 FT DOMAIN 724 770  
 FT DOMAIN 673 715  
 FT DOMAIN 287 345  
 FT SITE 759 762  
 FT DISULFID 291 341  
 FT DISULFID 300 324  
 FT DISULFID 316 337  
 FT CARBOHYD 542 542  
 FT CARBOHYD 571 571  
 FT FT  
 FT VARSPLIC 289 289  
 FT VARSPLIC 290 364  
 FT VARSPLIC 346 380  
 FT SEQUENCE 770 AA: 86752 MW: 26C50DE0890CAFA7A CRC64;

Query Match 89.8%; Score 44; DB 1; Length 770;  
 Best Local Similarity 100.0%; Pred. No. 0.22;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SEVKMDAEFR 9  
 |||||||||

DB 667 SEVKMDAEF 675

RESULT 10

AA\_RAT STANDARD: PRT; 770 AA.

ID A4\_RAT

DT 01-MUG-1988 (Rel. 08, Created)

DT 01-DEC-1992 (Rel. 24, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Alzheimer's disease amyloid A4 protein homolog precursor

DE (Amyloidogenic glycoprotein) (Ag).

GN App.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.

OX NCBI\_TaxID=10116;

RN [1]

RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.

RC TISSUE=Brain

RX MEDLINE=88312583; PubMed=2900758;

RA Shivers B.D., Hilbich C., Multhaup G., Salbaum J.M., Beyreuther K., Seeburg P.H.;

RT "Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brain suggests a role in cell contact.";

RT EMBO J. 7:1365-1370(1988).

RN [2]

RP SEQUENCE OF 289-364 FROM N.A.

RC TISSUE=Liver;

RX MEDLINE=89183625; PubMed=2648331;

RA Kang J., Mueller-Hill B.;

RT "The sequence of the two extra exons in rat preA4.";

RT Nucleic Acids Res. 17:2130-2130(1989).

CC -1- SUBCELLULAR LOCATION: Type I membrane protein.

CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS; APP(395), APP(563), APP(695), APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.

CC -1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF PHOSPHORYLATION (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.

CC -1- SIMILARITY: CONTAINS 1 BPT1/KUNTZ INHIBITOR DOMAIN.

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CC EMBL; X07648; CAA30488.1; -

DR EMBL; X14066; CAA32229.1; -

DR PIR: S00550; S00550.

DR PIR: S03607; S03607.

DR HSP; P05067; 1AAP.

DR InterPro: IPR001868; A4\_APP.

DR InterPro: IPR002223; Kuntz\_BPT1.

DR Pfam: PF02177; A4\_EXTRA; 1.

DR Pfam: PF00014; Kuntz\_BPT1; 1.

DR PRINTS: PR00203; AMYLOIDA4.

DR PRINTS: PR00759; BASICPTASE.

DR SMART: SM00006; A4\_EXTRA; 1.

DR SMART: SM00131; Ku; 1.

DR PROSITE: PS00319; A4\_EXTRA; 1.

DR PROSITE: PS00320; A4\_INTRA; 1.

DR PROSITE: PS00280; BPT1\_KUNTZ; 1.

DR PROSITE: PS50279; BPT1\_KUNTZ; 2; 1.

KW glycoprotein; Amyloid; Neurone; Transmembrane; Signal;

KW Alternative splicing; Serine protease inhibitor.

FT SIGNAL 1 17 BY SIMILARITY.

FT CHAIN 18 770 ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN

FT DOMAIN 18 699 HOMOLOG.

FT TRANSMEM 700 723 EXTRACELLULAR (POTENTIAL).

FT DOMAIN 724 770 POTENTIAL.

FT DOMAIN 673 715 CYTOSOLASMIC (POTENTIAL).

FT DOMAIN 287 345 ECTVLALENT OF BETA-AMYLOID PROTEIN.

FT SITE 759 762 BPT1/KUNTZ INHIBITOR.

FT DISULFID 291 341 CLATHRIN-BINDING (BY SIMILARITY).

FT DISULFID 300 324 BY SIMILARITY.

FT DISULFID 316 337 BY SIMILARITY.

FT CARBOHYD 542 542 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 571 571 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT VARSPPLIC 289 289 E -> V (IN ISOFORM APP(695)).

FT VARSPPLIC 290 364 MISSING (IN ISOFORM APP(695)).

SO SEQUENCE 770 AA; 86704 MW; C26C9D6BBD929A7 CRC64;

Query Match

Best Local Similarity 89.8%; Score 44; DB 1; Length 770;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEVKMDAEF 9

DB 667 SEVKMDAEF 675

QY 1 SEVKMDAEF 9

DB 667 SEVKMDAEF 675

RESULT 11

T2S1\_STREI STANDARD: PRT; 269 AA.

ID T2S1\_STREI

AC 052512;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Type II restriction enzyme SfiI (EC 3.1.21.4) (Endonuclease SfiI)

DE (K.SfiI).

GN SFIIR.

OS Streptomyces fimbriatus.

OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;

OC Actinomycetales; Streptomyces; Streptomycetaceae; Streptomyces.

OX NCBI\_TaxID=68197;

RN [1]

RP SEQUENCE FROM N.A.

RA van Cott E.M., Moran L.S., Slatko B.E., Wilson G.G.;

RT "Characterization of the SfiI restriction and modification genes.";

RT Submitted (DEC-1997) to the EMBL/Genbank/DBJ databases.

CC -1- FUNCTION: RECOGNIZES THE DOUBLE-STRANDED SEQUENCE GAGCANNNGCC

CC AND CLEAVES BEFORE N-9.

CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage of DNA to give specific double-stranded fragments with terminal 5'-phosphates.

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CC EMBL; AF039750; AAB95365.1; -

DR EMBL; AF039750; AAB95365.1; -

DR REBASE; 1655; SfiI.

DR Hydrolase: Endonuclease; Nuclease; Restriction system.

KW SEQUENCE 269 AA; 31044 MW; 3CA8499BAA5205EA CRC64;

Query Match

Best Local Similarity 75.5%; Score 37; DB 1; Length 269;

Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SEVKMDAEF 10

DB 115 SQPMDAEF 124

QY 1 SEVKMDAEF 10

DB 115 SQPMDAEF 124

RESULT 12



AC P04114; 000502; Q13787;  
 DT 01-NOV-1986 (Rel. 03, Created)  
 DT 01-NOV-1986 (Rel. 03, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Apolipoprotein B-100 precursor (Apo B-100) [contains: Apolipoprotein  
 B-48 (Apo B-48)].  
 GN APOB.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OC NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87016385; PubMed=3763409;  
 RA Knott T.C., Wallis S.C., Powell L.M., Pease R.J., Lusis A.J.,  
 RA Blackhart B., McCarthy B.J., Mahley R.W., Levy-Wilson B., Scott J.;  
 RT "Complete cDNA and derived protein sequence of human apolipoprotein  
 RT B-100.";  
 RL Nucleic Acids Res. 14:7501-7503(1986).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86803974; PubMed=3652907;  
 RA Ludwig E.H., Blackhart B.D., Plerotti V.R., Caiati L., Fortier C.,  
 RA Knott T., Scott J., Mahley R.W., Levy-Wilson B., McCarthy B.J.;  
 RT "DNA sequence of the human apolipoprotein B gene.";  
 RL DNA 6:363-372(1987).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87008488; PubMed=3759943;  
 RA Chen S.-H., Yang C.-Y., Chen P.-F., Setzer D., Tanimura M., Li W.-H.,  
 RA Goto A.M., Jr., Chan L.;  
 RT "The complete cDNA and amino acid sequence of human apolipoprotein  
 RT B-100.";  
 RL J. Biol. Chem. 261:12918-12921(1986).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87041416; PubMed=3464946;  
 RA Law S.W., Grant S.M., Higuchi K., Hospattankar A.V., Jackner K.J.,  
 RA Lee N., Brewer H.B., Jr.;  
 RT "Human liver apolipoprotein B-100 cDNA: complete nucleic acid and  
 RT derived amino acid sequence.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 83:8142-8146(1986).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87161758; PubMed=3030723;  
 RA Cladaras C., Hadjopoulou-Cladaras M., Nolte R.T., Atkinson D.,  
 RA Zannis V.I.;  
 RT "The complete sequence and structural analysis of human  
 RT apolipoprotein B-100: relationship between apob-100 and apob-48  
 RT forms.";  
 RL EMBO J. 5:3495-3507(1986).  
 RN [6]  
 RP SEQUENCE OF 709-906 FROM N.A.  
 RX MEDLINE=85270450; PubMed=3860836;  
 RA Deeb S.S., Motulsky A.G., Alpers J.J.;  
 RT "A partial cDNA clone for human apolipoprotein B.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 82:4983-4986(1985).  
 RN [7]  
 RP SEQUENCE OF 3056-3159 FROM N.A.  
 RX MEDLINE=86041888; PubMed=3903660;  
 RA Mehrabian M., Schumaker V.N., Fareed G.C., West R., Johnson D.F.,  
 RA Kirchgessner T.G., Lin H.-C., Wang X., Ma Y., Mendiaz E., Lusis A.J.;  
 RT "Human apolipoprotein B: identification of cDNA clones and  
 RT characterization of mRNA.";  
 RL Nucleic Acids Res. 13:6937-6953(1985).  
 RN [8]  
 RP SEQUENCE OF 1937-2018 AND 3811-4334 FROM N.A.  
 RX MEDLINE=86093680; PubMed=3841204;  
 RA Carlsson P., Olofsson S.O., Bonders G., Darnfors C., Wiklund O.,  
 RA Bjursell G.;  
 RT "Molecular cloning of human apolipoprotein B cDNA.";  
 RL Nucleic Acids Res. 13:8813-8826(1985).  
 RN [9]

RP SEQUENCE OF 3109-4563 FROM N.A.  
 RX MEDLINE=85300528; PubMed=2994225;  
 RA Knott T.J., Rall S.C. Jr., Innerarity T.L., Jacobson S.F.,  
 RA Ureña M.S., Levy-Wilson B., Powell L.M., Pease R.J., Edy R.,  
 RA Nakai H., Byers M., Priestley L.W., Robertson E., Rall L.B.,  
 RA Betsholtz C., Shows T.B., Mahley R.W., Scott J.;  
 RT "Human apolipoprotein B: structure of carboxyl-terminal domains,  
 RT sites of gene expression, and chromosomal localization.";  
 RL Science 230:37-43(1985).  
 RN [10]  
 RP SEQUENCE OF 1-291 FROM N.A.  
 RX MEDLINE=86149325; PubMed=3513177;  
 RA Protter A.A., Hardman D.A., Schilling J.W., Miller J., Appleby V.,  
 RA Chen G.C., Kirsher S.W., McIntroe G., Kane J.P.;  
 RT "Isolation of a cDNA clone encoding the amino-terminal region of  
 RT human apolipoprotein B.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 83:1467-1471(1986).  
 RN [11]  
 RP SEQUENCE OF 1-1670 FROM N.A.  
 RX MEDLINE=86287319; PubMed=3461454;  
 RA Protter A.A., Hardman D.A., Sato K.Y., Schilling J.W.,  
 RA Yamanaka M., Hori Y.J., Hjertild K.A., Chen G.C., Kane J.P.;  
 RT "Analysis of cDNA clones encoding the entire B-26 region of human  
 RT apolipoprotein B.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 83:5678-5682(1986).  
 RN [12]  
 RP PARTIAL SEQUENCE, AND IDENTIFICATION (APO-B48).  
 RX MEDLINE=88018019; PubMed=3659919;  
 RA Chen S.-H., Habib G., Yang C.-H., Gu Z.-W., Lee B.R., Weng S.-H.,  
 RA Silberman S.R., Cai S.-J., Deslypere J.P., Rosseneu M.,  
 RA Goto A.M., Jr., Li W.-H., Chan L.;  
 RT "Apolipoprotein B-48 is the product of a messenger RNA with an organ-  
 RT specific in-frame stop codon.";  
 RL Science 238:363-366(1987).  
 RN [13]  
 RP DOMAINS.  
 RX MEDLINE=87039351; PubMed=3773997;  
 RA Knott T.C., Pease R.J., Powell L.M., Wallis S.C., Rall S.C. Jr.,  
 RA Innerarity T.L., Blackhart B., Taylor W.R., Marcel Y., Milne R.,  
 RA Johnson D., Fuller M., Lusis A.J., McCarthy B.J., Mahley R.W.,  
 RA Levy-Wilson B., Scott J.;  
 RT "Complete protein sequence and identification of structural domains  
 RT of human apolipoprotein B.";  
 RL Nature 323:734-738(1986).  
 RN [14]  
 RP DOMAINS.  
 RA Yang C.-Y., Chen S.-H., Gianturco S.H., Bradley W.A., Sparrow J.T.,  
 RA Tanimura M., Li W.-H., Sparrow D.A., Deloof H., Rosseneu M.,  
 RA Lee F.-S., Gu Z.-W., Goto A.M., Jr., Chan L.;  
 RT "Sequence, structure, receptor-binding domains and internal repeats  
 RT of human apolipoprotein B-100.";  
 RL Nature 323:738-742(1986).  
 RN [15]  
 RP CALCULUM-BINDING DATA.  
 RX MEDLINE=86242245; PubMed=3087360;  
 RA Dashti N., Lee D.M., Mok T.;  
 RT "Apolipoprotein B is a calcium binding protein.";  
 RL Biochem. Biophys. Res. Commun. 137:493-499(1986).  
 RN [16]  
 RP VARIANT SER-4338.  
 RX MEDLINE=91071750; PubMed=1979313;  
 RA Navejas M., Laurent A.-M., Moreel J.-F., Ragab A., Cambou J.-P.,  
 RA Cuny G., Cambou F., Roizes G.;  
 RT "Detection by denaturing gradient gel electrophoresis of a new  
 RT polymorphism in the apolipoprotein B gene.";  
 RL Hum. Genet. 86:91-93(1990).  
 RN [17]  
 RP VARIANT FDB GLN-3527.  
 RX MEDLINE=89098975; PubMed=2563166;  
 RA Sorla L.F., Ludwig E.H., Clarke H.R.G., Vega G.L., Grundy S.M.,  
 RA McCarthy B.J.;  
 RT "Association between a specific apolipoprotein B mutation and  
 RT familial defective apolipoprotein B-100.";

Proc. Natl. Acad. Sci. U.S.A. 86:587-591(1989).  
 [18]  
 RP VARIANT LEU-2739. PubMed=2216805;  
 RX MEDLINE=91016974; PubMed=2216805;  
 RA Huang L.-S., Gavish D., Breslow J.L.;  
 RT "Sequence polymorphism in the human apob gene at position 8344.";  
 RL Nucleic Acids Res. 18:5922-5923(1990).  
 RN [19]  
 RP VARIANT FDB CYS-3558.  
 RX MEDLINE=95190020; PubMed=7883971;  
 RA Pullinger C.R., Hennessey L.K., Chatterton J.E., Liu W., Love J.A.,  
 RA Mendel C.M., Frost P.H., Malloy M.J., Schumaker V.N., Kane J.P.;  
 RT "Familial ligand-defective apolipoprotein B. Identification of a new  
 mutation that decreases LDL receptor binding affinity.";  
 RL J. Clin. Invest. 95:1225-1234(1995).  
 RN [20]  
 RP VARIANTS L-1437; S-1914; K-2566; T-3121; A-3945; M-4128 AND T-4481.  
 RX MEDLINE=97044521; PubMed=8889592;  
 RA Pollier O., Ricard S., Behague I., Souriau C., Evans A.E.,  
 RA Arveiler D., Marques-Vidal P., Luc G., Roizes G., Camden F.;  
 RT "Detection of new variants in the apolipoprotein B (Apo B) gene by  
 PCR-SSCP.";  
 RL Hum. Mutat. 8:282-285(1996).  
 RN [21]  
 RP VARIANTS FDB GLN-3527 AND CYS-3558.  
 RX MEDLINE=97403938; PubMed=9259199;  
 RA Rades J.P., Varret M., Saint-Jore B., Erlich D., Jondeau G.,  
 RA Krempf M., Giraudet P., Junien C., Boileau C.;  
 RT "Familial ligand-defective apolipoprotein B-100: simultaneous  
 detection of the ARG3500->GLN and ARG3531->CYS mutations in a  
 French population.";  
 RL Hum. Mutat. 10:160-163(1997).  
 RN [22]  
 RP VARIANTS S-1914; R-1923; L-2739; D-3319; T-3427; Q-3432 AND I-3921.  
 RX MEDLINE=98141125; PubMed=9490296;  
 RA Leren T.P., Bakken K.S., Hoel V., Hjermann I., Berg K.;  
 RT "Screening for mutations of the apolipoprotein B gene causing  
 hypocholesterolemia.";  
 RL Hum. Genet. 102:44-49(1998).  
 CC -1- FUNCTION: APOLOPROTEIN B IS A MAJOR PROTEIN CONSTITUENT OF  
 CHYLOMICRONS, VLDL AND LDL, IT FUNCTIONS AS A RECOGNITION SIGNAL  
 FOR THE CELLULAR BINDING AND INTERNALIZATION OF LDL PARTICLES BY  
 THE APOB/E RECEPTOR.  
 CC -1- DISEASE: DEFECTS IN APOB ARE A CAUSE OF FAMILIAL LIGAND-DEFECTIVE  
 APOLOPROTEIN B-100 (FDB). IT IS A DOMINANTLY INHERITED DISORDER  
 OF LIPOPROTEIN METABOLISM LEADING TO HYPERCHOLESTEROLEMIA AND  
 INCREASED PRONENESS TO CORONARY ARTERY DISEASE (CAD).  
 CC THE PLASMA CHOLESTEROL LEVELS ARE DRAMATICALLY ELEVATED DUE TO  
 IMPAIRED CLEARANCE OF LDL PARTICLES BY DEFECTIVE APOB/E RECEPTORS.  
 CC -1- DISEASE: DEFECTS IN APOB ASSOCIATED WITH OTHER GENE DEFECTS  
 (POLYGENIC) CAN BE THE CAUSE OF HYPOCHOLESTEROLEMIA.  
 CC -1- MISCELLANEOUS: APO B-48 WHICH IS SYNTHESIZED ONLY BY THE  
 INTESTINE, AND FOUND IN CHYLOMICRONS, IS A SHORTENED FORM OF APO  
 B.  
 Query Match 69.4%; Score 34; DB 1; Length 4563;  
 Best Local Similarity 66.7%; Pred. No. 1.6e+02;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 EVKMDAEFR 10  
 DB 1483 EVKIDGQFR 1491  
 RESULT 14  
 CC15\_SCHPO STANDARD; PRT; 927 AA.  
 AC 009822; 014365;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Cell division control protein 15.  
 GN CDC15 OR SPAC2068.05C.  
 OS Schizosaccharomyces pombe (fission yeast).

OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
 OC Schizosaccharomyces.  
 OX NCBI\_TaxID=4896;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=972;  
 RX MEDLINE=95360987; PubMed=7634333;  
 RA Fankhauser C., Raymond A., Cerrutti L., Utzig S., Hofmann K.;  
 RA Fankhauser C., Raymond A., Cerrutti L., Utzig S., Hofmann K.;  
 RT "The S. pombe cdc15 gene is a key element in the reorganization of F-  
 actin at mitosis.";  
 RL Cell 82:435-444(1995).  
 RN [2]  
 RP REVISIONS TO N-TERMINUS.  
 RA Fankhauser C., Raymond A., Cerrutti L., Utzig S., Hofmann K.;  
 RA Fankhauser C., Raymond A., Cerrutti L., Utzig S., Hofmann K.;  
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=972;  
 RA Badcock K., Churcher C.M., Wood V., Bartell B.G., Rajandream M.A.;  
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases  
 CC -1- FUNCTION: AFTER THE ONSET OF MITOSIS, FORMS A RING-LIKE STRUCTURE  
 WHICH CO-LOCALIZES WITH THE MEDIAL ACTIN RING. APPEARS TO MEDIALTE  
 CYTOSKELETAL REARRANGEMENTS REQUIRED FOR CYTOKINESIS. ESSENTIAL  
 FOR VIABILITY.  
 CC -1- DEVELOPMENTAL STAGE: PEAKS IN EARLY MITOSIS BEFORE SEPTATION.  
 CC -1- DOMAIN: THE N-TERMINAL REGION IS IN A COILED COIL STRUCTURE.  
 CC -1- PTM: PHOSPHORYLATED.  
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.  
 CC -1- SIMILARITY: SOME, TO S.POMBE SPB11C11.02 AND SPAC7D4.02C.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC -----  
 DR EMBL; X86179; CA60115.1; -;  
 DR EMBL; Z95334; CAB08599.2; -;  
 DR HSSP; P07751; ITUD.  
 DR InterPro; IPR001060; FCH.  
 DR InterPro; IPR001452; SH3.  
 DR Pfam; PF00611; FCH; 1.  
 DR Pfam; PF00018; SH3; 1.  
 DR PRINTS; PR00452; SH3DOMAIN.  
 DR SMART; SM00055; FCH; 1.  
 DR SMART; SM00326; SH3; 1.  
 DR PROSITE; PS50002; SH3; 1.  
 DR KWSites; Cytoskeleton; SH3 domain; Phosphorylation; Coiled coil.  
 FT DOMAIN 24 110 FCH.  
 FT DOMAIN 108 207 COILED COIL (POTENTIAL).  
 FT DOMAIN 866 927 SH3.  
 FT SEQUENCE 927 AA; 102119 MW; FDC7E0AAA3D247D CR664;  
 Query Match 67.3%; Score 33; DB 1; Length 927;  
 Best Local Similarity 85.7%; Pred. No. 48;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 KMDAEFR 10  
 DB 195 KMDAEFR 201  
 RESULT 15  
 Y683\_HALNT STANDARD; PRT; 263 AA.  
 ID Y683\_HALNT  
 AC 09HR12;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)

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DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative aldolase Yng0683c (EC 4.2.1.-).
GN YNG0683c.
OS Halobacterium sp. (strain NRC-1).
OC Archaea: Euryarchaeota; Halobacteriales; Halobacteriaceae;
OC Halobacterium.
OX NCBI_TaxID=64091;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20504483; PubMed=11016950;
RA Ng W.V., Kennedy S.P., Mahatas G.G., Bergquist B., Pan M.,
RA Shukla H.D., Lasky S.R., Ballig N.S., Thorsson V., Sbrogna J.,
RA Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
RA Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
RA Isebnarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
RA Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., Dassarma S.;
RA "genome sequence of Halobacterium species NRC-1."
RA Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
RL
CC -1- SIMILARITY: BELONGS TO THE DECO/FRAB FAMILY OF ALDOLASES.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
CC DR EMBL: AE005014; AA619176.1;
CC KW HYPOthetical protein; lyase; Schiff base; Complete proteome.
CC FT BINDING 177 177 SCHIFF-BASE (BY SIMILARITY).
CC SO SEQUENCE 263 AA; 28083 MW; 25FF044B6A77494F CRC64;
CC
CC Query Match 65.3%; Score 32; DB 1; Length 263;
CC Best Local Similarity 70.0%; Pred. No. 21;
CC Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Search completed: October 29, 2002, 10:27:28  
 Job time : 6 secs





GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 29, 2002, 10:23:11 ; Search time 18 Seconds  
(without alignments)  
96.108 Million cell updates/sec

Title: US-09-580-018-4  
Perfect score: 49  
Sequence: 1 SEVKMDAEFR 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: SP\_ARCHAEA:\*  
2: SP\_BACTERIA:\*  
3: SP\_FUNGI:\*  
4: SP\_HUMAN:\*  
5: SP\_INVERTEBRATE:\*  
6: SP\_MAMMAL:\*  
7: SP\_MNC:\*  
8: SP\_ORGANELLE:\*  
9: SP\_PHAGE:\*  
10: SP\_PLANT:\*  
11: SP\_PROTOZOA:\*  
12: SP\_VIRUS:\*  
13: SP\_VIRUS:\*  
14: SP\_UNCLASSIFIED:\*  
15: SP\_VIRUS:\*  
16: SP\_BACTERIAP:\*  
17: SP\_ARCHAEA:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	49	100.0	82	4 P78438	P78438 homo sapien
2	49	100.0	82	4 Q16014	Q16014 homo sapien
3	49	100.0	82	4 Q16019	Q16019 homo sapien
4	49	100.0	82	4 Q16020	Q16020 homo sapien
5	49	100.0	534	13 Q93296	Q93296 gallus gall
6	49	100.0	569	13 Q9PV11	Q9PV11 gallus gall
7	49	100.0	695	6 Q9SKN7	Q9SKN7 macaca fasc
8	49	100.0	695	11 Q60496	Q60496 cavia sp. P
9	49	100.0	695	13 Q9DCJ8	Q9DCJ8 gallus gall
10	49	100.0	751	13 Q9DCJ7	Q9DCJ7 gallus gall
11	49	100.0	770	6 Q9TUI0	Q9TUI0 sus scrofa
12	44	89.8	79	11 Q35463	Q35463 cricetus
13	44	89.8	607	11 Q99K32	Q99K32 mus musculu
14	44	89.8	695	11 P97487	P97487 mus musculu
15	43	87.8	693	13 Q98SG0	Q98SG0 xenopus lae
16	43	87.8	695	13 Q98SF9	Q98SF9 xenopus lae

17	43	87.8	747	13 Q91963	Q91963 xenopus. ap
18	42	85.7	423	2 Q52379	Q52379 raietonia s
19	42	85.7	423	2 Q45693	Q45693 burkholderi
20	39	79.6	142	5 Q16896	Q16896 caenorhabdi
21	36	73.5	630	2 Q93IK4	Q93IK4 vibrio sp.
22	35	71.4	317	17 Q96X72	Q96X72 sulfolobus
23	35	71.4	774	16 Q92CV7	Q92CV7 listeria in
24	34	69.4	239	10 Q9FNC2	Q9FNC2 arabidopsis
25	34	69.4	605	2 Q9LIF6	Q9LIF6 streptomyces
26	34	69.4	1192	10 Q94BS1	Q94BS1 arabidopsis
27	34	69.4	1261	10 Q9L030	Q9L030 arabidopsis
28	34	69.4	3262	4 Q13788	Q13788 homo sapien
29	33	67.3	302	9 Q37840	Q37840 bacterioph
30	33	67.3	438	2 Q9A1K4	Q9A1K4 biophila w
31	33	67.3	621	4 Q9H9T1	Q9H9T1 homo sapien
32	33	67.3	1027	4 Q9BMX2	Q9BMX2 homo sapien
33	33	67.3	1245	10 Q9C7F8	Q9C7F8 arabidopsis
34	32	65.3	143	4 Q9H935	Q9H935 homo sapien
35	32	65.3	161	16 Q98FE2	Q98FE2 rhizobium l
36	32	65.3	338	2 Q9A167	Q9A167 chlorobium
37	32	65.3	340	5 Q9U0X8	Q9U0X8 leishmania
38	32	65.3	350	2 Q9AL73	Q9AL73 chlorobium
39	32	65.3	350	2 Q9AL69	Q9AL69 chlorobium
40	32	65.3	350	2 Q9AL72	Q9AL72 chlorobium
41	32	65.3	376	12 Q9DVZ3	Q9DVZ3 plutella xy
42	32	65.3	405	4 Q9BU21	Q9BU21 homo sapien
43	32	65.3	436	17 Q9V2P8	Q9V2P8 pyrococcus
44	32	65.3	539	4 Q9NWD6	Q9NWD6 homo sapien
45	32	65.3	539	4 Q9NM45	Q9NM45 homo sapien

## ALIGNMENTS

RESULT 1  
P78438 PRELIMINARY; PRT; 82 AA.  
ID P78438  
AC P78438;  
DT 01-MAY-1997 (TREMBL) 03, Created  
DT 01-MAY-1997 (TREMBL) 03, Last sequence update  
DE 01-MAR-2001 (TREMBL) 16, Last annotation update  
DE AMYLOID PROTEIN (BETA-AMYLOID PROTEIN) (FRAGMENT).  
GN APP.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89392030; PubMed=2675837;  
RA Johnstone E.M., Chaney M.O., Moore R.E., Ward K.E., Norris F.H.,  
RA Little S.P.;  
RT "Alzheimer's disease amyloid peptide is encoded by two exons and shows  
RT similarity to soybean trypsin inhibitor."  
RL Biochem. Biophys. Res. Commun. 163:1248-1255(1989).  
RN [2]  
RP SEQUENCE OF 19-48 FROM N.A.  
RX MEDLINE=87120329; PubMed=2949367;  
RA Tanzi R.E., Gusella J.F., Watkins P.C., Bruns G.A., George-Hyslop P.,  
RA Van Keuren M.L., Patterson D., Pagan S., Kurnit D.M., Neve R.L.;  
RT "Amyloid beta protein gene: cDNA, mRNA distribution, and genetic  
RT linkage near the Alzheimer locus."  
RL Science 235:880-884(1987).  
RN [3]  
RP SEQUENCE OF 32-63 FROM N.A.  
RX MEDLINE=9305397; PubMed=1415269;  
RA Kamito K., Orr H.T., Payami H., Wajsmann E.M., Alonso M.E., Pulst S.M.,  
RA Anderson L., O'dahl S., Nemes E., White J.A.;  
RT "Linkage and mutational analysis of familial Alzheimer disease  
RT kindreds for the APP gene region."  
RL Am. J. Hum. Genet. 51:998-1014(1992).  
DR EMBL: M29270; AAA51768.1; -;  
DR EMBL: M29269; AAA51768.1; JOINED.

DR EMBL; M15532; AAA51564.1; -.  
 DR EMBL; S45136; AAB23646.1; -.  
 DR HSSP; P05067; 1BA4. 1  
 FT NON\_TER 1  
 SQ SEQUENCE 82 AA; 8994 MW; 8DA9E42B813A070E CRC64;

Query Match 100.0%; Score 49; DB 4; Length 82;  
 Best Local Similarity 100.0%; Pred. No. 0.009;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SEVKMDAEFR 10  
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 Db 12 SEVKMDAEFR 21

## RESULT 2

ID Q16014 PRELIMINARY; PRT; 82 AA.  
 AC Q16014;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE BETA-AMYLLOID PEPTIDE (FRAGMENT).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 GN NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93236601; PubMed=8476439;  
 RA Denman R.B., Rosenzweig R., Miller D.L.;  
 RT "A system for studying the effect(s) of familial Alzheimer disease  
 mutations on the processing of the beta-amyloid peptide precursor.";  
 RL Biochem. Biophys. Res. Commun. 192:96-103(1993).  
 DR EMBL; S60721; AAB26263.2; -.  
 DR HSSP; P05067; 1BA4. 1  
 FT NON\_TER 1  
 SQ SEQUENCE 82 AA; 8972 MW; F534AASB3EA9230A CRC64;

Query Match 100.0%; Score 49; DB 4; Length 82;  
 Best Local Similarity 100.0%; Pred. No. 0.009;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SEVKMDAEFR 10  
 |||||  
 Db 13 SEVKMDAEFR 22

## RESULT 3

ID Q16019 PRELIMINARY; PRT; 82 AA.  
 AC Q16019;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE BETA-AMYLLOID PEPTIDE (FRAGMENT).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 GN NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93236601; PubMed=8476439;  
 RA Denman R.B., Rosenzweig R., Miller D.L.;  
 RT "A system for studying the effect(s) of familial Alzheimer disease  
 mutations on the processing of the beta-amyloid peptide precursor.";  
 RL Biochem. Biophys. Res. Commun. 192:96-103(1993).  
 DR EMBL; S61380; AAB26264.2; -.  
 DR HSSP; P05067; 1BA4. 1  
 FT NON\_TER 1  
 SQ SEQUENCE 82 AA; 8972 MW; F534AASB3EA9230A CRC64;

SQ SEQUENCE 82 AA; 8938 MW; F534AAS0E579230A CRC64;

Query Match 100.0%; Score 49; DB 4; Length 82;  
 Best Local Similarity 100.0%; Pred. No. 0.009;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SEVKMDAEFR 10  
 |||||  
 Db 13 SEVKMDAEFR 22

## RESULT 4

ID Q16020 PRELIMINARY; PRT; 82 AA.  
 AC Q16020;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE BETA-AMYLLOID PEPTIDE (FRAGMENT).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 GN NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93236601; PubMed=8476439;  
 RA Denman R.B., Rosenzweig R., Miller D.L.;  
 RT "A system for studying the effect(s) of familial Alzheimer disease  
 mutations on the processing of the beta-amyloid peptide precursor.";  
 RL Biochem. Biophys. Res. Commun. 192:96-103(1993).  
 DR EMBL; S61383; AAB26265.2; -.  
 DR HSSP; P05067; 1BA4. 1  
 FT NON\_TER 1  
 SQ SEQUENCE 82 AA; 8882 MW; F534AASAE5D9230A CRC64;

Query Match 100.0%; Score 49; DB 4; Length 82;  
 Best Local Similarity 100.0%; Pred. No. 0.009;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SEVKMDAEFR 10  
 |||||  
 Db 13 SEVKMDAEFR 22

## RESULT 5

ID O93296 PRELIMINARY; PRT; 534 AA.  
 AC O93296;  
 DT 01-NOV-1998 (TREMBlrel. 08, Created)  
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE AMYLLOID PROTEIN (FRAGMENT).  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 GN NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98337885; PubMed=9671674;  
 RA Barnes N.Y., Li L., Yoshikawa K., Schwartz L.M., Oppenheim R.W.,  
 RA Milligan C.E.;  
 RT "Increased production of amyloid precursor protein provides a  
 substrate for caspase-3 in dying motoneurons.";  
 RL J. Neurosci. 18:5869-5880(1998).  
 DR EMBL; AF042098; AAC25052.1; -.  
 DR HSSP; P05067; 1BA4.  
 DR InterPro: IPR001868; A4 APP.  
 DR PRINTS: PR00203; AMYLOIDA4.  
 DR PROSITE: PS00319; A4\_EXTRA; 1.  
 DR PROSITE: PS00320; A4\_INTRA; 1.

FT NON\_TER 1 1  
SQ SEQUENCE 534 AA; 60597 MW; FB53EC2E66DC92 CRC64;

Query Match  
Best Local Similarity 100.0%; Score 49; DB 13; Length 534;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SEVKMDAER 10  
Db 431 SEVKMDAER 440

RESULT 6

O9PVL1 PRELIMINARY; PRT; 569 AA.

ID O9PVL1

AC O9PVL1

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE AMYLOID PROTEIN (FRAGMENT).

GN APP.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

NCBI\_TaxID=9031;

RN (1)

RP SEQUENCE FROM N.A.

RC TISSUE=BRAIN;

RA Coulson E.J., Paliga K., Beyreuther K., Masters C.L.;

RT tells us about its function.\*

RL Neurochem. Int. 0:0-0(2000).

DR EMBL; AF030341; AAF12698.1; -.

DR HSSP; P05067; 1BA4.

DR InterPro; IPR001868; A4\_APP.

DR Pfam; PF02177; A4\_EXTRA; 1.

DR PRINTS; PR00203; AMYLOIDA4.

DR SMART; SM00006; A4\_EXTRA; 1.

DR PROSITE; PS00319; A4\_EXTRA; 1.

DR PROSITE; PS00320; A4\_INTRA; 1.

FT NON\_TER 1

SQ SEQUENCE 569 AA; 64753 MW; 0AB8B851863A19D CRC64;

Query Match

Best Local Similarity 100.0%; Score 49; DB 13; Length 569;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SEVKMDAER 10  
Db 467 SEVKMDAER 476

RESULT 7

O95KN7 PRELIMINARY; PRT; 695 AA.

ID O95KN7

AC O95KN7

DT 01-DEC-2001 (TREMBLrel. 19, Created)

DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE AMYLOID B-PROTEIN PRECURSOR.

OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

OC Cercopithecoidea; Macaca.

NCBI\_TaxID=9541;

RN (1)

RP SEQUENCE FROM N.A.

RC TISSUE=CEREBELLUM;

RA Podlasky M.B., Tolan D.R., Selkoe D.J.;

RT "Homology of the amyloid beta protein precursor in monkey and human

RT supports a primate model for beta amyloidosis in Alzheimer's

RT disease.";

RL Am. J. Pathol. 138:1423-1435(1991).

DR EMBL; M58727; AAA36829.1; -.

FT SIGNAL 1 17 POTENTIAL.

FT CHAIN 597 636 POTENTIAL.

SQ SEQUENCE 695 AA; 78663 MW; 4F6EA0139F969D56 CRC64;

Query Match

Best Local Similarity 100.0%; Score 49; DB 6; Length 695;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SEVKMDAER 10  
Db 592 SEVKMDAER 601

RESULT 8

O60496 PRELIMINARY; PRT; 695 AA.

ID O60496

AC O60496

DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE PUTATIVE AMYLOID PRECURSOR PROTEIN.

OS Cavia sp.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Hystriognathia; Cavidae; Cavia.

NCBI\_TaxID=10143;

RN (1)

RP SEQUENCE FROM N.A.

RC TISSUE=BRAIN;

RA Beck M., Mueller D., Bigl V.;

RT "Amyloid precursor protein in Guinea pigs - complete cDNA sequence and

RT alternative splicing."

RL Biochim. Biophys. Acta 1351:17-21(1997).

DR EMBL; X97631; CA66230.1; -.

DR HSSP; P05067; 1BA4.

DR InterPro; IPR001868; A4\_APP.

DR Pfam; PF02177; A4\_EXTRA; 1.

DR PRINTS; PR00203; AMYLOIDA4.

DR SMART; SM00006; A4\_EXTRA; 1.

DR PROSITE; PS00319; A4\_EXTRA; 1.

DR PROSITE; PS00320; A4\_INTRA; 1.

SQ SEQUENCE 695 AA; 78701 MW; 5196A0C4017F16AB CRC64;

Query Match

Best Local Similarity 100.0%; Score 49; DB 11; Length 695;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SEVKMDAER 10  
Db 592 SEVKMDAER 601

RESULT 9

O9DGJ8 PRELIMINARY; PRT; 695 AA.

ID O9DGJ8

AC O9DGJ8

DT 01-MAR-2001 (TREMBLrel. 16, Created)

DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE BETA-AMYLOID PRECURSOR PROTEIN 695 ISOPFORM.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

NCBI\_TaxID=9031;

RN (1)

RP SEQUENCE FROM N.A.

RA Sakata M., Rodollos A., Sorribas V.;

RT "Cloning of full-length chicken beta-amyloid precursor protein

RT isoforms."

```

RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF289218; AAC00593.1; -.
DR HSP: P05067; 1BA4.
DR InterPro: IPR001868; A4_APP.
DR Pfam: PF02177; A4_EXTRA; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR SMART: SM00006; A4_EXTRA; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
SO SEQUENCE 695 AA; 78565 MW; F201ED02AEC86D95 CRC64;

Query Match
Best Local Similarity 100.0%; Score 49; DB 13; Length 695;
Pred. No. 0.079;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEVKMDAER 10
DB 592 SEVKMDAER 601

RESULT 10
Q9DGJ7 PRELIMINARY; PRT; 751 AA.
AC Q9DGJ7;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE BETA-AMYLOID PRECURSOR PROTEIN 751 ISOFORM.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Sarasa M., Rodolose A., Sorribas V.;
RT "Cloning of full-length chicken beta-amyloid precursor protein
RT isoforms."
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF289219; AAC00594.1; -.
DR HSP: P05067; 1BA4.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PRINTS: PR00759; BASICPTASE.
DR SMART: SM00006; A4_EXTRA; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS50279; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor.
SQ SEQUENCE 751 AA; 84705 MW; E78E9413A8033D84 CRC64;

Query Match
Best Local Similarity 100.0%; Score 49; DB 13; Length 751;
Pred. No. 0.085;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEVKMDAER 10
DB 648 SEVKMDAER 657

RESULT 11
Q9TU10 PRELIMINARY; PRT; 770 AA.
AC Q9TU10;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE AMYLOID PRECURSOR PROTEIN.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.

```

```

OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Kimura A., Takahashi T.;
RT "Amyloid Precursor Protein 770."
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB032550; BAA84580.1; -.
DR HSP: P05067; 1AAP.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PRINTS: PR00759; BASICPTASE.
DR SMART: SM00006; A4_EXTRA; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS50279; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor.
SQ SEQUENCE 770 AA; 86961 MW; 5F7A1DC82BCC583E CRC64;

Query Match
Best Local Similarity 100.0%; Score 49; DB 6; Length 770;
Pred. No. 0.088;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEVKMDAER 10
DB 667 SEVKMDAER 676

RESULT 12
O35463 PRELIMINARY; PRT; 79 AA.
ID O35463;
AC O35463;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE ALZHEIMER'S AMYLOID BETA PROTEIN (FRAGMENT).
GN BETA APP.
OS Cricetus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetus.
OX NCBI_TaxID=10029;
RN [1]
RP SEQUENCE FROM N.A.
RA Sambamurti K., Pinnix I., Gandhi S.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF030413; AAB86608.1; -.
DR HSP: P05067; 1BA4.
FT NON_TER 1
FT NON_TER 79
FT NON_TER 79
SQ SEQUENCE 79 AA; 8538 MW; 37F2C6C3BFF3F597 CRC64;

Query Match
Best Local Similarity 100.0%; Score 44; DB 11; Length 79;
Pred. No. 0.097;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEVKMDAER 9
DB 16 SEVKMDAER 24

RESULT 13
Q99K32 PRELIMINARY; PRT; 607 AA.
ID Q99K32;
AC Q99K32;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE HYPOTHETICAL 68.4 KDA PROTEIN (FRAGMENT).

```

SO	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=MAMMARY TUMOR. WAF-TGF ALPHA MODEL. 7 MONTHS OLD, CROSS
RC	TISSUE.;
RA	Straussberg R.;
RL	Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR	EMBL: BC005490; AA05490.1; -.
DR	HSSP: P05067; 1AAP.
DR	InterPro: IPR001868; A4_APP.
DR	InterPro: IPR002223; Kunitz_BPTI.
DR	Pfam: PF00014; Kunitz_BPTI; 1.
DR	PRINTS: PR00203; AMYLOIDA4.
DR	SMART: SM00131; KU; 1.
DR	PROSITE: PS00319; A4_EXTRA; 1.
DR	PROSITE: PS00320; A4_INTRA; 1.
DR	PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR	PROSITE: PS00279; BPTI_KUNITZ_2; 1.
KM	Hypothetical protein; Serine protease inhibitor.
FT	NON_TER
SO	SEQUENCE 607 AA; 68391 MW; BF80221ACBA7D172 CRC64;
Query Match	
Best Local Similarity 89.8%; Score 44; DB 11; Length 607;	
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 SEVKMDAEF 9
Db	504 SEVKMDAEF 512
RESULT 14	
ID	P97487 PRELIMINARY; PRT; 695 AA.
AC	P97487; P97942;
DT	01-MAY-1997 (TREMblrel, 03, Created)
DT	01-MAY-1997 (TREMblrel, 03, Last sequence update)
DE	01-DEC-2001 (TREMblrel, 19, Last annotation update)
DE	HIPPOCAMPAL AMYLOID PROTEIN.
GN	APP.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=HIPPOCAMPAL; TISSUE=HIPPOCAMPAL;
RC	TISSUE.
RA	Flood J.F., Kumar V.B., Sasser T., Word I., Morley J.E.;
RL	Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN	[2]
RP	SEQUENCE OF 581-662 FROM N.A.
RC	STRAIN=129SV;
RA	Wieg M.A., Busfield F., Duff K., Korenblat K., Capocchi M.,
RL	Loring J.F., Goate A.M.;
RL	Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR	EMBL: U84012; AABA1502.1; -.
DR	EMBL: U82624; AAB40919.1; -.
DR	HSSP: P05067; 1AWP.
DR	MGD: MGI:88059; APP.
DR	InterPro: IPR001868; A4_APP.
DR	Pfam: PF02177; A4_EXTRA; 1.
DR	PRINTS: PR00203; AMYLOIDA4.
DR	SMART: SM00006; A4_EXTRA; 1.
DR	PROSITE: PS00319; A4_EXTRA; 1.
DR	PROSITE: PS00320; A4_INTRA; 1.
SO	SEQUENCE 695 AA; 78414 MW; 9A5FBF2ED261236E CRC64;
Query Match	
Best Local Similarity 100.0%; Score 44; DB 11; Length 695;	
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	

Matches	9;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1 SEVKMDAEF 9								
Db	592 SEVKMDAEF 600								
RESULT	15								
Q98SGO									
1D	Q98SGO	PRELIMINARY;	PRF:	693 AA.					
AC	Q98SGO;								
DT	01-JUN-2001 (TEMBLrel. 17, Created)								
DT	01-JUN-2001 (TEMBLrel. 17, last sequence update)								
DT	01-DEC-2001 (TEMBLrel. 19, last annotation update)								
DE	BEFA-AMYLOID PRECURSOR PROTEIN A.								
GN	APP.								
OS	Xenopus laevis (African clawed frog).								
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;								
OC	Xenopodidae; Xenopus.								
OX	NCBI_TaxID=8355;								
RM	[1]								
RP	SEQUENCE FROM N.A.								
RA	Van den Hurk W.H.;								
RL	Thesis (2001), Department of Biological Sciences,								
RL	University of Nijmegen, Nijmegen, Netherlands.								
DR	EMBL; AJ298150; CAC37193.1; --								
DR	HSSP; P05067; 1H23.								
DR	InterPro; IPR001868; A4_APP.								
DR	Pfam; PF02177; A4_EXTRA; 1.								
DR	PRINTS; PRO0203; AMYLOIDA4.								
DR	SMART; SM00006; A4_EXTRA; 1.								
DR	PROSITE; PS00319; A4_EXTRA; 1.								
DR	PROSITE; PS00320; A4_INTRA; 1.								
KW	Signal.								
FT	SIGNAL								
SEQ	SEQUENCE	1	18	POTENTIAL.					
		693 AA;	78568 MW;	CALDID655C1AB653 CRC64;					
Query Match		87.8%;	Score 43;	DB 13;	Length 693;				
Matches	8;	Conservative	2;	Mismatches	0;	Gaps	0;		
QY	1 SEVKMDAEF 10								
Db	590 SEVKMDSEYR 599								

Search completed: October 29, 2002, 10:29:41  
Job time : 19.1429 secs

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      FT SIGNAL. 1 18 POTENTIAL.
      SQ SEQUENCE 693 AA: 78568 MW; CAPIDP655C1AB653 CRC64;

      Query Match 87.8%; Score 43; DB 13; Length 693;
      Best Local Similarity 80.0%; Pred. No. 1.4;
      Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0.

      QY 1 SEVKMDAEFR 10
         |||||:|:|
      DB 590 SEVKMDSEFR 599

Search completed: October 29, 2002, 10:29:41
Job time : 19.1429 secs

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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 29, 2002, 10:23:56 ; Search time 9 Seconds  
(without alignments)  
27.140 Million cell updates/sec

Title: US-09-580-018-4

Perfect score: 49

Sequence: 1 SEVKNDAEFR 10

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued\_Patents\_AA: \*  
1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep: \*  
2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep: \*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep: \*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep: \*  
5: /cgn2\_6/ptodata/1/1aa/PCrUS.COMB.pep: \*  
6: /cgn2\_6/ptodata/1/1aa/Backfill1est.pep: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	49	100.0	11	5	PCT-US94-07043A-7
2	49	100.0	12	5	PCT-US94-07043A-2
3	49	100.0	16	5	PCT-US94-07043A-1
4	49	100.0	27	1	US-08-141-324-11
5	49	100.0	27	1	US-08-541-902-11
6	49	100.0	45	1	US-08-462-859A-5
7	49	100.0	45	1	US-08-123-659A-5
8	49	100.0	45	1	US-08-464-247A-5
9	49	100.0	45	1	US-08-464-248A-5
10	49	100.0	58	1	US-08-371-930-25
11	49	100.0	58	5	PCT-US94-01712-25
12	49	100.0	63	1	US-08-462-859A-3
13	49	100.0	63	1	US-08-462-859A-4
14	49	100.0	63	1	US-08-123-659A-3
15	49	100.0	63	1	US-08-123-659A-4
16	49	100.0	63	1	US-08-464-247A-3
17	49	100.0	63	1	US-08-464-247A-4
18	49	100.0	63	1	US-08-464-248A-3
19	49	100.0	63	1	US-08-464-248A-4
20	49	100.0	105	2	US-08-729-345-1
21	49	100.0	117	2	US-08-729-345-3
22	49	100.0	152	6	5187153-4
23	49	100.0	162	6	5220013-4
24	49	100.0	162	6	5223482-4
25	49	100.0	264	1	US-07-990-893-5
26	49	100.0	487	1	US-08-462-859A-9
27	49	100.0	487	1	US-08-123-659A-9

28	49	100.0	487	1	US-08-464-247A-9	Sequence 9, Appli
29	49	100.0	487	1	US-08-464-248A-9	Sequence 9, Appli
30	49	100.0	492	1	US-08-462-859A-7	Sequence 7, Appli
31	49	100.0	492	1	US-08-123-659A-7	Sequence 7, Appli
32	49	100.0	492	1	US-08-464-247A-7	Sequence 7, Appli
33	49	100.0	492	1	US-08-464-248A-7	Sequence 7, Appli
34	49	100.0	537	1	US-08-453-552-4	Sequence 4, Appli
35	49	100.0	537	2	US-08-710-637-4	Sequence 4, Appli
36	49	100.0	537	5	PCT-US93-00907-4	Sequence 4, Appli
37	49	100.0	656	1	US-08-371-930-23	Sequence 23, Appli
38	49	100.0	656	5	PCT-US94-01712-23	Sequence 23, Appli
39	49	100.0	676	1	US-08-571-930-24	Sequence 24, Appli
40	49	100.0	676	5	PCT-US94-01712-24	Sequence 24, Appli
41	49	100.0	694	1	US-08-339-152A-18	Sequence 18, Appli
42	49	100.0	694	2	US-08-007-999B-5	Sequence 5, Appli
43	49	100.0	694	2	US-08-689-276A-5	Sequence 5, Appli
44	49	100.0	695	1	US-08-371-930-27	Sequence 27, Appli
45	49	100.0	695	1	US-08-123-702-2	Sequence 2, Appli

#### ALIGNMENTS

RESULT 1  
PCT-US94-07043A-7  
Sequence 7, Application PC/TUS9407043A  
GENERAL INFORMATION:  
APPLICANT: Tamburini, Paul P.; Benz, G nter; H bich,  
APPLICANT: Dieter; Dreyer, Robert N.; Koenig, Gerhard  
TITLE OF INVENTION: CATHEPSIN D IS AN AMYLOIDGENIC  
TITLE OF INVENTION: PROTEASE IN ALZHEIMER S DISEASE  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Miles Inc.  
STREET: 400 Morgan Lane  
CITY: West Haven  
STATE: Connecticut  
COUNTRY: USA  
ZIP: 06516  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 800 kb storage  
COMPUTER: Sharp PC 4600  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/07043A  
FILING DATE: June 21, 1994  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/10889  
FILING DATE: November 12, 1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/995,660  
FILING DATE: December 16, 1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/880,914  
FILING DATE: May 11, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Pamela A. Simonton  
REGISTRATION NUMBER: 31,060  
REFERENCE/DOCKET NUMBER: MTI 224.3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (203) 937-2340  
TELEFAX: (203) 937-2795  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
PCT-US94-07043A-7  
Query Match 100.0%; Score 49; DB 5; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.00045;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SEVKMDAER 10  
 |||||||||  
 Db 2 SEVKMDAER 11

RESULT 2  
 PCT-US94-07043A-2  
 : Sequence 2, Application PC/TUS9407043A  
 : GENERAL INFORMATION:  
 : APPLICANT: Tamburini, Paul P.; Benz, G nter; H bich,  
 : APPLICANT: Dieter; Dreyer, Robert N.; Koenig, Gerhard  
 : TITLE OF INVENTION: CATHEPSIN D IS AN AMYLOIDGENIC  
 : TITLE OF INVENTION: PROTEASE IN ALZHEIMER S DISEASE  
 : NUMBER OF SEQUENCES: 11  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: Miles Inc.  
 : STREET: 400 Morgan Lane  
 : CITY: West Haven  
 : STATE: Connecticut  
 : COUNTRY: USA  
 : ZIP: 06516  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Diskette, 3.50 inch, 800 kb storage  
 : COMPUTER: Sharp PC 4600  
 : OPERATING SYSTEM: MS-DOS  
 : SOFTWARE: WordPerfect 5.1  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: PCT/US94/07043A  
 : FILING DATE: June 21, 1994  
 : CLASSIFICATION:  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: PCT/US93/10889  
 : FILING DATE: November 12, 1993  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: 07/995,660  
 : FILING DATE: December 16, 1992  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: 07/880,914  
 : FILING DATE: May 11, 1992  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: Pamela A. Simonton  
 : REGISTRATION NUMBER: 31,060  
 : REFERENCE/DOCKET NUMBER: MTI 224.3  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: (203) 937-2340  
 : TELEFAX: (203) 937-2795  
 : INFORMATION FOR SEQ ID NO: 2:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 12 amino acids  
 : TYPE: amino acid  
 : TOPOLOGY: linear  
 : PCT-US94-07043A-2

Query Match 100.0%; Score 49; DB 5; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 0.0005;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SEVKMDAER 10  
 |||||||||  
 Db 2 SEVKMDAER 11

RESULT 3  
 PCT-US94-07043A-1  
 : Sequence 1, Application PC/TUS9407043A  
 : GENERAL INFORMATION:  
 : APPLICANT: Tamburini, Paul P.; Benz, G nter; H bich,  
 : APPLICANT: Dieter; Dreyer, Robert N.; Koenig, Gerhard  
 : TITLE OF INVENTION: CATHEPSIN D IS AN AMYLOIDGENIC  
 : TITLE OF INVENTION: PROTEASE IN ALZHEIMER S DISEASE  
 : NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Miles Inc.  
 STREET: 400 Morgan Lane  
 CITY: West Haven  
 STATE: Connecticut  
 COUNTRY: USA  
 ZIP: 06516  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 3.50 inch, 800 kb storage  
 COMPUTER: Sharp PC 4600  
 OPERATING SYSTEM: MS-DOS  
 SOFTWARE: WordPerfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US94/07043A  
 FILING DATE: June 21, 1994  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US93/10889  
 FILING DATE: November 12, 1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/995,660  
 FILING DATE: December 16, 1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/880,914  
 FILING DATE: May 11, 1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Pamela A. Simonton  
 REGISTRATION NUMBER: 31,060  
 REFERENCE/DOCKET NUMBER: MTI 224.3  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (203) 937-2340  
 TELEFAX: (203) 937-2795  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 16 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 PCT-US94-07043A-1

Query Match 100.0%; Score 49; DB 5; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 0.00067;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SEVKMDAER 10  
 |||||||||  
 Db 2 SEVKMDAER 11

RESULT 4  
 US-08-141-324-11  
 : Sequence 11, Application US/08141324  
 : Patent No. 5475097  
 : GENERAL INFORMATION:  
 : APPLICANT: Travis, James  
 : APPLICANT: Potempa, Jan S.  
 : APPLICANT: Barr, Philip J.  
 : APPLICANT: Pavloff, Nadine  
 : APPLICANT: Pike, Robert N.  
 : TITLE OF INVENTION: Lysine-specific Porphyromonas gingivalis  
 : TITLE OF INVENTION: Protease  
 : NUMBER OF SEQUENCES: 28  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: Greenlee and Winner, P.C.  
 : STREET: 5370 Manhattan Circle, Suite 201  
 : CITY: Boulder  
 : STATE: CO  
 : COUNTRY: US  
 : ZIP: 80303  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: PatentIn Release #1.0, Version #1.25



;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/141,324  
;; FILING DATE: 21-OCT-1993  
;; CLASSIFICATION: 424  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Ferber, Donna M.  
;; REGISTRATION NUMBER: 33,878  
;; REFERENCE/DOCKET NUMBER: 44-93  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 303-499-8080  
;; TELEFAX: 303-499-8089  
;; INFORMATION FOR SEQ ID NO: 11:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 27 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; HYPOTHETICAL: NO  
;; ANTI-SENSE: NO  
;; US-08-141-324-11

Query Match  
Best Local Similarity 100.0%; Score 49; DB 1; Length 27;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEVKMDAEFR 10  
Db 4 SEVKMDAEFR 13

RESULT 5  
US-08-541-902-11  
; Sequence 11, Application US/08541902  
; Patent No. 5707620  
; GENERAL INFORMATION:  
; APPLICANT: Travis, James  
; APPLICANT: Potempa, Jan S.  
; APPLICANT: Barr, Philip J.  
; APPLICANT: Pavloff, Nadine  
; APPLICANT: Pike, Robert N.  
; TITLE OF INVENTION: Lysine-specific Porphyromonas gingivalis  
; TITLE OF INVENTION: Protease  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Greenlee and Winner, P.C.  
; STREET: 5370 Manhattan Circle, Suite 201  
; CITY: Boulder  
; STATE: CO  
; COUNTRY: US  
; ZIP: 80303  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/541,902  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/141,324  
; FILING DATE: 21-OCT-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ferber, Donna M.  
; REGISTRATION NUMBER: 33,878  
; REFERENCE/DOCKET NUMBER: 44-93  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 303-499-8080  
; TELEFAX: 303-499-8089  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 27 amino acids

;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; HYPOTHETICAL: NO  
;; ANTI-SENSE: NO  
;; US-08-541-902-11

Query Match  
Best Local Similarity 100.0%; Score 49; DB 1; Length 27;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEVKMDAEFR 10  
Db 4 SEVKMDAEFR 13

RESULT 6  
US-08-462-859A-5  
; Sequence 5, Application US/08462859A  
; Patent No. 5652092  
; GENERAL INFORMATION:  
; APPLICANT: Jacobsen, J. S.  
; APPLICANT: Vitek, M. P.  
; TITLE OF INVENTION: No. 5652092el Amyloid Precursor and Method of  
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation  
; TITLE OF INVENTION: of B-Amyloid Peptide  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: American Cyanamid Company  
; STREET: One Cyanamid Plaza  
; CITY: Wayne  
; STATE: New Jersey  
; COUNTRY: United States  
; ZIP: 07470-8426  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/462,859A  
; FILING DATE: 05-JUN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Barnhard, Elizabeth M.  
; REGISTRATION NUMBER: 31,088  
; REFERENCE/DOCKET NUMBER: 31,844-04  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (201)831-3305  
; TELEFAX: (201)831-3246  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 45 amino acid  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
;; US-08-462-859A-5

Query Match  
Best Local Similarity 100.0%; Score 49; DB 1; Length 45;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEVKMDAEFR 10  
Db 5 SEVKMDAEFR 14

RESULT 7  
US-08-123-659A-5  
; Sequence 5, Application US/08123659A  
; Patent No. 5656477

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: GENERAL INFORMATION:
: APPLICANT: Jacobsen, J. S.
: TITLE OF INVENTION: No. 5656477el Amyloid Precursor and Method of
: TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
: NUMBER OF SEQUENCES: 19
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Anne Rosenblum
: STREET: 163 Delaware Avenue, Suite 212
: CITY: Delmar
: STATE: New York
: COUNTRY: U.S.A.
: ZIP: 12054
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/123,659A
: FILING DATE: 20-SEP-1993
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Rosenblum, Anne M.
: REGISTRATION NUMBER: 30,419
: REFERENCE/DOCKET NUMBER: 31,844-01
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (518)475-0611
: TELEFAX: (518)475-0619
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 45 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-123-659A-5

Query Match          100.0%; Score 49; DB 1; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEVKMDAEFR 10
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Db 5 SEVKMDAEFR 14

RESULT 8
US-08-464-247A-5
: Sequence 5, Application US/08464247A
: Patent No. 5693478
: GENERAL INFORMATION:
: APPLICANT: Jacobsen, J. S.
: TITLE OF INVENTION: No. 5693478el Amyloid Precursor and Method of
: TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
: NUMBER OF SEQUENCES: 19
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: American Cyanamid Company
: STREET: One Campus Drive
: CITY: Parsippany
: STATE: New Jersey
: COUNTRY: United States
: ZIP: 07054
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/464,247A
: FILING DATE: 05-JUN-1995

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: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Barnhard, Elizabeth M.
: REGISTRATION NUMBER: 31,088
: REFERENCE/DOCKET NUMBER: 31,844-03
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 201-683-2158
: TELEFAX: 201-683-4117
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 45 amino acids
: TYPE: amino acid
: STRANDEDNESS:
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-464-247A-5

Query Match          100.0%; Score 49; DB 1; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEVKMDAEFR 10
   |||||||
Db 5 SEVKMDAEFR 14

RESULT 9
US-08-464-248A-5
: Sequence 5, Application US/08464248A
: Patent No. 5703209
: GENERAL INFORMATION:
: APPLICANT: Jacobsen, J. S.
: TITLE OF INVENTION: No. 5703209el Amyloid Precursor and Method of
: TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
: NUMBER OF SEQUENCES: 19
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: American Cyanamid Company
: STREET: One Cyanamid Plaza
: CITY: Wayne New Jersey
: STATE: New Jersey
: COUNTRY: United States
: ZIP: 07470-8426
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/464,248A
: FILING DATE: 05-JUN-1995
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Barnhard, Elizabeth M.
: REGISTRATION NUMBER: 31,088
: REFERENCE/DOCKET NUMBER: 31,844-02
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (201)831-3246
: TELEFAX: (201)831-3305
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 45 amino acids
: TYPE: amino acid
: STRANDEDNESS:
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-464-248A-5

Query Match          100.0%; Score 49; DB 1; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 SEVKMAEPR 10  
DB 5 SEVKMAEPR 14

## RESULT 10

US-08-371-930-25  
Sequence 25, Application US/08371930  
Patent No. 5578451

## GENERAL INFORMATION:

APPLICANT: Nishimoto, Ikuro  
TITLE OF INVENTION: ALZHEIMER'S DISEASE THERAPEUTICS  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804

## COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM PS/2 Model 502 or 55SX  
OPERATING SYSTEM: MS-DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/371,930

## FILING DATE:

CLASSIFICATION: 436

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/019,208

FILING DATE: February 18, 1993

## ATTORNEY/AGENT INFORMATION:

NAME: Clark, Paul T.

REGISTRATION NUMBER: 30,162

REFERENCE/DOCKET NUMBER: 00786/154001

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 542-5070

TELEFAX: (617) 542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 25:

## SEQUENCE CHARACTERISTICS:

LENGTH: 58

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

US-08-371-930-25

## Query Match

Best local Similarity 100.0%; Score 49; DB 1; Length 58;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SEVKMAEPR 10  
DB 42 SEVKMAEPR 51

## RESULT 11

PCT-US94-01712-25

Sequence 25, Application PC/TUS9401712

## GENERAL INFORMATION:

APPLICANT: Nishimoto, Ikuro

TITLE OF INVENTION: ALZHEIMER'S DISEASE THERAPEUTICS

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson

STREET: 225 Franklin Street

CITY: Boston

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM PS/2 Model 502 or 55SX  
OPERATING SYSTEM: MS-DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/01712

## FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/019,208

FILING DATE: February 18, 1993

## ATTORNEY/AGENT INFORMATION:

NAME: Clark, Paul T.

REGISTRATION NUMBER: 30,162

REFERENCE/DOCKET NUMBER: 00786/154001

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 542-5070

TELEFAX: (617) 542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 25:

SEQUENCE CHARACTERISTICS:

LENGTH: 58

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

PCT-US94-01712-25

## Query Match

Best local Similarity 100.0%; Score 49; DB 5; Length 58;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SEVKMAEPR 10  
DB 42 SEVKMAEPR 51

## RESULT 12

US-08-462-859A-3

Sequence 3, Application US/08462859A

Patent No. 5652092

## GENERAL INFORMATION:

APPLICANT: Jacobsen, J. S.

TITLE OF INVENTION: No. 5652092el Amyloid Precursor and Method of

TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation

TITLE OF INVENTION: of B-Amyloid Peptide

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: American Cyanamid Company

STREET: One Cyanamid Plaza

CITY: Wayne

STATE: New Jersey

COUNTRY: United States

ZIP: 07470-8426

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/462,859A

FILING DATE: 05-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Barnhard, Elizabeth M.

REGISTRATION NUMBER: 31,088

REFERENCE/DOCKET NUMBER: 31,844-04

TELECOMMUNICATION INFORMATION:

TELEPHONE: (201)831-3246

TELEFAX: (201)831-3305

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 63 amino acids

TYPE: amino acid

STRANDEDNESS:  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-462-859A-3

Query Match  
 Best Local Similarity 100.0%; Score 49; DB 1; Length 63;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEVKMDAER 10  
 Db 5 SEVKMDAER 14

RESULT 13  
 US-08-462-859A-4  
 Sequence 4, Application US/08462859A

GENERAL INFORMATION:  
 APPLICANT: Jacobsen, J. S.  
 TITLE OF INVENTION: NO. 5652092el Amyloid Precursor and Method of  
 TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation  
 TITLE OF INVENTION: of B-Amyloid Peptide  
 NUMBER OF SEQUENCES: 19  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: American Cyanamid Company  
 STREET: One Cyanamid Plaza  
 CITY: Wayne  
 STATE: New Jersey  
 COUNTRY: United States  
 ZIP: 07470-8426

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/462,859A  
 FILING DATE: 05-JUN-1995  
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
 NAME: Barnhard, Elizabeth M.  
 REGISTRATION NUMBER: 31,088  
 REFERENCE/DOCKET NUMBER: 31,844-04  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (201)831-3246  
 TELEFAX: (201)831-3305  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 63 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein

US-08-462-859A-4

Query Match  
 Best Local Similarity 100.0%; Score 49; DB 1; Length 63;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEVKMDAER 10  
 Db 5 SEVKMDAER 14

RESULT 14  
 US-08-123-659A-3  
 Sequence 3, Application US/08123659A

GENERAL INFORMATION:  
 APPLICANT: Jacobsen, J. S.  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Vitek, M. P.

TITLE OF INVENTION: NO. 5656477el Amyloid Precursor and Method of  
 TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation  
 TITLE OF INVENTION: of B-Amyloid Peptide  
 NUMBER OF SEQUENCES: 19  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Anne Rosenblum  
 STREET: 163 Delaware Avenue, Suite 212  
 CITY: Delmar  
 STATE: New York  
 COUNTRY: U.S.A.  
 ZIP: 12054

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/123,659A  
 FILING DATE: 20-SEP-1993  
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
 NAME: Rosenblum, Anne M.  
 REGISTRATION NUMBER: 30,419  
 REFERENCE/DOCKET NUMBER: 31,844-01  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (518)475-0611  
 TELEFAX: (518)475-0619  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 63 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein

US-08-123-659A-3  
 Query Match  
 Best Local Similarity 100.0%; Score 49; DB 1; Length 63;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEVKMDAER 10  
 Db 5 SEVKMDAER 14

RESULT 15  
 US-08-123-659A-4  
 Sequence 4, Application US/08123659A

GENERAL INFORMATION:  
 APPLICANT: Jacobsen, J. S.  
 TITLE OF INVENTION: NO. 5656477el Amyloid Precursor and Method of  
 TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation  
 TITLE OF INVENTION: of B-Amyloid Peptide  
 NUMBER OF SEQUENCES: 19  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Anne Rosenblum  
 STREET: 163 Delaware Avenue, Suite 212  
 CITY: Delmar  
 STATE: New York  
 COUNTRY: U.S.A.  
 ZIP: 12054

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/123,659A  
 FILING DATE: 20-SEP-1993  
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
 NAME: Rosenblum, Anne M.

REGISTRATION NUMBER: 30,419  
REFERENCE/DOCKET NUMBER: 31,844-01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (518)475-0611  
TELEFAX: (518)475-0619  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 63 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-123-659A-4

Query Match 100.0%; Score 49; DB 1; Length 63;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 5 SEVKMDAER 14

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Job time : 9 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 29, 2002, 10:22:21 ; Search time 23.1429 Seconds  
(without alignments)  
47.995 Million cell updates/sec

Title: US-09-580-018-5  
Perfect score: 53  
Sequence: 1 EYKMDAEPFH 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	53	100.0	13	19	AAW70869 Beta-amyloid pepti
3	53	100.0	16	21	AAAB06315 Human beta-amyloid
4	53	100.0	16	21	AAAB06317 Human beta-amyloid
5	53	100.0	18	22	AAE00608 Human beta-amyloid
6	53	100.0	19	12	AAE00608 Brain-derived precu
7	53	100.0	20	21	AAE69713 Beta-APP alpha-sec
8	53	100.0	33	20	AAW98002 Amyloid precursor
9	53	100.0	39	21	AAE69717 Beta-APP alpha-sec
10	53	100.0	45	18	AAW26512 Amyloid precursor
11	53	100.0	45	18	AAW26392 Amyloid precursor

12	53	100.0	45	19	AAW44748 APP-REP 751 [BAP d
13	53	100.0	45	19	AAW42977 Deletion beta-amy1
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15	53	100.0	53	15	AAE55696 Sequence of uniden
16	53	100.0	53	15	AAE55697 Sequence of uniden
17	53	100.0	53	16	AAE64168 Variant beta amylo
18	53	100.0	54	21	AAE32126 Amyloid-beta precu
19	53	100.0	57	21	AAE10910 Human amyloid prec
20	53	100.0	58	15	AAE58937 Amyloid precursor
21	53	100.0	59	17	AAE05375 Amyloid precursor
22	53	100.0	59	19	AAW70863 Beta-amyloid precu
23	53	100.0	59	22	AAE84425 Partial sequence o
24	53	100.0	60	21	AAE69701 Beta-amyloid precu
25	53	100.0	63	18	AAE26511 Amyloid precursor
26	53	100.0	63	18	AAE26391 Amyloid precursor
27	53	100.0	63	19	AAW44747 APP-REP 751 [BAP E
28	53	100.0	63	19	AAW44746 APP-REP 751 [BAP E
29	53	100.0	63	19	AAW42975 Beta-amyloid pepti
30	53	100.0	63	19	AAW42976 Peptide derived fr
31	53	100.0	67	19	AAW71377 Novel human diago
32	53	100.0	93	22	ABE19083 Beta-amyloid precu
33	53	100.0	103	16	AAE74697 Natural beta-amylo
34	53	100.0	103	19	AAE51317 Beta-amyloid pepti
35	53	100.0	103	20	AAE89372 Beta-amyloid precu
36	53	100.0	103	21	AAE56103 Beta-amyloid precu
37	53	100.0	103	22	AAE12509 Amino acid sequenc
38	53	100.0	104	19	AAE51100 Familial Alzheimer
39	53	100.0	112	17	AAE93556 London-PAD APP pol
40	53	100.0	115	20	AAE97999 Flag-amyloid prote
41	53	100.0	117	19	AAE51102 Deduced sequence 1
42	53	100.0	162	9	AAE83151 Beta-amyloid-relat
43	53	100.0	162	12	AAE10023 Deduced from clone
44	53	100.0	162	14	AAE37863 Beta-amyloid precu
45	53	100.0	249	15	AAE5798

## ALIGNMENTS

## RESULT 1

AAA6209 standard: peptide; 10 AA.

AAA6209:

04-APR-2001 (first entry)

Human APP derived immunogenic peptide #5.

Amyloid deposit; APP, Abeta; brain; human; clearing response; nootropic;

Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;

amyloid precursor protein; Alzheimer's disease.

Homo sapiens.

WO200072880-A2.

07-DEC-2000.

26-MAY-2000: 2000WO-US14810.

28-MAY-1999: 99US-0322289.

(NEUR-) NEURALAB LTD.

Schenk DB, Bard F, Vasquez, NJ, Yednock T;

WPI; 2001-032104/04.

Preventing or treating a disease associated with amyloid deposits,

especially Alzheimer's disease, comprises administering amyloid

specific antibody -

PS Disclosure; Figure 19; 143bp; English.

XX This invention describes a novel method of preventing or treating a

CC disease associated with amyloid deposits of amyloid precursor protein

CC (APP) Abeta fragments in the brain of a patient, which comprises

CC administering to the patient: (a) an antibody that binds to Abeta, the

CC antibody binds to an amyloid deposit and induces a clearing response (Fc

CC receptor mediated phagocytosis) against it (b) a polypeptide containing

CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent

CC that induces an immunogenic response against residues 1-3 to 7-11 of

CC Abeta. The products of the invention have neurotropic and neuroprotective

CC activity. The method is also useful for monitoring a course of treatment

CC being administered to a patient e.g. active and passive immunization. The

CC methods are useful for prophylactic and therapeutic treatment of

CC Alzheimer's disease.

XX

SQ Sequence 10 AA;

Query Match 100.0%; Score 53; DB 22; Length 10;

Best Local Similarity 100.0%; Pred. NO. 0.00012;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EVKMDAEFRH 10

Db 1 EVKMDAEFRH 10

RESULT 2

AAW70869

ID AAW70869 standard; peptide: 13 AA.

XX

XX AAW70869;

XX

XX 04-FEB-1999 (first entry)

DT

XX

DE Beta-amyloid peptide to create a monoclonal antibody.

XX

KW Beta-amyloid precursor protein; beta-APP; beta-amyloid peptide;

KW antibody; amyloid deposit; Alzheimer's disease.

XX

OS Synthetic.

OS Homo sapiens.

XX

PN WO9844955-A1.

XX

PD 15-OCT-1998.

XX

PF 09-APR-1998; 98WO-US06900.

XX

PR 09-APR-1997; 97US-0041850.

XX

XX (MCIN/) MCINNIS P A.

PA (MIND-) MINDSET LTD.

XX

PI Chain DG;

XX

DR WPI; 1998-594476/50.

XX

PT Preventing or inhibiting progression of Alzheimer's Disease -

PT comprises use of recombinant DNA encoding an antibody specific for

PT the N- or C-terminus of an amyloid-beta peptide

XX

PS Example 1; Page 47; 58pp; English.

XX

CC The present sequence represents a peptide derived from beta-amyloid

CC precursor protein (beta-APP). The peptide is a beta-amyloid

CC peptide and is used to produce a monoclonal antibody. The specification

CC describes a method for prevention or inhibition of progression of

CC Alzheimer's disease. The method comprises administering a composition

CC comprising a recombinant DNA molecule containing a gene encoding a

CC recombinant antibody end-specific for the N-terminus or the C-terminus

CC of an amyloid-beta peptide, operably linked to a promoter which is

CC expressed in the central nervous system. The recombinant antibody

CC molecules prevent the accumulation of beta-amyloid peptides in the

CC extracellular space, interstitial fluid and cerebrospinal fluid and the

CC aggregation of such peptides into amyloid deposits in the brain. They

CC also inhibit the progression of Alzheimer's disease by inhibiting the

CC interaction of beta-amyloid peptides mediating Alzheimer's disease

CC induced neurotoxicity and inhibiting the Alzheimer's disease induced

CC complement activation and cytokine release involved in the inflammatory

CC process.

XX

SQ Sequence 13 AA;

Query Match 100.0%; Score 53; DB 19; Length 13;

Best Local Similarity 100.0%; Pred. NO. 0.00016;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EVKMDAEFRH 10

Db 4 EVKMDAEFRH 13

RESULT 3

AAB06315

ID AAB06315 standard; peptide: 16 AA.

XX

XX AAB06315;

XX

XX 03-OCT-2000 (first entry)

DT

XX

DE Human beta-amyloid precursor protein beta-secretase cleavage site.

XX

KW Human; beta-amyloid precursor protein; beta-APP; beta-secretase;

KW subtilisin-kexin isoenzyme 1; SKI-1;

KW pro-brain-derived neurotrophic factor; PROBDNF; anti-lipemic;

KW cytosolic; vasotropic; SKI-1 inhibitor; hypercholesterolemia;

KW liver steatosis; Ras-dependent cancer; restenosis;

KW amyloid protein formation.

XX

OS Homo sapiens.

XX

FT Key Location/Qualifiers

FT Cleavage-site 8..9

XX

PN WO200026348-A2.

XX

PD 11-MAY-2000.

XX

PF 04-NOV-1999; 99WO-CA01058.

XX

PR 04-NOV-1998; 98CA-2249648.

XX

XX (RECL-) INST RECH CLINIQUES MONTREAL.

PA Seidah N, Chretien M, Marcinkiewicz M, Laaksonen R, Davignon J;

PI WPI; 2000-365601/31.

XX

DR Novel soluble proteic fragment of subtilisin-kexin isoenzyme for

PT producing a polypeptide useful for treating hypercholesterolemia, liver

PT steatosis and amyloidosis, comprises a specific amino acid sequence -

XX

PS Example 4; Page 51; 119pp; English.

XX

CC The present sequence is the beta-secretase site of human beta-amyloid

CC precursor protein (beta-APP). The sequence may be cleaved

CC by a mammalian subtilase, specifically subtilisin-kexin isoenzyme 1

CC (SKI-1), a type-1 membrane-bound proteolase. Peptides which bind to and

CC are cleaved by SKI-1 may be used for monitoring SKI-1 activity, for

CC screening inhibitors of SKI-1 activity, or for screening enhancers of

CC SKI-1 activity. Proteic fragments of SKI-1 which bind to the SKI-1

CC catalytic site may be used as inhibitors of SKI-1 activity. They may be

CC used to treat diseases involving overexpression of SKI-1 or SKI-1

CC substrate. Such diseases include hypercholesterolemia, high levels of

CC fatty acids, lipids or larnesyl pyrophosphate, liver steatosis,



CC Ras-dependent cancer, restenosis and amyloid protein formation.

XX Sequence 16 AA;

Query Match 100.0%; Score 53; DB 21; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0.00019;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 EVKMDAEFRH 10  
Db 5 EVKMDAEFRH 14

RESULT 4  
AAB06317 standard; peptide: 16 AA.

XX AAB06317;  
XX 03-OCT-2000 (first entry)

DE Human beta-amyloid precursor protein beta-epsilon1-secretase site.

XX Human: beta-amyloid precursor protein; beta-APP;  
XX beta-epsilon1-secretase; subtilisin-kexin isoenzyme 1; SKI-1;  
XX pro-brain-derived neurotrophic factor; proBDNF; antilipemic;  
XX cytosolic; vasotropic; SKI-1 inhibitor; hypercholesterolaemia;  
XX liver steatosis; Ras-dependent cancer; restenosis;  
XX amyloid protein formation.

OS Homo sapiens.

EH Key Location/Qualifiers

FT Cleavage-site 8..9

PN WC020026348-A2.

PD 11-MAY-2000.

PF 04-NOV-1999; 99WO-CA01058.

PR 04-NOV-1998; 98CA-2249648.

XX (RECL-) INST RECH CLINIQUES MONTREAL.

XX Seidah N, Chretien M, Marcinkiewicz M, Laaksonen R, Davignon J;

XX WPI; 2000-365601/31.

PT Novel soluble proteic fragment of subtilisin-kexin isoenzyme for  
producing a polypeptide useful for treating hypercholesterolaemia, liver  
steatosis and amyloidosis, comprises a specific amino acid sequence -

XX Example 4; Page 51; 119pp; English.

XX The present sequence is the beta-epsilon1-secretase site of human  
beta-amyloid precursor protein (beta-APP). The sequence may be cleaved  
by a mammalian subtilase, specifically subtilisin-kexin isoenzyme 1  
(SKI-1), a type-1 membrane-bound proteinase. Peptides which bind to and  
are cleaved by SKI-1 may be used for monitoring SKI-1 activity, for  
screening inhibitors of SKI-1 activity, or for screening enhancers of  
SKI-1 activity. Proteic fragments of SKI-1 which bind to the SKI-1  
catalytic site may be used as inhibitors of SKI-1 activity. They may be  
used to treat diseases involving overexpression of SKI-1 or SKI-1  
substrate. Such diseases include hypercholesterolaemia, high levels of  
fatty acids, lipids or farnesyl pyrophosphate, liver steatosis,  
Ras-dependent cancer, restenosis and amyloid protein formation.

XX Sequence 16 AA;

Query Match 100.0%; Score 53; DB 21; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0.00019;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 EVKMDAEFRH 10  
Db 3 EVKMDAEFRH 12

RESULT 5  
AAE00608 standard; peptide: 18 AA.

XX AAE00608;  
XX 02-JUL-2001 (first entry)

DE Beta-amyloid precursor protein beta-secretase cleavage site.

XX Beta-amyloid precursor protein; beta-APP; caspase; beta-secretase;  
XX cysteine protease; apoptosis; caspase expression cassette; metastasis;  
XX tumour; cathepsin B; urokinase; proliferation; gene therapy;  
XX interdomain linker; cleavage site; Alzheimer's disease.

OS Unidentified.

PN WC0200129232-A2.

PD 26-APR-2001.

PF 19-OCT-2000; 2000WO-US28941.

PR 20-OCT-1999; 99US-0160559.

PR 14-AUG-2000; 2000US-0225564.

XX (SCIO-) SCIOS INC.

XX Corde11 B, Li Y;

XX WPI; 2001-290920/30.

PT Novel fusion polypeptide comprising first and second caspase subunit  
separated by cleavage site not associated in nature with caspase  
subunit, useful for cloning gene encoding enzymes involved in  
proteolytic cleavage -

XX Example 2; Page 26; 116pp; English.

XX The present sequence is a beta-secretase cleavage site of beta-amyloid  
precursor protein (beta-APP). This sequence is used to construct  
an artificially engineered chimeric cassette comprising human caspase-3  
with interdomain linker replaced by Swedish mutant beta-secretase  
cleavage site. This modified caspase-3 plays a pivotal role in  
Alzheimer's disease. Caspases are a family of cysteine proteases, that  
participate in the initiation and execution of apoptosis.  
The present invention relates to a method for functional cloning of genes  
encoding proteins or enzymes involved in proteolytic cleavage. The  
invention is based on the use of caspase expression cassettes comprising  
the coding sequence of a proteolytic cleavage site flanked by sequences  
encoding two caspase subunits. A fusion polypeptide comprising a first  
and a second caspase subunit, separated by a cleavage site not associated  
in nature, is useful for cloning gene encoding enzymes involved in  
proteolytic cleavage. An expression cassette containing fusion  
polypeptide is used to identify a mutant cell line deficient in an  
enzyme of interest and is also useful for diagnosis and suppression of  
CC proliferation or metastases of a tumour cell characterised by  
overexpression of a polypeptide (e.g. Cathepsin B or urokinase,  
selectively expressed in the tumour cells). DNA encoding fusion  
polypeptide is used in gene therapy.

XX Sequence 18 AA;

Query Match 100.0%; Score 53; DB 22; Length 18;  
Best Local Similarity 100.0%; Pred. No. 0.00022;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY      1 EVKMDAEFRH 10
        |||
        7 EVKMDAEFRH 16

RESULT 6
AAR14135
ID      AAR14135 standard; peptide: 19 AA.
AC      AAR14135;
DE      12-DEC-1991 (first entry)
XX      Brain-derived protease substrate contg. beta-APP cleavage site.
XX      Alzheimer's disease; chymase; multicatalytic protease;
KW      beta-amyloid precursor protein; A4.
XX      Synthetic.
OS      Key
FH      Location/Qualifiers
FT      Cleavage-site 4..5
FT      /note= "chymase and multicatalytic protease site"
PN      WO9113904-A.
PD      19-SEP-1991.
XX      04-MAR-1991; 91WO-US01474.
PF      05-MAR-1990; 90US-0489290.
PR      (CEPH-) CEPHALON INC.
XX      (CEPH-) CEPHALON INC.
PI      Siman R, Nelson RB, Kauer J, Potter H;
XX      WPI: 1991-295576/40.
DR      New chymotrypsin-like serine protease(s) - and their inhibitors
PT      are used to treat Alzheimer's disease
XX      Claim 41; Page 63; 86pp; English.
PS      This peptide is designed based on the sequence of beta-APP A4
XX      cleavage site. Cleavage by proteases in the brain releases beta-
CC      amyloid protein, the deposition of which is a feature of Alzheimer's
CC      disease neuropathology. The peptide is used to screen for candidate
CC      proteases which cleave between the Met and Asp residues. Two new
CC      proteases have been isolated having this cleavage specificity.
CC      Chymase was isolated from rat brains and multicatalytic protease was
CC      isolated from human cerebral cortex. See also AAR14136-9.
XX      SQ
XX      Sequence 19 AA:
XX      Query Match 100.0%; Score 53; DB 12; Length 19;
XX      Best Local Similarity 100.0%; Pred. NO. 0.00024;
XX      Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      1 EVKMDAEFRH 10
        |||
        1 EVKMDAEFRH 10

RESULT 7
AA69713
ID      AA69713 standard; peptide: 20 AA.
AC      AA69713;
DE      11-APR-2000 (first entry)
XX      Beta-APP alpha-secretase substrate [KM]-APP(-10,+10).
XX

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KW      Nootropic; neuroprotective; beta-amyloid precursor protein; metabolism;
KW      cleavage site; beta-secretase; neurodegenerative disease;
KW      Alzheimer's disease.
XX      Homo sapiens.
XX      WO9964587-A1.
XX      16-DEC-1999.
XX      04-JUN-1999; 99WO-FR01326.
XX      05-JUN-1998; 98FR-0007068.
PR      31-MAR-1999; 99US-0122599.
XX      (RHON ) RHONE-POULENC RORER SA.
XX      (UYPA-) UNIV CURIE PARIS VI P & M.
PI      Rhoulam M, Munoz-Gimenez N, Moutaouakil M, Cohen P, Bertrand P;
XX      WPI: 2000-097537/08.
XX      Polypeptide with beta-secretase activity, specific for wild-type
PT      amyloid precursor protein, useful in treating Alzheimer's disease
XX      Example 3; Page 24; 44pp; French.
XX      Peptides AA69702-169718 represent synthetic peptide substrates for a
CC      novel polypeptide with beta-secretase activity that can cleave
CC      specifically the natural beta-amyloid precursor protein (bAPP). Normal
CC      cleavage of the protein occurs between amino acids Met596-Asp597 and
CC      Val636-Ile637 (positions 4-5 and 44-45 of AA69701). The novel
CC      polypeptide is used to identify agents that interact specifically with
CC      it. These agents regulate metabolism of APP, particularly they slow down
CC      or reduce production of beta-amyloid, so can be used to treat
CC      neurodegenerative diseases, particularly Alzheimer's disease.
XX      SQ
XX      Sequence 20 AA:
XX      Query Match 100.0%; Score 53; DB 21; Length 20;
XX      Best Local Similarity 100.0%; Pred. No. 0.00025;
XX      Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      1 EVKMDAEFRH 10
        |||
        7 EVKMDAEFRH 16

RESULT 8
AA98002
ID      AA98002 standard; protein: 33 AA.
AC      AA98002;
XX      21-JUN-1999 (first entry)
XX      Amyloid precursor protein (aa656-678) with Swedish mutation.
DE      Amyloid precursor protein; APP; human; gene targeting;
XX      homologous recombination; transgenic mouse; transgenic animal;
KW      animal model; Alzheimer's disease.
XX      Mus musculus.
OS      WO9909150-A1.
XX      25-FEB-1999.
XX      18-AUG-1997; 97WO-US14507.
PF      18-AUG-1997; 97WO-US14507.
PR      (FARB ) BAYER CORP.
XX

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XX      Wlrrak DO;
PT      amyloid precursor protein, useful in treating Alzheimer's disease
XX      WPI: 1999-181029/15.
XX      Modification of target nucleic acids - by homologous recombination,
PT      used particularly for introducing a humanised amyloid precursor
PT      protein gene into rodents for producing models of Alzheimer's
PT      disease
XX
XX      Disclosure: Page 145; 209pp; English.
XX
XX      This polypeptide comprises residues 656-678 of a murine amyloid
CC      precursor protein (APP). The invention provides a novel gene
CC      targeting strategy that facilitates the introduction of one or
CC      more specific mutations into any gene in a single double reciprocal
CC      homologous recombination step. The method has been used
CC      particularly for introducing a humanised APP gene into rodents for
CC      producing animal models of Alzheimer's disease (AD). 4 independent
CC      lines of transgenic mice (lines ES5007, ES5103, ES5401 and ES5403)
CC      have been created using the gene targeting technique applied to
CC      embryonic stem cells. In each line, the mouse APP gene was modified
CC      to encode a mouse/human hybrid (m/hAPP) where amino acid residues
CC      666-770 of APP770 were encoded by human CDNA sequences instead of
CC      mouse genomic exons (exons 16-18). Within these residues, only 3
CC      amino acid differences exist between the mouse and human proteins,
CC      i.e. Gly-676 to Arg, Phe-681 to Thr and Arg-684 to His. The
CC      exon-cDNA fusion gene therefore encodes an APP containing a
CC      humanised beta-amyloid domain. Swedish- and/or London-PAD APP
CC      mutations have also been introduced (see also AAW97997-W98001).
XX
XX      Sequence 33 AA;
SQ
Query Match 100.0%; Score 53; DB 20; Length 33;
Best Local Similarity 100.0%; Pred No. 0.00043;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EVKMDAEFRH 10
DB 13 EVKMDAEFRH 22

```

```

XX      RESULT 10
XX      AAW26512
XX      AAW26512 standard; Peptide: 45 AA.
XX
XX      AAW26512;
XX
XX      06-JAN-1998 (first entry)
XX
XX      Amyloid precursor protein fragment APP-RBP 751 (BAP del11-28).
DE
XX      Amyloid precursor protein; APP; beta-amyloid protein; BAP;
KW      substrate; mutlein; secretase; Alzheimer's disease; human.
XX
XX      Chimeric Homo sapiens.
OS      Chimeric synthetic.
XX
XX      Key location/Qualifiers
FH      Cleavage-site 7..8 /note="secretase cleavage site"
FT      Peptide 10..33 /label="BAP(del11-28)"
FT      Domain 20..42 /note="truncated beta-amyloid protein"
XX      /label="Transmembrane"
XX
XX      US5656477-A.
XX      12-AUG-1997.
XX
XX      01-MAY-1992; 92US-0877675.
XX
XX      20-SEP-1993; 93US-0123659.
XX      01-MAY-1992; 92US-0877675.
XX
XX      (AMCY ) AMERICAN CYANAMID CO.
XX
XX      Jacobsen JS, Vitek MP;
XX      WPI: 1997-414594/38.
XX
XX      Nucleic acid encoding amyloid precursor mutlein(s) - comprising
PT      reporter gene and coding sequence, for identifying compounds which
PT      modify the activity of proteolytic enzymes which cleave APP
XX      Disclosure: Fig 5A; 84pp; English.
XX
XX      Polypeptide with beta-secretase activity, specific for wild-type
PT      amyloid precursor protein, useful in treating Alzheimer's disease
XX      Example 3; Page 24; 44pp; French.
XX
XX      Peptides AAY69702-Y69718 represent synthetic peptide substrates for a
CC      novel polypeptide with beta-secretase activity that can cleave
CC      specifically the natural beta-amyloid precursor protein (BAP). Normal
CC      cleavage of the protein occurs between amino acids Met396 Asp597 and
CC      Val386-Ile637 (positions 4-3 and 44-45 of AAY69701). The novel
CC      polypeptide is used to identify agents that interact specifically with
CC      it. These agents regulate metabolism of APP, particularly they slow down
CC      or reduce production of beta-amyloid, so can be used to treat
CC      neurodegenerative diseases, particularly Alzheimer's disease.
XX
XX      Sequence 39 AA;
SQ
Query Match 100.0%; Score 53; DB 21; Length 39;
Best Local Similarity 100.0%; Pred No. 0.00052;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EVKMDAEFRH 10
DB 16 EVKMDAEFRH 25

```

CC This peptide sequence shows the region of amyloid precursor protein  
 CC (APP) that includes a truncated beta-amyloid protein (BAP) lacking  
 CC the native secretase cleavage/recognition site. In an attempt to  
 CC engineer an APP non-cleavable substrate for secretase, an  
 CC APP-reporter (APP-RFP) protein that carries the BAP deletion has  
 CC been expressed in recombinant host cells. Deletion of these 18  
 CC amino acids, however, still resulted in the secretion of an  
 CC N-terminal APP-reporter fragment into the cytoplasm. Non-  
 CC cleavable APP substrates can be used to detect other putative  
 CC abnormal APP processing events. They can also be used to  
 CC investigate cellular post-translational modifications to APP in  
 CC order to determine the potential influence on normal secretase and  
 CC abnormal BAP 'clipping' activities.

XX Sequence 45 AA:

Query Match 100.0%; Score 53; DB 18; Length 45;  
 Best Local Similarity 100.0%; Pred. No. 0.0006;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMDAEFRH 10  
 |||

DB 6 EVKMDAEFRH 15

#### RESULT 11

AAW26392  
 ID AAW26392 standard; Peptide: 45 AA.

XX AAW26392;

DT 15-DEC-1997 (first entry)

DE Amyloid precursor protein fragment APP-RFP 751 (BAP del11-28).

KW Amyloid precursor protein; APP; beta-amyloid protein; BAP;

KM substrate; muteln; secretase; Alzheimer's disease; human.

OS Chimeric Homo sapiens;

OS Chimeric synthetic.

FH Key Location/Qualifiers

FT Cleavage-site 7.8 /note= "secretase cleavage site"

FT Peptide 10..33 /label= BAP(del11-28)

FT /note= "truncated beta-amyloid protein"

FT Domain 20..42 /label= Transmembrane

PN US5652092-A.

PD 29-JUL-1997.

PF 01-MAY-1992; 92US-0877675.

PR 20-SEP-1993; 93US-0123659.

PR 01-MAY-1992; 92US-0877675.

PR 05-JUN-1995; 95US-0462859.

PA (AMCY ) AMERICAN CYANAMID CO.

PI Jacobsen JS, Vitek MP;

DR WPI; 1997-392937/36.

PT Screening for compounds which reduce beta-amyloid protein formation

PT - using cells which express a construct encoding a marker and an

PT amyloid precursor muteln derived from APP isoforms

PS Disclosure; Fig 5A; 84pp; English.

XX This peptide sequence shows the region of amyloid precursor protein

CC (APP) that includes a truncated beta-amyloid protein (BAP) lacking  
 CC the native secretase cleavage/recognition site. In an attempt to  
 CC engineer an APP non-cleavable substrate for secretase, an  
 CC APP-reporter (APP-RFP) protein that carries the BAP deletion has  
 CC been expressed in recombinant host cells. Deletion of these 18  
 CC amino acids, however, still resulted in the secretion of an  
 CC N-terminal APP-reporter fragment into the cytoplasm. Non-  
 CC cleavable APP substrates can be used to detect other putative  
 CC abnormal APP processing events. They can also be used to  
 CC investigate cellular post-translational modifications to APP in  
 CC order to determine the potential influence on normal secretase and  
 CC abnormal BAP 'clipping' activities.

XX Sequence 45 AA:

Query Match 100.0%; Score 53; DB 18; Length 45;  
 Best Local Similarity 100.0%; Pred. No. 0.0006;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMDAEFRH 10  
 |||

DB 6 EVKMDAEFRH 15

#### RESULT 12

AAW44748  
 ID AAW44748 standard; Protein: 45 AA.

XX AAW44748;

DT 01-JUN-1998 (first entry)

DE APP-RFP 751 [BAP delta(11-28)] peptide.

KW Amyloid precursor protein; APP; APP 751 isoform; deletion; substrate P;

KM epitope; Met-enkephalin; detection; secretase; beta-amyloid protein; BAP;

KW Alzheimer's disease; cleavage.

OS Homo sapiens.

OS Synthetic.

FH Key Location/Qualifiers

FT Cleavage-site 7.8 /note= "putative secretase cleavage site"

FT Misc-difference 19..20 /note= "residues 11-28 of the wild type BAP sequence

FT are deleted from between these positions"

PN US5693478-A.

PD 02-DEC-1997.

PF 05-JUN-1995; 95US-0464247.

PR 20-SEP-1993; 93US-0123659.

PR 01-MAY-1992; 92US-0877675.

PR 05-JUN-1995; 95US-0464247.

PA (AMCY ) AMERICAN CYANAMID CO.

PI Jacobsen JS, Vitek MP;

DR WPI; 1998-031744/03.

PT Amyloid precursor muteln reporter molecule assay containing antibody

PT recognised marker - used to study pathways associated with

PT Alzheimer's disease

PS Disclosure; Fig 5A; 84pp; English.

XX This sequence represent the beta-amyloid protein sequence from the

CC construct APP-RFP751 [BAP delta(11-28)]. The mutant sequence contains

CC a deletion of the wild type BAP residues 11-28. This causes a

CC shortening of the BAP sequence. This may affect cleavage of the BAP by  
 CC the "secretase" dependent on whether the "secretase" recognises the  
 CC cleavage site by a positional effect or by sequence. The mutant sequence  
 CC can be used in a method to study secretase and beta-amyloid protein  
 CC (BAP)-generating pathways associated with Alzheimer's disease by  
 CC studying proteolytic cleavage of the reporter polypeptides (e.g.  
 CC AAM44744 and AAM44745).

XX Sequence 45 AA;

Query Match 100.0%; Score 53; DB 19; Length 45;  
 Best Local Similarity 100.0%; Pred. No. 0.0006;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMDAEFRH 10  
 |||||  
 DB 6 EVKMDAEFRH 15

#### RESULT 13

ID AAM42977 standard; peptide; 45 AA.

AC AAM42977;

DT 01-MAY-1998 (first entry)

DE Deletion beta-amyloid peptide (BAP) derived from APP-RFP 751.

XX Beta-amyloid peptide; BAP; extracellular BAP plaque;

KM cerebrovascular deposit; Alzheimer's disease; Downs syndrome;

KM amyloid precursor protein; APP; secretase; BAP aggregation;

KM abnormal proteolytic cleavage.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Domain 20..43 /note="putative transmembrane domain"

PN US5703209-A.

PD 30-DEC-1997.

PF 05-JUN-1995; 95US-0464248.

PR 20-SEP-1993; 93US-0123659.

PR 01-MAY-1992; 92US-0877675.

PA (AMCY ) AMERICAN CYANAMID CO.

PI Jacobsen JS, Vittek MP;

PT WPI; 1998-076482/07.

PS Amyloid precursor protein fusion polypeptides - comprising APP  
 fragment and marker, useful for research and drug screening

XX Disclosure; Fig 5A; 84pp; English.

CC The present sequence represents a beta-amyloid peptide (BAP), with  
 CC a deletion amino acids 11-28 (numbered according to AAM42976). Abnormal

CC accumulation of extracellular BAP in plaques and cerebrovascular  
 CC deposits is characteristic in brains of individuals suffering from

CC Alzheimer's disease and Downs syndrome. BAP is a poorly soluble,  
 CC self-aggregating protein which is derived from a larger amyloid precursor

CC protein (APP). APP is expressed as an integral membrane protein, and is  
 CC cleaved by secretase, between BAP 16lys and 17leu. Cleavage at this site

CC precludes amyloidogenesis and results in the release of the  
 CC amino-terminal APP fragment. Three major isoforms of APP exist: APP-695,

CC APP-751 and APP-770. These isoforms are derived by alternative splicing.  
 CC APP-RFP 751 is a deletion construct of APP-751, which has a deletion of  
 CC 276 amino acids to within 15 amino acids of the BAP domain. APP can be

CC used as a substrate for studying abnormal proteolytic cleavage which  
 CC results in the release of BAP, and also to screen for drugs that will  
 CC inhibit such cleavage.

XX Sequence 45 AA;

Query Match 100.0%; Score 53; DB 19; Length 45;  
 Best Local Similarity 100.0%; Pred. No. 0.0006;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMDAEFRH 10  
 |||||  
 DB 6 EVKMDAEFRH 15

#### RESULT 14

ID AAR55695 standard; Protein; 53 AA.

AC AAR55695;

DT 29-DEC-1994 (first entry)

DE Sequence of unidentified protein sequence ID number 20.

XX Amyloid precursor protein; APP; plaque; beta/A4; Alzheimer's;

KM transgene; ss.

OS Synthetic.

PN W09412627-A.

PD 09-JUN-1994.

PF 24-NOV-1993; 93WO-US11480.

PR 25-NOV-1992; 92US-0989850.

PR 09-NOV-1993; 93US-0149222.

PA (CEPH-) CEPHALON INC.

PI Howland DS, Scott RW;

DR WPI; 1994-200256/24.

PT Transgenic animal model for Alzheimer's disease - contains  
 of synapsin gene promoter

PS Example; Page 54; 94pp; English.

CC There was no apparent reference to sequence ID numbers 20, 21 or 22  
 CC in the specification. The specification describes a transgenic

CC animal model for Alzheimer's disease. A transgenic animal  
 CC harbouring a transgene coding for an amyloid protein under the

CC control of a promoter is claimed. The amyloid protein can be  
 CC APP695, APP751 or APP770. The coding sequence may contain a

CC mutation, including the hereditary cerebral haemorrhage with  
 CC amyloidosis - Dutch type (HCHWA-DT) and familial Alzheimer's

CC disease (FAD). Perhaps SQ IDS 20-22 corresp. to wt, HCHWA-DT  
 CC and FAD?

XX Sequence 53 AA;

Query Match 100.0%; Score 53; DB 15; Length 53;  
 Best Local Similarity 100.0%; Pred. No. 0.00072;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMDAEFRH 10  
 |||||  
 DB 1 EVKMDAEFRH 10

Result	ID	Accession	Description	Score	DB	Length	Positives	Negatives	Indels	Gaps
15	AA055696	AA055696	standard; protein; 53 AA.	100.0%	53	153	153	0	0	0
16	AA055696	AA055696	standard; protein; 53 AA.	100.0%	53	153	153	0	0	0
17	AA055696	AA055696	standard; protein; 53 AA.	100.0%	53	153	153	0	0	0
18	AA055696	AA055696	standard; protein; 53 AA.	100.0%	53	153	153	0	0	0
19	AA055696	AA055696	standard; protein; 53 AA.	100.0%	53	153	153	0	0	0
20	AA055696	AA055696	standard; protein; 53 AA.	100.0%	53	153	153	0	0	0
21	AA055696	AA055696	standard; protein; 53 AA.	100.0%	53	153	153	0	0	0
22	AA055696	AA055696	standard; protein; 53 AA.	100.0%	53	153	153	0	0	0
23	AA055696	AA055696	standard; protein; 53 AA.	100.0%	53	153	153	0	0	0
24	AA055696	AA055696	standard; protein; 53 AA.	100.0%	53	153	153	0	0	0
25	AA055696	AA055696	standard; protein; 53 AA.	100.0%	53	153	153	0	0	0
26	AA055696	AA055696	standard; protein; 53 AA.	100.0%	53	153	153	0	0	0
27	AA055696	AA055696	standard; protein; 53 AA.	100.0%	53	153	153	0	0	0
28	AA055696	AA055696	standard; protein; 53 AA.	100.0%	53	153	153	0	0	0
29	AA055696	AA055696	standard; protein; 53 AA.	100.0%	53	153	153	0	0	0
30	AA055696	AA055696	standard; protein; 53 AA.	100.0%	53	153	153	0	0	0
31	AA055696	AA055696	standard; protein; 53 AA.	100.0%	53	153	153	0	0	0
32	AA055696	AA055696	standard; protein; 53 AA.	100.0%	53	153	153	0	0	0
33	AA055696	AA055696	standard; protein; 53 AA.	100.0%	53	153	153	0	0	0
34	AA055696	AA055696	standard; protein; 53 AA.	100.0%	53	153	153	0	0	0
35	AA055696	AA055696	standard; protein; 53 AA.	100.0%	53	153	153	0	0	0
36	AA055696	AA055696	standard; protein; 53 AA.	100.0%	53	153	153	0	0	0
37	AA055696	AA055696	standard; protein; 53 AA.	100.0%	53	153	153	0	0	0
38	AA055696	AA055696	standard; protein; 53 AA.	100.0%	53	153	153	0	0	0
39	AA055696	AA055696	standard; protein; 53 AA.	100.0%	53	153	153	0	0	0
40	AA055696	AA055696	standard; protein; 53 AA.	100.0%	53	153	153	0	0	0
41	AA055696	AA055696	standard; protein; 53 AA.	100.0%	53	153	153	0	0	0
42	AA055696	AA055696	standard; protein; 53 AA.	100.0%	53	153	153	0	0	0
43	AA055696	AA055696	standard; protein; 53 AA.	100.0%	53	153	153	0	0	0
44	AA055696	AA055696	standard; protein; 53 AA.	100.0%	53	153	153	0	0	0
45	AA055696	AA055696	standard; protein; 53 AA.	100.0%	53	153	153	0	0	0
46	AA055696	AA055696	standard; protein; 53 AA.	100.0%	53	153	153	0	0	0
47	AA055696	AA055696	standard; protein; 53 AA.	100.0%	53	153	153	0	0	0
48	AA055696	AA055696	standard; protein; 53 AA.	100.0%	53	153	153	0	0	0
49	AA055696	AA055696	standard; protein; 53 AA.	100.0%	53	153	153	0	0	0
50	AA055696	AA055696								

Search completed: October 29, 2002, 10:26:44  
Job time : 24.1429 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 29, 2002, 10:23:36 ; Search time 10.4286 Seconds  
(without alignments)  
92.140 Million cell updates/sec

Title: US-09-580-018-5  
Perfect score: 53  
Sequence: 1 EVKMDAEFRH 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues  
Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	53	100.0	57	2 E60045	Alzheimer's disease
2	53	100.0	57	2 F60045	Alzheimer's disease
3	53	100.0	57	2 G60045	Alzheimer's disease
4	53	100.0	57	2 D60045	Alzheimer's disease
5	53	100.0	57	2 A60045	Alzheimer's disease
6	53	100.0	57	2 B60045	Alzheimer's disease
7	53	100.0	82	2 P00438	Alzheimer's disease
8	53	100.0	695	1 AA9795	Alzheimer's disease
9	53	100.0	770	1 Q8R0A4	Alzheimer's disease
10	47	88.7	747	2 JH0773	Alzheimer's disease
11	46	86.8	33	2 S23094	Alzheimer's disease
12	46	86.8	695	2 A27485	beta-amyloid prote
13	46	86.8	695	2 S00550	Alzheimer's disease
14	39	73.6	142	2 E89026	Alzheimer's disease
15	38	71.7	427	2 C83591	Alzheimer's disease
16	35	60.0	402	2 S38477	protein F13A2.1 [i
17	35	60.0	582	2 S72637	rdsl protein - fis
18	35	60.0	774	2 AG1565	hypothetical ABC e
19	35	66.0	782	2 A34219	autolysin (amidase
20	34	64.2	442	2 PN0512	Bic-D protein - fir
21	34	64.2	246	2 AG1140	beta-amyloid prote
22	34	64.2	400	2 S70187	transcription regu
23	34	64.2	423	2 C84991	44.7K vira protein
24	34	64.2	647	2 T26240	elongation factor
25	34	64.2	763	2 JC4376	hypothetical prote
26	34	64.2	1237	2 AE1915	beta-glucosidase (
27	34	64.2	1256	2 AB2042	hypothetical prote
28	34	64.2	4563	1 LPHUB	hypothetical prote
29	33	62.3	97	1 RCBP22	apolipoprotein B-1
					abc2 protein - pha

30	33	62.3	177	2 AB3649	hypothetical prote
31	33	62.3	255	2 G90509	dolichol-phosphate
32	33	62.3	294	2 T34048	hypothetical prote
33	33	62.3	384	2 F96601	hypothetical prote
34	33	62.3	426	2 B69876	acetylornithine de
35	33	62.3	626	2 AF0358	conserved hypothet
36	33	62.3	912	2 H71931	hypothetical prote
37	33	62.3	927	2 T38127	phosphoprotein - f
38	33	62.3	1265	2 T51498	hypothetical prote
39	33	62.3	1579	2 S59801	protein kinase SSK
40	33	62.3	1906	2 AD2443	hypothetical prote
41	32	60.4	113	2 AH0923	conserved hypothet
42	32	60.4	132	2 UQ0737	RnpA protein - Mic
43	32	60.4	173	2 G64318	hypothetical prote
44	32	60.4	139	2 S76960	hypothetical prote
45	32	60.4	350	2 G75421	probable serine/ch

## ALIGNMENTS

RESULT 1  
E60045 Alzheimer's disease amyloid beta/A4 protein precursor - sheep (fragment)  
C:Species: Ovis sp. (sheep)  
C:Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 28-Jul-1995  
C:Accession: E60045  
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
Brain Res. Mol. Brain Res. 10, 299-305, 1991  
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d  
A:Reference number: A60045; MUID:92017079  
A:Accession: E60045  
A:Molecule type: mRNA  
A:Residues: 1-57 <JOH>  
A:Cross-References: EMBL:X56130  
C:Superfamily: Alzheimer's disease amyloid beta protein; animal knitz-type proteinas  
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 53; DB 2; Length 57;  
Best Local Similarity 100.0%; Pred. No. 0.00053;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMDAEFRH 10  
Db 2 EVKMDAEFRH 11  
|||||  
RESULT 2  
F60045 Alzheimer's disease amyloid beta/A4 protein precursor - pig (fragment)  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 13-Aug-1999  
C:Accession: F60045  
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
Brain Res. Mol. Brain Res. 10, 299-305, 1991  
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d  
A:Reference number: A60045; MUID:92017079  
A:Accession: F60045  
A:Molecule type: mRNA  
A:Residues: 1-57 <JOH>  
A:Cross-References: EMBL:X56127; NID:q1895; PIDN:CAA39592.1; PID:q1896  
C:Superfamily: Alzheimer's disease amyloid beta protein; animal knitz-type proteinas  
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 53; DB 2; Length 57;  
Best Local Similarity 100.0%; Pred. No. 0.00053;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMDAEFRH 10  
Db 2 EVKMDAEFRH 11  
|||||

RESULT 3  
G60045  
Alzheimer's disease amyloid beta/A4 protein precursor - guinea pig (fragment)  
C:Species: *Canis porcellus* (guinea pig)  
C:Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 28-Jul-1995  
C:Accession: G60045  
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
Brain Res. Mol. Brain Res. 10, 299-305, 1991  
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,  
A:Reference number: A60045; MUID:92017079  
A:Accession: G60045  
A:Molecule type: mRNA  
A:Residues: 1-57 <JOH>  
A:Cross-references: EMBL:X56126  
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase  
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 53; DB 2; Length 57;  
Best Local Similarity 100.0%; Pred. No. 0.00053;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMDAEFRH 10  
Db 2 EVKMDAEFRH 11  
|||||

RESULT 4  
D60045  
Alzheimer's disease amyloid beta/A4 protein precursor - bovine (fragment)  
C:Species: *Bos primigenius taurus* (cattle)  
C:Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 28-Jul-1995  
C:Accession: D60045  
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
Brain Res. Mol. Brain Res. 10, 299-305, 1991  
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,  
A:Reference number: A60045; MUID:92017079  
A:Accession: D60045  
A:Molecule type: mRNA  
A:Residues: 1-57 <JOH>  
A:Cross-references: EMBL:X56124  
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase  
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 53; DB 2; Length 57;  
Best Local Similarity 100.0%; Pred. No. 0.00053;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMDAEFRH 10  
Db 2 EVKMDAEFRH 11  
|||||

RESULT 5  
A60045  
Alzheimer's disease amyloid beta/A4 protein precursor - dog (fragment)  
C:Species: *Canis lupus familiaris* (dog)  
C:Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 28-Jul-1995  
C:Accession: A60045  
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
Brain Res. Mol. Brain Res. 10, 299-305, 1991  
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,  
A:Reference number: A60045; MUID:92017079  
A:Accession: A60045  
A:Molecule type: mRNA  
A:Residues: 1-57 <JOH>  
A:Cross-references: EMBL:X56125  
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase  
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 53; DB 2; Length 57;  
Best Local Similarity 100.0%; Pred. No. 0.00053;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMDAEFRH 10  
Db 2 EVKMDAEFRH 11  
|||||

RESULT 6  
B60045  
Alzheimer's disease amyloid beta/A4 protein precursor - polar bear (fragment)  
C:Species: *Ursus maritimus* (polar bear)  
C:Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 13-Aug-1999  
C:Accession: B60045  
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
Brain Res. Mol. Brain Res. 10, 299-305, 1991  
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d  
A:Reference number: A60045; MUID:92017079  
A:Accession: B60045  
A:Molecule type: mRNA  
A:Residues: 1-57 <JOH>  
A:Cross-references: EMBL:X56128; NID:92165; PIDN:CA439593.1; PID:92166  
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas  
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 53; DB 2; Length 57;  
Best Local Similarity 100.0%; Pred. No. 0.00053;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMDAEFRH 10  
Db 2 EVKMDAEFRH 11  
|||||

RESULT 7  
P00438  
Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)  
C:Species: *Oryctolagus cuniculus* (domestic rabbit)  
C:Date: 30-Sep-1993 #sequence\_revision 19-Oct-1995 #text\_change 19-Oct-1995  
C:Accession: P00438; C60045  
R:Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.E.  
Biochem. Biophys. Res. Commun. 188, 905-911, 1992  
A:Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precurs  
A:Reference number: P00438; MUID:93075180  
A:Accession: P00438  
A:Molecule type: DNA  
A:Residues: 1-82 <DAV>  
A:Cross-references: GB:M83558; GB:M83657  
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
Brain Res. Mol. Brain Res. 10, 299-305, 1991  
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d  
A:Reference number: A60045; MUID:92017079  
A:Accession: C60045  
A:Molecule type: mRNA  
A:Residues: 12-68 <JOH>  
A:Cross-references: EMBL:X56129  
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas  
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match 100.0%; Score 53; DB 2; Length 82;  
Best Local Similarity 100.0%; Pred. No. 0.0008;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMDAEFRH 10  
Db 13 EVKMDAEFRH 22  
|||||

RESULT 8  
A49795  
Alzheimer's disease amyloid beta protein precursor - crab-eating macaque  
C:Species: *Macaca fascicularis* (crab-eating macaque)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C:Accession: A49795  
R:Podlisky, M.B.; Tolian, D.R.; Selkoe, D.J.  
Am. J. Pathol. 138, 1423-1435, 1991



A>Title: Homology of the amyloid beta protein precursor in monkey and human supports a  
 A:Reference number: A49795; MUID:91273117  
 A:Accession: A49795  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-695 <PDB>  
 A:Cross-references: GB:M58727; NID:q342062; PIDN:AAA36829.1; PID:q342063  
 C:superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1  
 C:Keywords: alternative splicing

Query Match 100.0%; Score 53; DB 1; Length 695;  
 Best local similarity 100.0%; Prec. No. 0.0089;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMAEPRH 10  
 |||||  
 Db 593 EVKMAEPRH 602

RESULT 9  
 ORF044  
 Alzheimer's disease amyloid beta protein precursor [validated] - human  
 N:Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor Xla inhibi  
 N:Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vascular  
 protein precursor splice form APP(770)  
 C:Species: Homo sapiens (man)  
 C>Date: 30-Jun-1987 #sequence-revision 28-Jul-1995 #text-change 15-Sep-2000  
 C:Accession: S02260; S05194; A32277; A33486; I39452; I39453; I59562; A44  
 4668; A28583; A29302; A60805; J00082; S06121; A60355; A59011; A38384; S29076; S38252; S3  
 R:Lemaire, H.G.; Salbaum, J.M.; Multhaupt, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.; Bey  
 Nucleic Acids Res. 17, 517-522, 1989  
 A>Title: The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded b  
 A:Reference number: S02260; MUID:89128427  
 A:Accession: S02260  
 A:Molecule type: DNA  
 A:Residues: 1-288, 'V', 365-770 <LEMI>  
 A:Cross-references: EMBL:X13466  
 A>Note: alternative splice form APP(695)  
 R:Lemaire, H.G.  
 submitted to the EMBL Data Library, November 1988  
 A:Reference number: S05194  
 A:Accession: S05194  
 A:Molecule type: DNA  
 A:Residues: 1-14, 'VW', 17-288, 'V', 365-770 <LEM2>  
 A:Cross-references: EMBL:X13466; NID:q35598; PIDN:CAA31830.1; PID:q871360  
 A>Note: alternative splice form APP(695)  
 R:La Pauci, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.  
 Biochem. Biophys. Res. Commun. 159, 297-304, 1989  
 A>Title: Characterization of the 5'-end region and the first two exons of the beta-prote  
 A:Reference number: A32277; MUID:89165870  
 A:Accession: A32277  
 A:Molecule type: DNA  
 A:Residues: 1-75 <LAF>  
 A:Cross-references: GB:M24546; GB:M24547; NID:q34102; PIDN:AA313654.1; PID:q516074  
 R:Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.  
 Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989  
 A>Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows similarit  
 A:Reference number: A33260; MUID:89392030  
 A:Accession: A33260  
 A:Molecule type: DNA  
 A:Residues: 656-737 <JOH>  
 A:Cross-references: GB:M29270; NID:q178863; PIDN:AAA51768.1; PID:q178865  
 R:Prelli, F.; Levy, E.; van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B.  
 Biochem. Biophys. Res. Commun. 170, 301-307, 1990  
 A>Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid of  
 A:Reference number: A35486; MUID:90321244  
 A:Accession: A35486  
 A:Molecule type: DNA  
 A:Residues: 672-710 <PREI>  
 A>Note: 693-Gln was found in DNA isolated from HCMA-D patients  
 R:Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.  
 Gene 87, 257-263, 1990  
 A>Title: Genomic organization of the human amyloid beta-protein precursor gene.

A:Reference number: I39451; MUID:90236318  
 A:Accession: I39452  
 A>Status: nucleic acid sequence not shown; translation not shown; translated from GB/  
 A:Molecule type: DNA  
 A:Residues: 1-770 <YOS1>  
 A:Cross-references: GB:M3112; NID:q178613; PIDN:AAB59502.1; PID:q178616  
 A:Accession: I39451  
 A>Status: nucleic acid sequence not shown; translation not shown; translated from GB/  
 A:Molecule type: DNA  
 A:Residues: 1-530, 'QWLMPEVPAWEAKVR' <YOS2>  
 A:Cross-references: GB:M34875; NID:q178608; PIDN:AAB59501.1; PID:q178615  
 R:Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.  
 Gene 102, 291-292, 1991  
 A:Reference number: A59020; MUID:91340168  
 A:Contents: annotation; erratum  
 A>Note: revised physical map for reference I39451  
 R:Levy, E.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van Du  
 Science 248, 1124-1126, 1990  
 A>Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemo  
 A:Reference number: I39453; MUID:90260663  
 A:Accession: I39453  
 A>Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 656-737 <LEV>  
 A:Cross-references: GB:M37896; NID:q178618; PIDN:AAA51727.1; PID:q178620  
 A>Note: a mutation with 693-Gln is presented  
 R:Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.  
 Science 254, 97-99, 1991  
 A>Title: A mutation in the amyloid precursor protein associated with hereditary Alzhe  
 A:Reference number: I59562; MUID:92022553  
 A:Accession: I59562  
 A>Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 689-716, 'F', 718-737 <MUR>  
 A:Cross-references: GB:S57665; NID:q236720; PIDN:AAB19991.1; PID:q236721  
 R:Kamino, K.; Orr, H.T.; Payant, H.; Wilsman, E.M.; Alonso, M.E.; Pulst, S.M.; Anders  
 drakis, S.E.; Korenberg, J.R.; Sharma, V.; Kukull, W.; Larson, E.; Heston, L.L.; Mart  
 Am. J. Hum. Genet. 51, 998-1014, 1992  
 A>Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for t  
 A:Reference number: A44017; MUID:93035397  
 A:Accession: A44017  
 A:Molecule type: DNA  
 A:Residues: 687-692, 'G', 694-718 <KAM1>  
 A:Cross-references: GB:S45135; NID:q257377; PIDN:AAB23645.1; PID:q257378  
 A:Experimental source: familial Alzheimer disease family SB  
 A>Note: sequence extracted from NCBI backbone (NCBI:P.115374)  
 A:Accession: B44017  
 A:Molecule type: DNA  
 A:Residues: 687-718 <KAM2>  
 A:Cross-references: GB:S45136; NID:q257379; PIDN:AAB23646.1; PID:q257380  
 A:Experimental source: familial Alzheimer disease family LIT  
 A>Note: sequence extracted from NCBI backbone (NCBI:P.115376)  
 A>Note: this sequence has a silent mutation  
 R:Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.  
 Nature 325, 733-736, 1987  
 A>Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-sur  
 A:Reference number: A03134; MUID:87144572  
 A:Accession: A03134  
 A:Molecule type: mRNA  
 A:Residues: 1-288, 'V', 365-770 <KAN>  
 A:Cross-references: GB:I00264; NID:q28525; PIDN:CAA6374.1; PID:q28526  
 A>Note: alternative splice form APP(695)  
 R:Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.  
 Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987  
 A>Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascula  
 A:Reference number: A29030; MUID:87231971  
 A:Accession: A29030  
 A:Molecule type: mRNA  
 A:Residues: 284-288, 'V', 365-646, 'E', 648-770 <ROB>  
 A:Cross-references: GB:M16765; NID:q178539; PIDN:AAA51722.1; PID:q178540  
 A>Note: the authors translated the codon GAG for residue 647 as Asp  
 R:Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Salafioti, U.; Gajdusek, D.C.  
 Science 255, 877-880, 1987

A:Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid  
A:Reference number: A47584; MUID:87120328  
A:Accession: A47584  
A:Molecule type: mRNA  
A:Residues: 674-756, 'S', 758-770 <GOL>  
A:Cross-references: GB:M1553; NID:q178706; PIDN:AAA35540.1; PID:q178707  
A:Note: Experimental source: brain  
R:Tanzil, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van Ke  
Science 235, 880-884, 1987  
A:Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near th  
A:Reference number: A47585; MUID:87120329  
A:Accession: A47585  
A:Molecule type: mRNA  
A:Residues: 674-703 <TAN1>  
A:Cross-references: GB:M15532; NID:q177957; PIDN:AAA51564.1; PID:q177958  
R:Dyrks, T.; Weidemann, A.; Muthaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Muelle  
EMBO J. 7, 949-957, 1988  
A:Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 prec  
A:Reference number: S02638; MUID:88296437  
A:Accession: S02638  
A:Molecule type: mRNA  
A:Residues: 672-678 <DYP>  
R:Tanzil, R.E.; McClatchey, A.I.; Lampertl, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Newe  
Nature 331, 528-530, 1988  
A:Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associat  
A:Reference number: S00707; MUID:88122640  
A:Accession: S00707  
A:Molecule type: mRNA  
A:Residues: 286-344, 'I', 365-366 <TAN2>  
A:Cross-references: EMBL:X06982; NID:q28817; PIDN:CAA30042.1; PID:q929612  
A:Note: Experimental source: promyelocytic leukemia cell line HL60  
A:Note: alternative splice form APP(751)  
R:Porte, P.; Gonzalez-Delgado, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.; Da  
Nature 331, 525-527, 1988  
A:Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibit  
A:Reference number: S00925; MUID:88122639  
A:Accession: S00925  
A:Molecule type: mRNA  
A:Residues: 1-344, 'I', 365-770 <PO2>  
A:Cross-references: GB:X06989; EMBL:Y00297; NID:q28720; PIDN:CAA30050.1; PID:q28721  
A:Note: alternative splice form APP(751)  
R:Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.  
Nature 331, 530-532, 1988  
A:Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibit  
A:Reference number: A38949; MUID:88122641  
A:Accession: A38949  
A:Molecule type: mRNA  
A:Residues: 287-367 <KIT>  
A:Cross-references: GB:X06981; NID:q28816; PIDN:CAA30041.1; PID:q929611  
A:Note: Experimental source: glioblastoma cell line  
A:Note: alternative splice form APP(770)  
R:Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ashton  
Brain Res. Mol. Brain Res. 4, 121-131, 1998  
A:Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of three F  
A:Reference number: A30320  
A:Accession: A30320  
A:Molecule type: mRNA  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 284-288, 'V', 365-770 <VIT1>  
A:Accession: B30320  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 122-288, 'V', 365-770 <VIT2>  
A:Accession: C30320  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 606-770 <VIT3>  
R:Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta, C.A  
Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988  
A:Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease br  
A:Reference number: A31087; MUID:88124954  
A:Accession: A31087  
A:Molecule type: mRNA

A:Residues: 507-770 <A1>  
A:Cross-references: GB:M18734; NID:q178572; PIDN:AAA51726.1; PID:q178573  
A:Note: the authors translated the codon GAA for residue 599 as Gly, ACC for residue  
8 as Val, GTG for residue 609 as Asn, AAT for residue 610 as Gly, and GGT for residue  
A:Note: the cited Genbank accession number, J03594, is not in release 101.0  
R:Maisters, C.L.; Muthaup, G.; Simms, G.; Pottinger, J.; Martins, R.N.; Beyreuther,  
Query Match 100.0%; Score 53; DB 1; Length 770;  
Best Local Similarity 100.0%; Pred. No. 0.01;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 EVKMDAEFRH 10  
|||||||  
Db 668 EVKMDAEFRH 677  
RESULT 10  
JH0773  
Alzheimer's disease amyloid beta protein precursor - African clawed frog  
C:Species: Xenopus laevis (African clawed frog)  
C>Date: 10-Jun-1993 #sequence\_revision 10-Jun-1993 #text\_change 13-Aug-1999  
C:Accession: JH0773  
R:Okado, H.; Okamoto, H.  
Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992  
A:Title: A Xenopus homologue of the human beta-amyloid precursor protein: development  
A:Reference number: JH0773; MUID:93129227  
A:Accession: JH0773  
A:Molecule type: mRNA  
A:Residues: 1-747 <OKA>  
A:Cross-references: GB:S52417; NID:q263150; PIDN:AAA24853.1; PID:q263151  
A:Experimental source: larva  
A:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas  
C:Keywords: alternative splicing; amyloid  
F:287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>  
Query Match 88.7%; Score 47; DB 2; Length 747;  
Best Local Similarity 80.0%; Pred. No. 0.17;  
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
OY 1 EVKMDAEFRH 10  
|||||||  
Db 645 EVKMDSEYRH 654  
RESULT 11  
S23094  
beta-amyloid protein precursor - rat  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 03-May-1996  
C:Accession: S23094  
R:Kojima, S.; Omori, M.  
FEBS Lett. 304, 57-60, 1992  
A:Title: Two-way cleavage of beta-amyloid protein precursor by multicatalytic protein  
A:Reference number: S23094; MUID:92316198  
A:Accession: S23094  
A:Molecule type: protein  
A:Residues: 1-33 <KOJ>  
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas  
Query Match 86.8%; Score 46; DB 2; Length 33;  
Best Local Similarity 90.0%; Pred. No. 0.008;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 1 EVKMDAEFRH 10  
|||||||  
Db 2 EVKMDAEFRH 11  
RESULT 12  
A27485  
Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse  
N:Alternate names: proteinase nexin II  
C:Species: Mus musculus (house mouse)

C>Date: 31-Mar-1989 #sequence\_revision 31-Mar-1989 #text\_change 13-Aug-1999  
 C:Accession: A27485; S19727; 149485  
 R:Yamada, T.; Sasaki, H.; Furuya, H.; Miyata, T.; Goto, I.; Sakaki, Y.  
 Biochem. Biophys. Res. Commun. 149, 665-671, 1987  
 A:Title: Complementary DNA for the mouse homolog of the human amyloid beta protein precursor  
 A:Reference number: A27485; MUID:88106489  
 A:Accession: A27485  
 A:Molecule type: mRNA  
 A:Residues: 1-695 <YAM>  
 A:Cross-references: GB:M18373; NID:9191568; PIDN:AAA37139.1; PID:9309085  
 A:Experimental source: brain  
 A:Strooper, B.; van Leuven, F.; van den Berghe, H.  
 Biochem. Biophys. Acta 1129, 141-143, 1991  
 A:Title: The amyloid beta protein precursor or proteinase nexin II from mouse is closer  
 A:Reference number: S19727; MUID:92096458  
 A:Accession: S19727  
 A:Molecule type: mRNA  
 A:Residues: 1-210 'G', 212-220 'S', 222-396 'A', 398-402 'T', 404-448 'A', 450-695 <STR>  
 A:Cross-references: EMBL:X59379  
 R:Iizumi, R.; Yamada, T.; Yoshikawa, S.; Sasaki, H.; Hattori, M.; Sakaki, Y.  
 Gene 112, 189-195, 1992  
 A:Title: Positive and negative regulatory elements for the expression of the Alzheimer's  
 A:Reference number: 149485; MUID:92209998  
 A:Accession: 149485  
 A>Status: translated from GB/EMBL/DBD  
 A:Molecule type: DNA  
 A:Residues: 1-19 <RES>  
 A:Cross-references: GB:D10603; NID:9220328; PIDN:BA01456.1; PID:9220329  
 C:Genetics:  
 A:Map position: 16c3  
 C:Superfamily: Alzheimer's disease amyloid beta protein, animal Kunitz-type proteinase I  
 C:Keywords: alternative splicing; amyloid; transmembrane protein

Query Match 86.8%; Score 46; DB 2; Length 695;  
 Best Local Similarity 90.0%; Pred. No. 0.25; Indels 0; Gaps 0;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 EYKMDAEPFH 10  
 Db 593 EYKMDAEPFH 602

RESULT 13  
 S00550  
 Alzheimer's disease amyloid beta protein precursor - rat  
 N:Alternate names: beta-A4 amyloid protein  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 13-Aug-1999  
 C:Accession: S00550; A41245; A39820; S46251  
 R:Shivers, B.D.; Hlilich, C.; Mulhapp, G.; Salbaum, M.; Beyreuther, K.; Seeburg, P.H.  
 EMBO J. 7, 1365-1370, 1988  
 A:Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brain  
 A:Reference number: S00550; MUID:88312583  
 A:Accession: S00550  
 A:Molecule type: mRNA  
 A:Residues: 1-695 <SHI>  
 A:Cross-references: EMBL:X07648; NID:955616; PIDN:CAA30488.1; PID:955617  
 R:Schubert, D.; Schröder, R.; Lacobriere, M.; Salton, T.; Cole, G.  
 Science 241, 223-226, 1988  
 A:Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan core  
 A:Reference number: A41245; MUID:88264430  
 A:Accession: A41245  
 A:Molecule type: protein  
 A:Residues: 18-37 'X', 39-40 'X', 42-44 <SCH>  
 A:Note: evidence for heparan sulfate attachment  
 R:Hesse, L.; Behner, D.; Masters, C.L.; Mulhapp, G.  
 FEBS Lett. 349, 109-116, 1994  
 A:Title: The beta-A4 amyloid precursor protein binding to copper.  
 A:Reference number: S46251; MUID:94320627  
 A:Contents: annotation; copper binding sites  
 A:Note: rat peptides were isolated but not sequenced  
 R:Potempska, A.; Styles, J.; Mehta, P.; Kim, K.S.; Miller, D.L.  
 J. Biol. Chem. 266, 8464-8469, 1991

A:Title: Purification and tissue level of the beta-amyloid peptide precursor of rat b  
 A:Reference number: A39820; MUID:91217087  
 A:Accession: A39820  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 18-32 <POT>  
 A:Experimental source: brain  
 C:Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques is  
 C:Superfamily: Alzheimer's disease amyloid beta protein, animal Kunitz-type proteinas  
 C:Keywords: alternative splicing; amyloid; glycoprotein; transmembrane protein  
 F:625-648/Domain: transmembrane #status predicted <YAM>

Query Match 86.8%; Score 46; DB 2; Length 695;  
 Best Local Similarity 90.0%; Pred. No. 0.25;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 EYKMDAEPFH 10  
 Db 593 EYKMDAEPFH 602

RESULT 14  
 E89026  
 protein F13A2.1 [imported] - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C>Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 10-May-2001  
 C:Accession: E89026  
 R:Anonymous, The C. elegans Sequencing Consortium.  
 Science 282, 2012-2018, 1998  
 A:Title: Genome sequence of the nematode C. elegans: a platform for investigating bio  
 A:Reference number: A75000; MUID:99069613; PMID:9851916  
 A:Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/projects/C\_  
 A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999;  
 A:Accession: E89026  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-142 <STO>  
 A:Cross-references: GB:chr\_V; PIDN:AAB69895.1; PID:92384795; GSPDB:GN00023; CESP:F13A  
 C:Genetics:  
 A:Gene: F13A2.1  
 A:Map position: 5

Query Match 73.6%; Score 39; DB 2; Length 142;  
 Best Local Similarity 77.8%; Pred. No. 1.1;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 EYKMDAEPFH 9  
 Db 56 EYKMDAEPFH 64

RESULT 15  
 C83591  
 N-carbamoyl-beta-alanine amidohydrolyase PA0444 [imported] - Pseudomonas aeruginosa (s  
 C:Species: Pseudomonas aeruginosa  
 C>Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
 C:Accession: C83591  
 R:Stover, C.K.; Pham, X.Q.; Errlin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.;  
 Adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lathig, K.; L  
 .; Lory, S.; Olson, M.V.  
 Nature 406, 959-964, 2000  
 A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa  
 A:Reference number: A82950; MUID:20437337  
 A:Accession: C83591  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-427 <STO>  
 A:Cross-references: GB:AE004481; GB:AE004091; NID:99946293; PIDN:AA03833.1; GSPDB:GN  
 A:Experimental source: strain PA01  
 C:Genetics:  
 A:Gene: PA0444  
 C:Superfamily: N-carbamyl-L-amino acid amidohydrolyase

Query Match 71.78; Score 38; DB 2; Length 427;  
 Best Local Similarity 70.08; Pred. No. 6.4;  
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EYKMDAERRH 10  
 ||| :|||  
 Db 289 EYKMTLDFRH 298

Search completed: October 29, 2002, 10:31:02  
 Job time : 11.4286 secs

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OM protein - protein search, using sw model

Run on: October 29, 2002, 10:22:36 ; Search time 5 seconds  
(without alignments)  
77.439 Million cell updates/sec

Title: US-09-580-018-5  
Perfect score: 53  
Sequence: 1 EVKMAEFRRH 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	53	100.0	57	1 A4_PIG	Q29023 sus scrofa
2	53	100.0	57	1 A4_URDMA	Q29149 ursus marit
3	53	100.0	58	1 A4_CANFA	Q28280 canis famill
4	53	100.0	58	1 A4_RABIT	Q28748 oryctolagus
5	53	100.0	59	1 A4_SHEEP	Q28757 ovis aries
6	53	100.0	59	1 A4_BOVIN	Q28053 bos taurus
7	53	100.0	751	1 A4_SALSC	Q95241 salmtr sci
8	53	100.0	770	1 A4_HUMAN	P05067 homo sapien
9	46	86.8	770	1 A4_MOUSE	P12023 mus musculu
10	46	86.8	770	1 A4_RAT	P08582 rattus norv
11	35	66.0	402	1 R0SL_SCHPO	P53693 schizosacch
12	35	66.0	782	1 BICD_DROME	P16568 drosophila
13	34	64.2	269	1 T2SI_STRFI	O52512 streptomyce
14	34	64.2	394	1 EFTU_BUCAT	O31297 buchnera ap
15	34	64.2	4563	1 APB_HUMAN	P04114 homo sapien
16	33	62.3	97	1 ABC2_BPP22	P11191 bacterioph
17	33	62.3	927	1 CC15_SCHPO	O09892 schizosacch
18	33	62.3	1579	1 SSK2_YEAST	P53599 saccharomyc
19	32	60.4	132	1 RNP4_MICLU	P21172 micrococcc
20	32	60.4	173	1 Y150_MENJA	O57614 methanococ
21	32	60.4	354	1 BCPA_CHLIT	O46195 chlorobium
22	32	60.4	365	1 BCPA_CHLIT	O46393 chlorobium
23	32	60.4	502	1 YGCL_ECOLI	O46901 escherichia
24	32	60.4	780	1 K6PL_HUMAN	P17858 homo sapien
25	31	58.5	198	1 TNE4_MOUSE	P43488 mus musculu
26	31	58.5	323	1 DHBX_MOUSE	P70694 mus musculu
27	31	58.5	323	1 PE2R_RABIT	P80508 oryctolagus
28	31	58.5	351	1 VA0D_HUMAN	P12953 homo sapien
29	31	58.5	351	1 VA0D_HUMAN	P51863 mus musculu
30	31	58.5	478	1 G6PD_BORBU	O51581 borrelia bu
31	31	58.5	479	1 Y098_MYCPN	P75535 mycoplasma
32	31	58.5	757	1 ECR_ILICCU	O18531 lucilia cup
33	31	58.5	1451	1 A2M2_MOUSE	P28666 mus musculu

34	31	58.5	1476	1 A2M1_MOUSE	P28665 mus musculu
35	31	58.5	1477	1 A113_RAP	P14046 rattus norv
36	31	58.5	3562	1 PGCV_CHICK	O90953 gallus galli
37	31	58.5	4644	1 DYHC_MOUSE	O91044 mus musculu
38	31	58.5	4644	1 DYHC_RAT	P38650 rattus norv
39	30.5	57.5	376	1 AROC_YEAST	P28777 saccharomyc
40	30	56.6	78	1 RL31_RICCN	O92140 rickettsia
41	30	56.6	78	1 RL31_RICPR	O92647 rickettsia
42	30	56.6	177	1 BLC_CITFR	O46036 citrobacter
43	30	56.6	177	1 BLC_ECOLI	P39281 escherichia
44	30	56.6	193	1 YEXN_AERSA	P45785 aeromonas s
45	30	56.6	197	1 OM26_HAEIN	O57483 haemophilus

## ALIGNMENTS

## RESULT 1

A4\_PIG STANDARD: PRT: 57 AA.

AC Q29023;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid protein (beta-Ap) (A-beta)] (Fragment).  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain.  
RX MEDLINE=92017079; PubMed=1656157;  
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;  
RT "Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis."  
RT Brain Res. Mol. Brain Res. 10:299-305(1991).  
RL

CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN G(O) (BY SIMILARITY).  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.  
CC  
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CC  
CC EMBL: X56127; CAA39592.1; -.  
CC HSSP: P05067; 1RA4.  
DR InterPro: IPR001868; A4\_APP.  
DR PROSITE: PS00319; A4\_EXTRA; PARTIAL.  
DR PROSITE: PS00320; A4\_INTRA; PARTIAL.  
KW Glycoprotein; Amyloid; Neutone; Transmembrane.  
FT CHAIN 1 48 BETA-AMYLOID PROTEIN (POTENTIAL).  
FT DOMAIN 34 33 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 34 57 POTENTIAL.  
FT NON\_TER 57 57  
SQ SEQUENCE 57 AA; 6172 MW; 84209DB8BEA82DFA CRC64;

Query Match 100.0%; Score 53; DB 1; Length 57;  
Best Local Similarity 100.0%; Pred. No. 0.00046;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMAEFRRH 10  
|||||

```
Db      2 EVKMDAEFRH 11

RESULT 2
A4_URSWA      STANDARD:      PRT:      57 AA.
ID_029149;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
protein (Beta-Ap4) (A-beta)] (Fragment).
GN App.
OS Ursus maritimus (Polar bear) (Thalarchos maritimus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.
OX NCBI_TaxID=29073;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
G(O) (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
-----
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CC or send an email to license@isb-sib.ch).
-----
DR EMBL: X56128; CAA39593.1; -.
DR HSSP: P05067; 1BA4.
DR InterPro: IPR001868; A4_APP.
DR PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR PROSITE: PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.
FT NON_TER 1
FT CHAIN 1 48 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 34 57 POTENTIAL.
FT NON_TER 57
SQ SEQUENCE 57 AA; 6172 MW; 84209D88BA82DFA CRC64;

Query Match 100.0%; Score 53; DB 1; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.00046;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 EVKMDAEFRH 10
Db      2 EVKMDAEFRH 11

RESULT 3
A4_CANFA      STANDARD:      PRT:      58 AA.
ID_028280;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
protein (Beta-Ap4) (A-beta)] (Fragment).
GN App.
OS Canis familiaris (Dog).
OS Canis familiaris (Dog).

Oy      1 EVKMDAEFRH 10
Db      2 EVKMDAEFRH 11

RESULT 4
A4_RABIT      STANDARD:      PRT:      58 AA.
ID_028748;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
protein (Beta-Ap4) (A-beta)] (Fragment).
GN App.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
G(O) (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
-----
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-----
DR EMBL: X56125; CAA39590.1; -.
DR HSSP: P05067; 1BA4.
DR InterPro: IPR001868; A4_APP.
DR PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR PROSITE: PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.
FT NON_TER 1
FT CHAIN 1 49 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 34 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 35 58 POTENTIAL.
FT NON_TER 58
SQ SEQUENCE 58 AA; 6285 MW; 8469D489A2E12DFA CRC64;

Query Match 100.0%; Score 53; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.00047;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 EVKMDAEFRH 10
Db      3 EVKMDAEFRH 12

RESULT 4
A4_RABIT      STANDARD:      PRT:      58 AA.
ID_028748;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
protein (Beta-Ap4) (A-beta)] (Fragment).
GN App.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
G(O) (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
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CC or send an email to license@isb-sib.ch).
-----
DR EMBL: X56125; CAA39590.1; -.
DR HSSP: P05067; 1BA4.
DR InterPro: IPR001868; A4_APP.
DR PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR PROSITE: PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.
FT NON_TER 1
FT CHAIN 1 49 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 34 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 35 58 POTENTIAL.
FT NON_TER 58
SQ SEQUENCE 58 AA; 6285 MW; 8469D489A2E12DFA CRC64;
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CC      G(O) (BY SIMILARITY).
CC      -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC      -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC      -----
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CC      -----
DR      EMBL: X56129; CAA39594.1; -.
DR      HSSP: P05067; IBA4.
DR      InterPro: IPR001868; A4_APP.
DR      PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR      PROSITE: PS00320; A4_INTRA; PARTIAL.
KW      Glycoprotein; Amyloid; Neurone; Transmembrane.
FT      NON_TER 1
FT      CHAIN 1 48 BETA-AMYLOID PROTEIN (POTENTIAL).
FT      DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
FT      TRANSEM 34 57 POTENTIAL.
FT      DOMAIN 58 >58 CYTOPLASMIC (POTENTIAL).
FT      NON_TER 58
SQ      SEQUENCE 58 AA; 6300 MW; F434209D88BBA82D CRC64;

Query Match          100.0%; Score 53; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.00047;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 EVKMDAEFRH 10
        |||||
Db      2 EVKMDAEFRH 11

RESULT 5
A4_SHEEP
ID      A4_SHEEP      STANDARD;      PRT;      58 AA.
AC      Q28757;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      30-MAY-2000 (Rel. 39, Last annotation update)
DE      Alzheimer's disease amyloid A4 protein homolog [contains: Beta-amyloid
DE      protein (Beta-Ap) (A-beta)] (Fragment).
OS      App.
OS      Ovis aries (Sheep).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC      Bovidae; Caprinae; Ovis.
OX      NCBI_TaxID=9940;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Heart;
RX      MEDLINE=92017079; PubMed=1656157;
RA      Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT      "Conservation of the sequence of the Alzheimer's disease amyloid
RT      peptide in dog, polar bear and five other mammals by cross-species
RT      polymerase chain reaction analysis.";
RL      Brain Res. Mol. Brain Res. 10:299-305(1991).
CC      -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC      INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC      G(O) (BY SIMILARITY).
CC      -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC      -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC      -----
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CC      -----

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DR      EMBL: X56130; CAA39595.1; -.
DR      HSSP: P05067; IAML.
DR      InterPro: IPR001868; A4_APP.
DR      PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR      PROSITE: PS00320; A4_INTRA; PARTIAL.
KW      Glycoprotein; Amyloid; Neurone; Transmembrane.
FT      NON_TER 1
FT      CHAIN 1 48 BETA-AMYLOID PROTEIN (POTENTIAL).
FT      DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
FT      TRANSEM 34 57 POTENTIAL.
FT      DOMAIN 58 >58 CYTOPLASMIC (POTENTIAL).
FT      NON_TER 58
SQ      SEQUENCE 58 AA; 6300 MW; F434209D88BBA82D CRC64;

Query Match          100.0%; Score 53; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.00047;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 EVKMDAEFRH 10
        |||||
Db      2 EVKMDAEFRH 11

RESULT 6
A4_BOVIN
ID      A4_BOVIN      STANDARD;      PRT;      59 AA.
AC      Q28053;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      30-MAY-2000 (Rel. 39, Last annotation update)
DE      Alzheimer's disease amyloid A4 protein homolog [contains: Beta-amyloid
DE      protein (Beta-Ap) (A-beta)] (Fragment).
OS      App.
OS      Bos taurus (Bovine).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC      Bovidae; Bovinae; Bos.
OX      NCBI_TaxID=9913;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Brain;
RX      MEDLINE=92017079; PubMed=1656157;
RA      Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT      "Conservation of the sequence of the Alzheimer's disease amyloid
RT      peptide in dog, polar bear and five other mammals by cross-species
RT      polymerase chain reaction analysis.";
RL      Brain Res. Mol. Brain Res. 10:299-305(1991).
CC      -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC      INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC      G(O) (BY SIMILARITY).
CC      -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC      -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC      -----
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CC      -----
DR      EMBL: X56124; CAA39589.1; -.
DR      EMBL: X56126; CAA39591.1; -.
DR      HSSP: P05067; IBA4.
DR      InterPro: IPR001868; A4_APP.
DR      PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR      PROSITE: PS00320; A4_INTRA; PARTIAL.
KW      Glycoprotein; Amyloid; Neurone; Transmembrane.
FT      NON_TER 1
FT      CHAIN 1 49 BETA-AMYLOID PROTEIN (POTENTIAL).
FT      DOMAIN <1 34 EXTRACELLULAR (POTENTIAL).
FT      TRANSEM 35 58 POTENTIAL.
FT      DOMAIN 59 >59 CYTOPLASMIC (POTENTIAL).

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FT NON_TER 59 59
SQ SEQUENCE 59 AA; 6414 MW; F43469D488A2E12D CRC64;

Query Match
Best Local Similarity 100.0%; Score 53; DB 1; Length 59;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMDAEFRH 10
   |||||
Db 3 EVKMDAEFRH 12

RESULT 7
A4_SAIISC STANDARD: PRT; 751 AA.
ID A4_SAIISC
AC Q95241;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein precursor [Contains: Beta-
  amyloid protein (beta-APP) (A-beta)].
GN APP.
OS Saimiri sciureus (Common squirrel monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.
OX NCBI_TaxID=9521;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Liver, and kidney;
RX MEDLINE=96108492; PubMed=8532114;
RX Levy E., Anorim A., Frangione B., Walker L.C.;
RX "Beta-amyloid precursor protein gene in squirrel monkeys with
  cerebral amyloid angiopathy.";
RX Neurobiol. Aging 16:805-808(1995).
RL
CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
  INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
  G(O).
CC
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC
CC -1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
  WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
  RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
  NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
  PHOSPHORYLATION (BY SIMILARITY)
CC
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC
CC -1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
CC
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  or send an email to license@isb-sib.ch).
CC
CC EMBL; S81024; AADI347.1; -.
DR HSSP; P05067; IAP.
DR InterPro; IPR001868; A4_APP.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00006; A4_EXTRA; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00320; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_2; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
KW Glycoprotein; Amyloid; Neurone; Transmembrane; Alternative splicing;
KW Signal; Serine protease inhibitor.
FT SIGNAL 1 17 BY SIMILARITY.
FT CHAIN 18 751 A4 PROTEIN.
FT CHAIN 653 695 BETA-AMYLOID PROTEIN (POTENTIAL).

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FT DOMAIN 18 680 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 681 704 POTENTIAL.
FT DOMAIN 705 751 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 287 345 BPTI/KUNITZ INHIBITOR.
FT SITE 740 743 CLATHRIN-BINDING (BY SIMILARITY).
FT ACT_SITE 301 302 REACTIVE BOND.
FT DISULFID 291 341 BY SIMILARITY.
FT DISULFID 300 324 BY SIMILARITY.
FT DISULFID 316 337 BY SIMILARITY.
FT CARBOHYD 523 523 N-LINKED (GLCNAC. . .) (PROBABLE).
FT CARBOHYD 552 552 N-LINKED (GLCNAC. . .) (PROBABLE).
SQ SEQUENCE 751 AA; 84893 MW; 6C3E431089569049 CRC64;

Query Match
Best Local Similarity 100.0%; Score 53; DB 1; Length 751;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMDAEFRH 10
   |||||
Db 649 EVKMDAEFRH 658

RESULT 8
A4_HUMAN STANDARD: PRT; 770 AA.
ID A4_HUMAN
AC P05067; P09000; Q16011;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein precursor (Protease nexin-II)
DE (PN-II) (APP1) [Contains: Beta-amyloid protein (beta-APP) (A-beta)].
GN APP OR A4 OR CVA4 OR ADL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Brain;
RX MEDLINE=87144572; PubMed=2881207;
RX Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L.,
RX Grieschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.;
RX "The precursor of Alzheimer's disease amyloid A4 protein resembles a
  cell-surface receptor.";
RX Nature 325:733-736(1987).
RL
RL [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88122639; PubMed=2893289;
RX Ponte P., Gonzalez-Dewhilt P., Schilling J., Miller J., Hsu D.,
RX Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F.,
RX Cordell B.;
RX "A new A4 amyloid mRNA contains a domain homologous to serine
  proteinase inhibitors.";
RX Nature 331:525-527(1988).
RL
RL [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=89128427; PubMed=2783775;
RX Lemaire H.-G., Salbaum J.M., Multhaup G., Kang J., Beyreuther K.,
RX Unterbeck A., Beyreuther K., Mueller-Hill B.;
RX "The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid
  is encoded by 16 exons.";
RX Nucleic Acids Res. 17:517-522(1989).
RL
RL [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=97263807; PubMed=9108164;
RX Hattori M., Tsukahara F., Furuhata Y., Tanahashi H., Hirose M.,
RX Saito M., Tsukuni S., Sakaki Y.;
RX "A novel method for making nested deletions and its application for
  sequencing of a 300 kb region of human APP locus.";
RX Nucleic Acids Res. 25:1802-1808(1997).
RL
RL [5]
RP SEQUENCE OF 286-345 AND 365-366 FROM N.A.
RX MEDLINE=88122640; PubMed=2893290;

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RA Tanzi R.E., McClatchey A.I., Lampertl E.D., Villa-Komaroff L.,  
 RA Gusella J.F., Neve R.L.;  
 RT "Protease inhibitor domain encoded by an amyloid protein precursor  
 RT mRNA associated with Alzheimer's disease.";  
 RL Nature 331:528-530(1988).  
 RN [6]  
 RA SEQUENCE OF 287-367 FROM N.A.  
 RX MEDLINE=8812841; PubMed=2893291;  
 RA Kitauchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.;  
 RT "Novel precursor of Alzheimer's disease amyloid protein shows  
 RT protease inhibitory activity.";  
 RL Nature 331:530-532(1988).  
 RN [7]  
 RP SEQUENCE OF 284-289 AND 365-770 FROM N.A.  
 RX MEDLINE=87231971; PubMed=3035574;  
 RA Robakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;  
 RT "Molecular cloning and characterization of a cDNA encoding the  
 RT cerebrovascular and the neuritic plaque amyloid peptides.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).  
 RN [8]  
 RP SEQUENCE OF 507-770 FROM N.A.  
 RX MEDLINE=88124954; PubMed=2893379;  
 RA Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,  
 RA Marotta C.A.;  
 RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer  
 RT disease brain: coding and noncoding regions of the fetal precursor  
 RT mRNA are expressed in the cortex.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).  
 RN [9]  
 RP SEQUENCE OF 672-681.  
 RX MEDLINE=88035004; PubMed=3312495;  
 RA Partridge W.M., Vinters H.V., Yang J., Eisenberg J., Choi T.B.,  
 RA Tountelliotte W.W., Huebner V., Shively J.E.;  
 RT "Amyloid angiopathy of Alzheimer's disease: amino acid composition  
 RT and partial sequence of a 4,200-dalton peptide isolated from cortical  
 RT microvessels.";  
 RL J. Neurochem. 49:1394-1401(1987).  
 RN [10]  
 RP SEQUENCE OF 739-770 FROM N.A.  
 RX MEDLINE=90236318; PubMed=2110105;  
 RA Yoshikaki S.-I., Sasaki H., Doh-Ura K., Furuya H., Sakaki Y.;  
 RT "Genomic organization of the human amyloid beta-protein precursor  
 RT gene.";  
 RL Gene 87:257-263(1990).  
 RN [11]  
 RP SEQUENCE OF 1-10 FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=89016647; PubMed=3140222;  
 RA Schon E.A., Mita S., Sadlock J., Herbert J.;  
 RT "A cDNA specifying the human amyloid beta precursor protein (ABPP)  
 RT encodes a 95-kDa polypeptide.";  
 RL Nucleic Acids Res. 16:9351-9351(1988).  
 RN [12]  
 RP SEQUENCE OF 18-50.  
 RX MEDLINE=87250462; PubMed=3597385;  
 RA van Nostrand W.E., Cunningham D.D.;  
 RT "Purification of protease nexin II from human fibroblasts.";  
 RL J. Biol. Chem. 262:8508-8514(1987).  
 RN [13]  
 RP IDENTITY OF APP WITH NEXIN-II.  
 RX MEDLINE=89384866; PubMed=2506449;  
 RA Oltersdorf T., Fritz L.C., Schenk D.B., Lieberburg I.,  
 RA Johnson-Wood K.L., Beattie E.C., Ward P.J., Blacher R.W., Dovey H.F.,  
 RA Sinha S.;  
 RT "The secreted form of the Alzheimer's amyloid precursor protein with  
 RT the Kunitz domain is protease nexin-II.";  
 RL Nature 341:144-147(1989).  
 RN [14]  
 RP PROTEASE-SPECIFICITY OF INHIBITOR DOMAIN.  
 RX MEDLINE=90211252; PubMed=1969731;  
 RA Kido H., Fukutomi A., Schilling J., Wang Y., Cordell B., Katunuma N.;  
 RT "Protease-specificity of Kunitz inhibitor domain of Alzheimer's  
 RT disease amyloid protein precursor.";

RL Biochem. Biophys. Res. Commun. 167:716-721(1990).  
 RN [15]  
 RP COMPLEX WITH G(O).  
 RX MEDLINE=93188965; PubMed=8446172;  
 RA Nishimoto I., Okamoto T., Matsura Y., Takahashi S., Okamoto T.,  
 RA Murayama Y., Ogata E.;  
 RT "Alzheimer amyloid protein precursor complexes with brain GTP-binding  
 RT protein G(O).";  
 RL Nature 362:75-79(1993).  
 RN [16]  
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 28-133.  
 RX MEDLINE=99215582; PubMed=10201399;  
 RA Rossjohn J., Cappai R., Fell S.C., Henry A., McKinsty M.J.,  
 RA Galatis D., Hesse L., Multhaup G., Beyreuther K., Masters C.L.,  
 RA Parker M.W.;  
 RT "Crystal structure of the N-terminal, growth factor-like domain of  
 RT Alzheimer amyloid precursor protein.";  
 RL Nat. Struct. Biol. 6:327-331(1999).  
 RN [17]  
 RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF 287-344.  
 RX MEDLINE=91104913; PubMed=2125487;  
 RA Hynes T.R., Randal M., Kennedy L.A., Eigenbrodt C., Kosiakof A.A.;  
 RT "X-ray crystal structure of the protease inhibitor domain of  
 RT Alzheimer's amyloid beta-protein precursor.";  
 RL Biochemistry 29:10018-10022(1990).  
 RN [18]  
 RP STRUCTURE BY NMR OF 289-344.  
 RX MEDLINE=92031488; PubMed=1718421;  
 RA Heald S.L., Tilton R.F., Jr., Hammond L.S., Lee A., Bayney R.M.,  
 RA Kamarek M.E., Ramabhadran T.V., Dreyer R.N., Davis G., Unterbeck A.,  
 RA Tamburini P.P.;  
 RT "Sequential NMR resonance assignment and structure determination of  
 RT the Kunitz-type inhibitor domain of the Alzheimer's beta-amyloid  
 RT precursor protein.";  
 RL Biochemistry 30:10467-10478(1991).  
 RN [19]  
 RP STRUCTURE BY NMR OF 672-699.  
 RX MEDLINE=94281210; PubMed=7516706;  
 RA Talafoos J., Marchowski K.J., Klopman G., Zagorski M.G.;  
 RT "Solution structure of residues 1-28 of the amyloid beta-peptide.";  
 RL Biochemistry 33:7788-7796(1994).  
 RN [20]  
 RP STRUCTURE BY NMR OF 696-706.  
 RX MEDLINE=97128622; PubMed=8973180;  
 RA Kohno T., Kobayashi K., Maeda T., Sato K., Takashima A.;  
 RT "Three-dimensional structures of the amyloid beta peptide (25-35) in  
 RT membrane-mimicking environment.";  
 RL Biochemistry 35:16094-16104(1996).  
 RN [21]  
 RP STRUCTURE BY NMR OF 672-711.  
 RX MEDLINE=98359783; PubMed=9693002;  
 RA Coles M., Bicknell W., Watson A.A., Fairlie D.P., Craik D.J.;  
 RT "Solution structure of amyloid beta-peptide(1-40) in a water-miscible  
 RT environment. Is the membrane-spanning domain where we think it is?";  
 RL Biochemistry 37:11064-11077(1998).  
 RN [22]  
 RP STRUCTURE BY NMR OF 672-699.  
 RX MEDLINE=20400066; PubMed=10940222;  
 RA Poulsen S.-A., Watson A.A., Craik D.J.;  
 RT "Solution structures in aqueous SDS micelles of two amyloid beta  
 RT peptides of Abeta(1-28) mutated at the alpha-secretase cleavage  
 RT site.";  
 RL J. Struct. Biol. 130:142-152(2000).  
 RN [23]  
 RP STRUCTURE BY NMR OF 681-706.  
 RX MEDLINE=20400065; PubMed=10940221;  
 RA Zhang S., Iwata K., Lachenmann M.J., Peng J.W., Li S., Stimson E.R.,  
 RA Lu Y., Felix A.M., Maglio J.E., Lee J.P.;  
 RT "The Alzheimer's peptide a beta adopts a collapsed coil structure in  
 RT water.";  
 RL J. Struct. Biol. 130:130-141(2000).  
 RN [24]  
 RP SIGNAL SEQUENCE CLEAVAGE SITE, AND TOPOLOGY.

RA MEDLINE=88296437; PubMed=2900137;  
RA Dyrys T., Weitemann A., Muthaup G., Salbaum J.M., Lemaire H.-G.,  
RA Kang J., Mueller-Hill B., Masters C.L., Beyreuther K.;  
RT "Identification, transmembrane orientation and biogenesis of the  
RT amyloid A4 precursor of Alzheimer's disease.";  
Query Match 100.0%; Score 53; DB 1; Length 770;  
Best Local Similarity 100.0%; Pred. No. 0.0067;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 EVKMDAEFRH 10  
Db 668 EVKMDAEFRH 677  
RESULT 9  
A4\_MOUSE STANDARD; PRT; 770 AA.  
AC P12023;  
DT 01-OCT-1989 (Rel. 12, Created)  
DT 01-DEC-1992 (Rel. 24, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Alzheimer's disease amyloid A4 protein homolog precursor  
DE (Amyloidogenic glycoprotein) (AG).  
GN APP.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_Taxid=10090;  
RN [1]  
RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.  
RC STRAIN-BALB/C; TISSUE-Brain;  
RA MEDLINE=92096458; PubMed=1756177;  
RT de Strooper B., van Leuven F., van den Bergh H.;  
RT "The amyloid beta protein precursor or proteinase nexin II from mouse  
RT is closer related to its human homolog than previously reported.";  
RL Biochim. Biophys. Acta 1129:141-143(1991).  
RN [2]  
RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.  
RC TISSUE-Brain;  
RA MEDLINE=88106489; PubMed=3322280;  
RT Yamada T., Sasaki H., Furuya H., Miyata T., Goto I., Sasaki Y.;  
RT "Complementary DNA for the mouse homolog of the human amyloid beta  
RT protein precursor.";  
RL Biochem. Biophys. Res. Commun. 149:665-671(1987).  
RN [3]  
RP REVISIONS.  
RA Yamada T.;  
RL Submitted (MAR-1988) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE OF 289-364 FROM N.A.  
RC STRAIN-CD-1; TISSUE-Placenta;  
RA MEDLINE=89345111; PubMed=2569710;  
RT Fukuchi K., Martin G.M., Deeb S.S.;  
RT "Sequence of the protease inhibitor domain of the A4 amyloid protein  
RT precursor of Mus domestica.";  
RL Nucleic Acids Res. 17:5396-5396(1989).  
RN [5]  
RP SEQUENCE OF 1-19 FROM N.A.  
RC MEDLINE=92209998; PubMed=1555768;  
RA Izumi R., Yamada T., Yoshikai S.I., Sasaki H., Hattori M.,  
RA Sakai Y.;  
RT "Positive and negative regulatory elements for the expression of the  
RT Alzheimer's disease amyloid precursor-encoding gene in mouse.";  
RL Gene 112:189-195(1992).  
RN [6]  
RP SEQUENCE OF 281-380 FROM N.A., AND ALTERNATIVE SPLICING.  
RC TISSUE-Brain, and Kidney;  
RA MEDLINE=89149813; PubMed=2493250;  
RT Yamada T., Sasaki H., Dohura K., Goto I., Sasaki Y.;  
RT "Structure and expression of the alternatively-spliced forms of mRNA  
RT for the mouse homolog of Alzheimer's disease amyloid beta protein  
RT precursor.";

RL Biochem. Biophys. Res. Commun. 158:906-912(1989).  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS, APP(395), APP(563), APP(695),  
CC APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE  
CC SPLICING.  
CC -1- TISSUE SPECIFICITY: AAA(770) IS EXPRESSED IN KIDNEY. AAA(751) IS  
CC WIDELY EXPRESSED. AAA(695) IS EXPRESSED IN BRAIN, KIDNEY AND  
CC LIVER.  
CC -1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION  
CC WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC  
CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE  
CC NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF  
CC PHOSPHORYLATION (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.  
CC -1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.  
-----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
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CC EMBL: X59379; -; NOT\_ANNOTATED\_CDS.  
CC DR EMBL: M18373; AAA37139.1; -;  
CC DR EMBL: X15210; CAA33280.1; -;  
CC DR EMBL: D10603; BAA01456.1; -;  
CC DR EMBL: M24397; AAA39929.1; -;  
CC DR PIR: A27485; A27485.  
CC DR PIR: S04855; S04855.  
CC DR PIR: S19727; S19727.  
CC DR HSSP: P05067; IQCM.  
CC DR MGD: MGI:88059; APP.  
CC DR InterPro: IPR001868; A4\_APP.  
CC DR InterPro: IPR002223; Kunitz\_BPTI.  
CC DR Pfam: PF02177; A4\_EXTRA; 1.  
CC DR Pfam: PF00014; Kunitz\_BPTI; 1.  
CC DR PRINTS: PR00203; AMYLOIDA4.  
CC DR PRINTS: PR00759; BASICPTASE.  
CC DR SMART: SM00006; A4\_EXTRA; 1.  
CC DR SMART: SM00131; Ku; 1.  
CC DR PROSITE: PS00319; A4\_EXTRA; 1.  
CC DR PROSITE: PS00320; A4\_INTRA; 1.  
CC DR PROSITE: PS00280; BPTI\_KUNITZ\_1; 1.  
CC DR PROSITE: PS50279; BPTI\_KUNITZ\_2; 1.  
CC KW Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;  
CC KW Alternative splicing; Serine protease inhibitor.  
CC FT SIGNAL 1 17  
CC FT CHAIN 18 770  
CC FT FT  
CC FT FT  
CC FT DOMAIN 18 699  
CC FT TRANSLEM 700 723  
CC FT DOMAIN 724 770  
CC FT DOMAIN 673 715  
CC FT DOMAIN 287 345  
CC FT SITE 759 762  
CC FT DISULFID 291 341  
CC FT DISULFID 300 324  
CC FT DISULFID 316 337  
CC FT CARBOHYD 542 542  
CC FT CARBOHYD 571 571  
CC FT CARBOHYD 571 571  
CC FT VASAPLIC 289 289  
CC FT VASAPLIC 290 364  
CC FT VASAPLIC 346 380  
CC SO SEQUENCE 770 AA; 86752 MW; 26C50DE0890CA7A CR64;  
Query Match 86.8%; Score 46; DB 1; Length 770;  
Best Local Similarity 90.0%; Pred. No. 0.16;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Oy 1 EVKMDAEFRH 10  
|||||||

DB 668 EVKMDAEFGH 677

RESULT 10

ID A4\_RAT STANDARD: PRT: 770 AA.

AC P08592;

DT 01-AUG-1988 (Rel. 08, Created)

DT 01-DEC-1992 (Rel. 24, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Alzheimer's disease amyloid A4 protein homolog precursor

DE (Amyloidogenic glycoprotein) (Ag).

GN APP.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI\_TaxId=10116;

XX [1]

RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.

RC TISSUE=Brain;

RX MEDLINE=88312583; PubMed=2900758;

RA Shivers B.D., Hilbich C., Multhaup G., Salbaum J.M., Beyreuther K.,

RA Seeburg P.H.,

RT "Alzheimer's disease amyloidogenic glycoprotein: expression pattern

RT in rat brain suggests a role in cell contact.";

RL EMBO J. 7:1365-1370(1988).

RN [2]

RP SEQUENCE OF 289-364 FROM N.A.

RC TISSUE=Liver;

RX MEDLINE=89183625; PubMed=2648331;

RA Kang J., Mueller-Hill B.;

RT "The sequence of the two extra exons in rat preA4.";

RL Nucleic Acids Res. 17:2130-2130(1989).

CC -1- SUBCELLULAR LOCATION: Type I membrane protein.

CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS: APP(395), APP(563), APP(695),

CC APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE

CC SPLICING.

CC -1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION

CC WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC

CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE

CC NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF

CC PHOSPHORYLATION (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.

CC -1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.

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CC -----

CC EMBL: X07648; CAA30488.1; -

CC EMBL: X14066; CAA32229.1; -

CC PIR: S00550; S00550.

CC PIR: S03607; S03607.

CC HSSP: P05067; IAAP.

DR InterPro: IPR001868; A4\_APP.

DR InterPro: IPR002223; Kunitz\_BPTI.

DR Pfam: PF02177; A4\_EXTRA; 1.

DR Pfam: PF00014; Kunitz\_BPTI; 1.

DR PRINTS: PR00203; AMYLOIDA4.

DR PRINTS: PR00759; BASICPTASE.

DR SMART: SM00006; A4\_EXTRA; 1.

DR SMART: SM00131; KU; 1.

DR PROSITE: PS00319; A4\_EXTRA; 1.

DR PROSITE: PS00320; A4\_INTRA; 1.

DR PROSITE: PS00280; BPTI\_KUNITZ\_1; 1.

DR PROSITE: PS50279; BPTI\_KUNITZ\_2; 1.

KW Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;

KW Alternative splicing; Serine protease inhibitor.

FT SIGNAL 1 17 BY SIMILARITY.

FT CHAIN 18 770

FT DOMAIN 18 699

FT TRANSMEM 700 723

FT DOMAIN 724 770

FT DOMAIN 673 715

FT DOMAIN 287 345

FT SITE 759 762

FT DISULFID 291 341

FT DISULFID 300 324

FT DISULFID 316 337

FT CARBOHYD 542 542

FT CARBOHYD 571 571

FT VARSPLIC 289 289

FT VARSPLIC 290 364

SO SEQUENCE 770 AA; 86704 MW; C26C9D5HB2D929A7 CRC64;

Query Match 86.8%; Score 46; DB 1; Length 770;

Best Local Similarity 90.0%; Pred. No. 0.16;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EVKMDAEFRH 10

DB 668 EVKMDAEFGH 677

RESULT 11

RDSL\_SCHPO

ID RDSL\_SCHPO STANDARD: PRT: 402 AA.

AC P53693; Q9U78;

DT 01-OCT-1996 (Rel. 34, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Rds1 protein.

GN RDS1 OR SPAC343.12.

OS Schizosaccharomyces pombe (Fission yeast).

OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;

OC Schizosaccharomycetales; Schizosaccharomycetaceae;

OX NCBI\_TaxId=4896;

XX [1]

RP SEQUENCE FROM N.A.

RP STRAIN=972;

RX MEDLINE=96004765; PubMed=7565608;

RA Ludin K.M., Hilti N., Schweingruber M.E.;

RT "Schizosaccharomyces pombe rds1, an adenine-repressible gene

RT regulated by glucose, ammonium, phosphate, carbon dioxide and

RT temperature.";

RL Mol. Gen. Genet. 248:439-445(1995).

RN [2]

RP SEQUENCE FROM N.A.

RP STRAIN=972;

RA Murphy L., Harris D., Wood V., Rajandream M.A., Barrell B.G.;

RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases

CC -1- FUNCTION: MAY HAVE A FUNCTION IN STRESS-RELATED RESPONSES OF THE

CC CELL.

CC -1- INDUCTION: WHEN CELLS ARE STARVED FOR GLUCOSE, AMMONIUM, OR

CC PHOSPHATE, WHEN THEY ARE EXPOSED TO A CARBON DIOXIDE ATMOSPHERE,

CC WHEN THEY ARE SHIFTED TO HIGHER TEMPERATURES OR WHEN THEY ENTER

CC STATIONARY PHASE. ADENINE-REPRESSIBLE.

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CC -----

CC EMBL: X77328; CAA54544.1; -

CC EMBL: AL109739; CAB52275.1; -

DR CONFLICT 17 17 R -> G (IN REF. 1).

FT SEQUENCE 402 AA; 43827 MW; 564343EDD7B4BECA CRC64;

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Query Match          66.0%; Score 35; DB 1; Length 402;
Best Local Similarity 60.0%; Pred. No. 13;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 1 EVKMDAEFRH 10
    |::|::|
Db 110 EAQIDAENRH 119

RESULT 12
ID BICD_DROME STANDARD; PRT; 782 AA.
AC P16568; O9YJ05;
DT 01-AUG-1990 (Rel. 15, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cytoskeleton-like bicaudal D protein.
GN BICD OR CG6605.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI-TaxId=7227;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90075232; PubMed=2550944;
RA Wharton R.P., Struhl G.;
RT "Structure of the Drosophila Bicadald protein and its role in
RT localizing the the posterior determinant nanos.";
RL Cell 59:881-892(1989).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=OREGON-R;
RX MEDLINE=90152340; PubMed=2576013;
RA Suter B., Romberg L.M., Steward R.;
RT "Bicadual-D, a Drosophila gene involved in developmental asymmetry:
RT localized transcript accumulation in ovaries and sequence similarity
RT to myosin heavy chain tail domains.";
RL Genes Dev. 3:1957-1968(1989).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Bailew R.M., Basu A.V., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
RA Chert J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dooson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriere S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heilmann T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegam C.,
RA Jaitani M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liao X., Lele Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mekulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclab J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

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RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
CC -1- FUNCTION: THIS PROTEIN IS ESSENTIAL FOR DIFFERENTIATION. IT
CC MAY PLAY A ROLE IN LOCALIZING OF NANOS (A MATERNAL DETERMINANT)
CC ACTIVITY IN OOCYTES. BICD MUTATIONS CAUSE NANOS MISLOCALIZATION
CC AND THUS BICAUDAL DEVELOPMENT.
CC -1- DEVELOPMENTAL STAGE: OOGENESIS.
CC -1- SIMILARITY: OF C-TERMINAL HALF TO VARIOUS MYOSIN HEAVY CHAINS AND
CC SOME INTERMEDIATE FILAMENT PROTEINS.
CC -----
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CC -----
DR EMBL; M31684; AAA28393.1; -;
DR EMBL; X51652; CAA35964.1; -;
DR EMBL; AE003655; AAF53616.1; -;
DR PIR; A33636; A33636.
DR FLYBASE; FBgn0000183; BICD.
KW coiled coil; developmental protein.
FT DOMAIN 3 263
FT FT 319 477 COILED COIL (POTENTIAL).
FT FT 601 746 COILED COIL (POTENTIAL).
FT FT 746 746 COILED COIL (POTENTIAL).
FT FT 296 296 A -> S (IN REF. 1).
FT FT 318 318 L -> P (IN REF. 1).
FT FT 477 477 H -> R (IN REF. 1).
FT FT 477 477
SQ SEQUENCE 782 AA; 88953 MW; 5A7176171DF58E6 CRC64;

Query Match          66.0%; Score 35; DB 1; Length 782;
Best Local Similarity 60.0%; Pred. No. 23;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 1 EVKMDAEFRH 10
    |::|::|
Db 739 EMEKDEMRH 748

RESULT 13
ID T2S1_STRFI STANDARD; PRT; 269 AA.
AC 052512;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Type II restriction enzyme SfiI (EC 3.1.21.4) (Endonuclease SfiI)
GN SfiI.
OS Streptomyces fimbriatus.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomyces; Streptomycetaceae; Streptomyces.
OX NCBI-TaxId=68197;
[1]
RP SEQUENCE FROM N.A.
RA van Cott E.M., Moran L.S., Slatko B.E., Wilson G.G.;
RT "Characterization of the SfiI restriction and modification genes.";
RT Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: RECOGNIZES THE DOUBLE-STRANDED SEQUENCE GGGCCNNNNNGGCC
CC AND CLEAVES BEFORE N-9.
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage of DNA to give
CC specific double-stranded fragments with terminal 5'-phosphates.
CC -----
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DR EMBL: AF039750; AAB95365.1; -  
DR REBASE: 1655; SflI.  
RW HydroLase; Endonuclease; Nuclease; Restriction system.  
SQ SEQUENCE 269 AA; 31044 MW; 3C48499BA5205EA CRC64;

Query Match  
Best Local Similarity 64.2%; Score 34; DB 1; Length 269;  
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 EVKMDAEFRH 10  
Db 116 QLPMDAEFRN 125  
:: |||||

RESULT 14  
EFVU\_BUCAL STANDARD; PRT; 394 AA.  
ID EFVU\_BUCAL  
AC 031297;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Elongation factor Tu (EF-Tu).  
GN TUF OR B0526.  
OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum  
OS symbiotic bacterium).  
OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.  
OX NCBI\_TaxID=118099;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=TOKYO 1998;  
RX MEDLINE=20445173; PubMed=10993077;  
RA Shigenobu S., Matanabe H., Hattori M., Sakaki Y., Ishikawa H.;  
RT "Genome sequence of the endocellular bacterial symbiont of aphids  
RL Buchnera sp. APS.";  
RN Nature 407:81-86(2000).  
RN [2]  
RP SEQUENCE OF 20-384 FROM N.A.  
RX MEDLINE=98242088; PubMed=9580987;  
RA Brynne E.U., Kurland C.G., Moran N.A., Andersson S.G.;  
RT "Evolutionary rates for tuf genes in endosymbionts of aphids.";  
RL Mol. Biol. Evol. 15:574-582(1998).  
CC -1- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING OF  
CC AMINOACYL-tRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN  
CC BIOSYNTHESIS.  
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -1- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.  
CC EF-TU/EF-1A SUBFAMILY.  
CC -----  
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DR EMBL: AP001119; BAB13219.1; ALT\_INIT.  
DR EMBL: Y13307; CAAT2974.1; -  
DR HSSP: P02990; IETU.  
DR InterPro: IPR000795; GMP\_EFTU.  
DR Pfam: PF00009; GTP\_EFTU; 1.  
DR PRINTS: PR00315; ELONGACTFCT.  
DR PROSITE: PS00301; EFACOR\_GTP; 1.  
RW Elongation factor; Protein biosynthesis; GTP-binding;  
KW Complete proteome.

FT NP\_BIND 19 26 GTP (BY SIMILARITY).  
FT NP\_BIND 81 85 GTP (BY SIMILARITY).  
FT NP\_BIND 136 139 GTP (BY SIMILARITY).  
FT CONFLICT 89 89 I -> M (IN REF. 2).  
SQ SEQUENCE 394 AA; 43465 MW; 09B73EADCA0DF5F6 CRC64;

Query Match  
Best Local Similarity 64.2%; Score 34; DB 1; Length 394;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 VKMDAEFRH 10  
Db 68 VEYDFEFRH 76  
1: | |||

RESULT 15  
APB\_HUMAN STANDARD; PRT; 4563 AA.  
ID APB\_HUMAN  
AC P04114; 000502; Q13787;  
DT 01-NOV-1986 (Rel. 03, Created)  
DT 01-NOV-1986 (Rel. 03, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Apolipoprotein B-100 precursor (Apo B-100) [Contains: Apolipoprotein  
DE B-48 (Apo B-48)].  
GN APOB.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=87016385; PubMed=3763409;  
RA Knott T.C., Wallis S.C., Powell L.M., Pease R.J., Lusis A.J.;  
RA Blackhart B., McCarthy B.J., Mahley R.W., Levy-Wilson B., Scott J.;  
RT "Complete cDNA and derived protein sequence of human apolipoprotein  
RT B-100.";  
RN B-100.";  
RN Nucleic Acids Res. 14:7501-7503(1986).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88003974; PubMed=3652907;  
RA Ludwig E.H., Blackhart B.D., Plerotli V.R., Caiati L., Portier C.,  
RA Knott T., Scott J., Mahley R.W., Levy-Wilson B., McCarthy B.J.;  
RT "DNA sequence of the human apolipoprotein B gene.";  
RN DNA 6:363-372(1987).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=87008488; PubMed=3759943;  
RA Chen S.-H., Yang C.-Y., Chen P.-F., Setzer D., Tanimura M., Li W.-H.,  
RA Gotto A.M., Jr., Chan L.;  
RT "The complete cDNA and amino acid sequence of human apolipoprotein  
RT B-100.";  
RN J. Biol. Chem. 261:12918-12921(1986).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=87041416; PubMed=3464946;  
RA Law S.W., Grant S.M., Higuchi K., Hospattankar A.V., Lackner K.J.,  
RA Lee N., Brewer H.B., Jr.;  
RT "Human liver apolipoprotein B-100 cDNA: complete nucleic acid and  
RT derived amino acid sequence.";  
RN Proc. Natl. Acad. Sci. U.S.A. 83:8142-8146(1986).  
RN [5]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=87161758; PubMed=3030729;  
RA Cladaras C., Hadzopoulou-Cladaras M., Nolte R.T., Atkinson D.,  
RA Zannis V.I.;  
RT "The complete sequence and structural analysis of human  
RT apolipoprotein B-100: relationship between apob-100 and apob-48  
RT forms.";  
RN EMBO J. 5:3495-3507(1986).  
RN [6]  
RP SEQUENCE OF 709-906 FROM N.A.  
RX MEDLINE=85270450; PubMed=3860836;  
RW Deeb S.S., Motulsky A.G., Albers J.J.;

RT "A partial cDNA clone for human apolipoprotein B.";

RL Proc. Natl. Acad. Sci. U.S.A. 82:4983-4986(1985).

RN [77]

RP SEQUENCE OF 3056-3159 FROM N.A.

RX MEDLINE=86041888; PubMed=3903660;

RA Meuthabian M., Schumaker V.N., Fareed G.C., West R., Johnson D.F.,

RT Kirchgessner T.G., Lin H.-C., Wang X., Ma Y., Mendiaz E., Lusis A.J.,

RT "Human apolipoprotein B: identification of cDNA clones and

RT characterization of mRNA.";

RL Nucleic Acids Res. 13:6937-6953(1985).

RN [8]

RP SEQUENCE OF 1937-2018 AND 3811-4334 FROM N.A.

RX MEDLINE=86093680; PubMed=3841204;

RA Carlsson P., Olofsson S.O., Bondjers G., Darnfors C., Wiklund O.,

RT Bjursell G.,

RT "Molecular cloning of human apolipoprotein B cDNA.";

RL Nucleic Acids Res. 13:8813-8826(1985).

RN [9]

RP SEQUENCE OF 3109-4563 FROM N.A.

RX MEDLINE=85300528; PubMed=2994225;

RA Knott T.J., Rall S.C. Jr., Innerarity T.L., Jacobson S.F.,

RA Uredea M.S., Levy-Wilson B., Powell L.M., Pease R.J., Eddy R.,

RA Nakai H., Byers M., Priestley L.M., Robertson E., Rall L.B.,

RA Bersholtz C., Shows T.B., Mahley R.W., Scott J.,

RT "Human apolipoprotein B: structure of carboxyl-terminal domains,

RT sites of gene expression, and chromosomal localization.";

RL Science 230:37-43(1985).

RN [10]

RP SEQUENCE OF 1-291 FROM N.A.

RX MEDLINE=86149325; PubMed=3513177;

RA Procter A.A., Hardman D.A., Schilling J.W., Miller J., Appleby V.,

RT Chen G.C., Kirsher S.W., McEnroe G., Kane J.P.,

RT "Isolation of a cDNA clone encoding the amino-terminal region of

RT human apolipoprotein B.";

RL Proc. Natl. Acad. Sci. U.S.A. 83:1467-1471(1986).

RN [11]

RP SEQUENCE OF 1-1670 FROM N.A.

RX MEDLINE=86287319; PubMed=346154;

RA Procter A.A., Hardman D.A., Sato K.Y., Schilling J.W.,

RA Yamanaka M., Hort Y.J., Herrild K.A., Chen G.C., Kane J.P.,

RT "Analysis of cDNA clones encoding the entire B-26 region of human

RT apolipoprotein B.";

RL Proc. Natl. Acad. Sci. U.S.A. 83:5678-5682(1986).

RN [12]

RP PARTIAL SEQUENCE AND IDENTIFICATION (APO-B48).

RX MEDLINE=88018019; PubMed=3659919;

RA Chen S.-H., Habb G., Yang C.-H., Gu Z.-W., Lee B.R., Wang S.-H.,

RA Silberman S.R., Cai S.-J., Deslypere J.P., Rosseneu M.,

RA Gotto A.M. Jr., Li W.-H., Chan L.,

RT "Apolipoprotein B-48 is the product of a messenger RNA with an organ-

RT specific in-frame stop codon.";

RL Science 238:363-366(1987).

RN [13]

RP DOMAINS.

RX MEDLINE=87039351; PubMed=3773997;

RA Knott T.C., Pease R.J., Powell L.M., Wallis S.C., Rall S.C. Jr.,

RA Innerarity T.L., Blackhart B., Taylor W.R., Marcel Y., Milne R.,

RA Johnson D., Fuller M., Lusis A.J., McCarthy B.J., Mahley R.W.,

RA Levy-Wilson B., Scott J.,

RT "Complete protein sequence and identification of structural domains

RT of human apolipoprotein B.";

RL Nature 323:734-738(1986).

RN [14]

RP DOMAINS.

RX MEDLINE=86242245; PubMed=3087360;

RA Yang C.-Y., Chen S.-H., Gianturco S.H., Bradley W.A., Sparrow J.T.,

RA Tanimura M., Li W.-H., Sparrow D.A., Deloof H., Rosseneu M.,

RA Lee F.-S., Gu Z.-W., Gotto A.M. Jr., Chan L.,

RT "Sequence, structure, receptor-binding domains and internal repeats

RT of human apolipoprotein B-100.";

RL Nature 323:738-742(1986).

RN [15]

RP CALCIUM-BINDING DATA.

RA Dashti N., Lee D.M., Mok T.,

RT "Apolipoprotein B is a calcium binding protein.";

RL Biochem. Biophys. Res. Commun. 137:493-499(1986).

RN [16]

RP VARIANT SER-4338.

RX MEDLINE=91071750; PubMed=1979313;

RA Navajas M., Laurent A.-M., Moreel J.-F., Ragab A., Cambou J.-P.,

RT Cuny G., Cambien F., Roizes G.,

RT "Detection by denaturing gradient gel electrophoresis of a new

RT polymorphism in the apolipoprotein B gene.";

RL Hum. Genet. 86:91-93(1990).

RN [17]

RP VARIANT FDB GLN-3527.

RX MEDLINE=89098975; PubMed=2563166;

RA Scoria L.F., Ludwig E.H., Clarke H.R.G., Vega G.L., Grundy S.M.,

RA McCarthy B.J.,

RT "Association between a specific apolipoprotein B mutation and

RT familial defective apolipoprotein B-100.";

RL Proc. Natl. Acad. Sci. U.S.A. 86:587-591(1989).

RN [18]

RP VARIANT LEU-2739.

RX MEDLINE=91016974; PubMed=2216805;

RA Huang L.-S., Gavish D., Breslow J.L.,

RT "Sequence polymorphism in the human apob gene at position 8344.";

RL Nucleic Acids Res. 18:5922-5922(1990).

RN [19]

RP VARIANT FDB CYS-3558.

RX MEDLINE=95190020; PubMed=7883971;

RA Pullinger C.R., Hennessy L.K., Chatterton J.E., Liu W., Love J.A.,

RA Mendel C.M., Frost P.H., Malloy M.J., Schumaker V.N., Kane J.P.,

RT "Familial ligand-defective apolipoprotein B. Identification of a new

RT mutation that decreases LDL receptor binding affinity.";

RL J. Clin. Invest. 95:1225-1234(1995).

RN [20]

RP VARIANTS L-1437; S-1914; K-2566; T-3121; A-3945; M-4128 AND T-4481.

RX MEDLINE=97044521; PubMed=8889592;

RA Poirier O., Ricard S., Behague I., Souriau C., Evans A.E.,

RA Aveller D., Marques-Vidal P., Luc G., Roizes G., Cambien F.,

RT "Detection of new variants in the apolipoprotein B (Apo B) gene by

RT PCR-SSCP.";

RL Hum. Mutat. 8:282-285(1996).

RN [21]

RP VARIANTS FDB GLN-3527 AND CYS-3558.

RX MEDLINE=97403938; PubMed=9259199;

RA Rabes J.P., Varret M., Saint-Jore B., Erlich D., Jondeau G.,

RA Kempf M., Giraudet P., Junien C., Bolleau C.,

RT "Familial ligand-defective apolipoprotein B-100: simultaneous

RT detection of the ARG3500-->Gln and ARG3531-->Cys mutations in a

RT French population.";

RL Hum. Mutat. 10:160-163(1997).

RN [22]

RP VARIANTS S-1914; R-1923; L-2739; D-3319; T-3427; Q-3432 AND I-3921.

RX MEDLINE=98141125; PubMed=9490296;

RA Leren T.P., Bakken K.S., Hoel V., Hjermann I., Berg K.,

RT "Screening for mutations of the apolipoprotein B gene causing

RT hypocholesterolemia.";

RL Hum. Genet. 102:44-49(1998).

RN [23]

RP FUNCTION: APOLIPOPROTEIN B IS A MAJOR PROTEIN CONSTITUENT OF

CC CHYLOMICRONS, VLDL AND LDL. IT FUNCTIONS AS A RECOGNITION SIGNAL

CC FOR THE CELLULAR BINDING AND INTERNALIZATION OF LDL PARTICLES BY

CC THE APOB/E RECEPTOR.

CC -1- DISEASE: DEFECTS IN APOB ARE A CAUSE OF FAMILIAL LIGAND-DEFECTIVE

CC APOLIPOPROTEIN B-100 (FDB). IT IS A DOMINANTLY INHERITED DISORDER

CC OF LIPOPROTEIN METABOLISM LEADING TO HYPERCHOLESTEROLEMIA AND

CC INCREASED PRONESS TO CORONARY ARTERY DISEASE (CAD).

CC THE PLASMA CHOLESTEROL LEVELS ARE DRAMATICALLY ELLEVATED DUE TO

CC IMPAIRED CLEARANCE OF LDL PARTICLES BY DEFECTIVE APOB/E RECEPTORS.

CC -1- DISEASE: DEFECTS IN APOB ASSOCIATED WITH OTHER GENE DEFECTS

CC (POLYGENIC) CAN BE THE CAUSE OF HYPOCHOLESTEROLEMIA.

CC MISCELLANEOUS: APO B-48 WHICH IS SYNTHESIZED ONLY BY THE

CC INTESTINE, AND FOUND IN CHYLOMICRONS, IS A SHORTENED FORM OF APO

Query Match

64.2%; Score 34; DB 1; Length 4563;

Best Local Similarity 66.7%; Pred. No. 2.5e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 EVKMDAEFR 9  
| | | | : | |  
Db 1483 EVKIDGQFR 1491

Search completed: October 29, 2002, 10:27:30  
Job time : 7 secs

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•  
•  
•



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OM protein - protein search, using sw model

Run on: October 29, 2002, 10:23:11 : Search time 18 Seconds  
(without alignments)  
96.108 Million cell updates/sec

Title: US-09-580-018-5  
Perfect score: 53  
Sequence: 1 EVKMAEEFRH 10

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 17294929 residues  
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_19:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mmc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_protent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	100.0	82	4	P78438
2	53	100.0	82	4	P78438
3	53	100.0	82	4	P78438
4	53	100.0	82	4	P78438
5	53	100.0	82	4	P78438
6	53	100.0	82	4	P78438
7	53	100.0	82	4	P78438
8	53	100.0	82	4	P78438
9	53	100.0	82	4	P78438
10	53	100.0	82	4	P78438
11	53	100.0	82	4	P78438
12	53	100.0	82	4	P78438
13	53	100.0	82	4	P78438
14	53	100.0	82	4	P78438
15	53	100.0	82	4	P78438
16	53	100.0	82	4	P78438

17	46	86.8	423	2	Q45693
18	46	86.8	697	11	Q99K32
19	46	86.8	695	11	P97487
20	39	73.6	142	5	O16896
21	38	71.7	427	16	Q91673
22	35	66.0	582	35	Q91673
23	35	66.0	582	35	P74939
24	35	66.0	774	16	Q92CV7
25	34	64.2	19	4	Q9UC8
26	34	64.2	28	4	Q9UCD1
27	34	64.2	30	4	Q9UC9
28	34	64.2	33	4	Q9UC33
29	34	64.2	105	10	Q9UCJ9
30	34	64.2	239	10	Q9FNG2
31	34	64.2	265	34	Q9A0L8
32	34	64.2	347	12	Q9LFD6
33	34	64.2	400	2	Q52295
34	34	64.2	407	2	Q9E8V1
35	34	64.2	431	2	Q935K0
36	34	64.2	439	2	Q9L5I6
37	34	64.2	454	5	Q9UN07
38	34	64.2	452	5	Q9Y198
39	34	64.2	475	5	Q90343
40	34	64.2	612	13	Q919E7
41	34	64.2	634	5	Q909Y8
42	34	64.2	647	5	Q62395
43	34	64.2	676	5	Q9W106
44	34	64.2	738	13	Q90W28
45	34	64.2	763	3	Q12653

## ALIGNMENTS

RESULT 1  
P78438 PRELIMINARY; PRT; 82 AA.  
AC P78438;  
DT 01-MAY-1997 (TRENBERG, 03, Created)  
DT 01-MAY-1997 (TRENBERG, 03, Last sequence update)  
DT 01-MAR-2001 (TRENBERG, 16, Last annotation update)  
DE AMYLOID PROTEIN (BETA-AMYLOID PROTEIN) (FRAGMENT).  
GN APP.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Johnson E.M., Chaney M.O., Moore R.E., Ward K.E., Norris F.H., Little S.P.;  
RT "Alzheimer's disease amyloid peptide is encoded by two exons and shows similarity to soybean trypsin inhibitor.";  
RL Biochem. Biophys. Res. Commun. 163:1248-1255(1989).  
RN [2]  
RP SEQUENCE OF 19-48 FROM N.A.  
RA MEDLINE=87120329; PubMed=2949367;  
RA Tanzi R.E., Gusella J.F., Watkins P.C., Bruns G.A., George-Hyslop P., Van Keuren M.L., Patterson D., Pagan S., Kurnit D.M., Neve R.L.;  
RT "Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near the Alzheimer locus.";  
RL Science 235:880-884(1987).  
RN [3]  
RP SEQUENCE OF 32-63 FROM N.A.  
RA MEDLINE=93035397; PubMed=1415269;  
RA Kamino K., Orr H.T., Payami H., Witsman E.M., Alonso M.E., Pulst S.M., Anderson L., O'dahl S., Nemens E., White J.A.;  
RT "Linkage and mutational analysis of familial Alzheimer disease kindreds for the APP gene region.";  
RL Am. J. Hum. Genet. 51:998-1014(1992).  
DR EMBL; M29270; AAA51768.1; -;  
DR EMBL; M29269; AAA51768.1; JOINED.

DR EMBL: M15532; AAA51564.1; -  
 DR EMBL: S45136; AAB23646.1; -  
 DR HSSP: P05067; 1BA4.  
 FT NON\_TER  
 SQ SEQUENCE 82 AA; 8994 MW; 8DA9E42B813A070E CRC64;

Query Match 100.0%; Score 53; DB 4; Length 82;  
 Best Local Similarity 100.0%; Pred. No. 0.0023;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EVKMDAEFRH 10  
 DB 13 EVKMDAEFRH 22

RESULT 2  
 ID 016014 PRELIMINARY; PRT; 82 AA.  
 AC 016014;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE BETA-AMYLOID PEPTIDE (FRAGMENT).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93236601; PubMed=8476439;  
 RA Denman R.B., Rosenzwaig R., Miller D.L.;  
 RT "A system for studying the effect(s) of familial Alzheimer disease  
 mutations on the processing of the beta-amyloid peptide precursor";  
 RL Biochem. Biophys. Res. Commun. 192:96-103(1993).  
 DR EMBL: S60721; AAB26263.2; -  
 DR HSSP: P05067; 1BA4.  
 FT NON\_TER 1  
 FT NON\_TER 82  
 SQ SEQUENCE 82 AA; 8972 MW; F534AA5B3EA9230A CRC64;

Query Match 100.0%; Score 53; DB 4; Length 82;  
 Best Local Similarity 100.0%; Pred. No. 0.0023;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EVKMDAEFRH 10  
 DB 14 EVKMDAEFRH 23

RESULT 3  
 ID 016019 PRELIMINARY; PRT; 82 AA.  
 AC 016019;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE BETA-AMYLOID PEPTIDE (FRAGMENT).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93236601; PubMed=8476439;  
 RA Denman R.B., Rosenzwaig R., Miller D.L.;  
 RT "A system for studying the effect(s) of familial Alzheimer disease  
 mutations on the processing of the beta-amyloid peptide precursor";  
 RL Biochem. Biophys. Res. Commun. 192:96-103(1993).  
 DR EMBL: S61380; AAB26264.2; -  
 DR HSSP: P05067; 1BA4.  
 FT NON\_TER 1  
 FT NON\_TER 82

SQ SEQUENCE 82 AA; 8938 MW; F534AA50E579230A CRC64;

Query Match 100.0%; Score 53; DB 4; Length 82;  
 Best Local Similarity 100.0%; Pred. No. 0.0023;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EVKMDAEFRH 10  
 DB 14 EVKMDAEFRH 23

RESULT 4  
 ID 016020 PRELIMINARY; PRT; 82 AA.  
 AC 016020;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE BETA-AMYLOID PEPTIDE (FRAGMENT).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93236601; PubMed=8476439;  
 RA Denman R.B., Rosenzwaig R., Miller D.L.;  
 RT "A system for studying the effect(s) of familial Alzheimer disease  
 mutations on the processing of the beta-amyloid peptide precursor";  
 RL Biochem. Biophys. Res. Commun. 192:96-103(1993).  
 DR EMBL: S61383; AAB26265.2; -  
 DR HSSP: P05067; 1BA4.  
 FT NON\_TER 1  
 FT NON\_TER 82  
 SQ SEQUENCE 82 AA; 8882 MW; F534AA5AE5D9230A CRC64;

Query Match 100.0%; Score 53; DB 4; Length 82;  
 Best Local Similarity 100.0%; Pred. No. 0.0023;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EVKMDAEFRH 10  
 DB 14 EVKMDAEFRH 23

RESULT 5  
 ID 093296 PRELIMINARY; PRT; 534 AA.  
 AC 093296;  
 DT 01-NOV-1998 (TREMBLrel. 08, Created)  
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE AMYLOID PROTEIN (FRAGMENT).  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98337885; PubMed=9671674;  
 RA Barnes N.Y., Li L., Yoshikawa K., Schwartz L.M., Oppenheim R.W.,  
 RA Milligan C.E.;  
 RT "Increased production of amyloid precursor protein provides a  
 substrate for caspase-3 in dying motoneurons";  
 RL J. Neurosci. 18:5869-5880(1998).  
 DR EMBL: AF042098; AAC25052.1; -  
 DR HSSP: P05067; 1BA4.  
 DR InterPro: IPR001868; A4\_APP.  
 DR PRINTS: PR00203; AMYLOIDR4.  
 DR PROSITE: PS00319; A4\_EXTRA; 1.  
 DR PROSITE: PS00320; A4\_INTRA; 1.

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FT NON_TER 1 1
SQ SEQUENCE 534 AA; 60597 MW; FB53ECC2E6D4C92 CRC64;

Query Match
Best Local Similarity 100.0%; Score 53; DB 13; Length 534;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMDAEFRH 10
   |||||
Db 432 EVKMDAEFRH 441

RESULT 6
Q9PVL1 PRELIMINARY; PRT; 569 AA.
AC Q9PVL1:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE AMYLOID PROTEIN (FRAGMENT).
GN APP.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RX [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Coulson E.J., Paliaga K., Beyreuther K., Masters C.L.;
RT "What the evolution of the amyloid protein precursor supergene family
RL tells us about its function.";
RL Neurochem. Int. 0:0-0(2000).
DR EMBL: AF030341; AAF12698.1; -
DR HSSP: P05067; 1BA4
DR InterPro: IPR001868; A4_APP.
DR Pfam: PF02177; A4_EXTRA; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR SMART: SM00006; A4_EXTRA; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
FT NON_TER 1 1
SQ SEQUENCE 569 AA; 64753 MW; 0AB8BB851863A19D CRC64;

Query Match
Best Local Similarity 100.0%; Score 53; DB 13; Length 569;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMDAEFRH 10
   |||||
Db 468 EVKMDAEFRH 477

RESULT 7
Q95KN7 PRELIMINARY; PRT; 695 AA.
AC Q95KN7:
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE AMYLOID B-PROTEIN PRECURSOR.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9541;
RX [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CEREBELLUM;
RX MEDLINE=91273117; PubMed=1905108;
RA Podlinsky M.B., Tolan D.R., Selkoe D.J.;
RT "Homology of the amyloid beta protein precursor in monkey and human
RT supports a primate model for beta amyloidosis in Alzheimer's

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RT disease.";
RL Am. J. Pathol. 138:1423-1435(1991).
DR EMBL: M58727; AAA36829.1; -.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 597 636 POTENTIAL.
SQ SEQUENCE 695 AA; 78663 MW; 4F6EA0139F969D56 CRC64;

Query Match
Best Local Similarity 100.0%; Score 53; DB 6; Length 695;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMDAEFRH 10
   |||||
Db 593 EVKMDAEFRH 602

RESULT 8
Q60496 PRELIMINARY; PRT; 695 AA.
AC Q60496:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE PUTATIVE AMYLOID PRECURSOR PROTEIN.
OS Cavia sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.
OX NCBI_TaxID=10143;
RX [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=97236426; PubMed=9116031;
RA Beck M., Mueller D., Bigl V.;
RT "Amyloid precursor protein in Guinea pigs - complete cDNA sequence and
RL alternative splicing.";
RL Biochim. Biophys. Acta 1351:17-21(1997).
DR EMBL: X97631; CAA66230.1; -
DR HSSP: P05067; 1BA4
DR InterPro: IPR001868; A4_APP.
DR Pfam: PF02177; A4_EXTRA; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR SMART: SM00006; A4_EXTRA; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
SQ SEQUENCE 695 AA; 78701 MW; 5196A0C4017F16AB CRC64;

Query Match
Best Local Similarity 100.0%; Score 53; DB 11; Length 695;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMDAEFRH 10
   |||||
Db 593 EVKMDAEFRH 602

RESULT 9
Q9DGB8 PRELIMINARY; PRT; 695 AA.
AC Q9DGB8:
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE BETA-AMYLOID PRECURSOR PROTEIN 695 ISOFORM.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RX [1]
RP SEQUENCE FROM N.A.
RA Sarasa M., Rodolosse A., Sorribas V.;
RT "Cloning of full-length chicken beta-amyloid precursor protein
RT isoforms.";

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RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF289218; AAG00593.1; -.  
 DR HSSP: P05067; 1BA4.  
 DR InterPro: IPR001868; A4\_APP.  
 DR Pfam: PF02177; A4\_EXTRA; 1.  
 DR PRINTS: PR00203; AMYLOIDA4.  
 DR SMART: SM00006; A4\_EXTRA; 1.  
 DR PROSITE: PS00319; A4\_EXTRA; 1.  
 SQ SEQUENCE 695 AA; 78565 MW; F201ED02AEC6ED95 CRC64;

Query Match 100.0%; Score 53; DB 13; Length 695;  
 Best Local Similarity 100.0%; Pred. NO. 0.022;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EVKMDAEFRH 10  
 |||||  
 DB 593 EVKMDAEFRH 602

RESULT 10  
 ID 09DGI7 PRELIMINARY; PRT; 751 AA.

AC 09DGI7; 01-MAR-2001 (TREMBlrel. 16, Created)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE BETA-AMYLOID PRECURSOR PROTEIN 751 ISOFORM.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Sarasa M., Rodolosse A., Sorribas V.:  
 RT "Cloning of full-length chicken beta-amyloid precursor protein  
 isoforms.";  
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF289219; AAG00594.1; -.  
 DR HSSP: P05067; 1BA4.  
 DR InterPro: IPR001868; A4\_APP.  
 DR InterPro: IPR002223; Kunitz\_BPTI.  
 DR Pfam: PF02177; A4\_EXTRA; 1.  
 DR Pfam: PF00014; Kunitz\_BPTI; 1.  
 DR PRINTS: PR00203; AMYLOIDA4.  
 DR PRINTS: PR00759; BASICPTASE.  
 DR SMART: SM00006; A4\_EXTRA; 1.  
 DR SMART: SM00131; KU; 1.  
 DR PROSITE: PS00280; BPTI\_KUNITZ\_1; 1.  
 DR PROSITE: PS0279; BPTI\_KUNITZ\_2; 1.  
 KW Serine protease inhibitor.  
 SQ SEQUENCE 751 AA; 84705 MW; E78E9A13A8033D84 CRC64;

Query Match 100.0%; Score 53; DB 13; Length 751;  
 Best Local Similarity 100.0%; Pred. NO. 0.023;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EVKMDAEFRH 10  
 |||||  
 DB 649 EVKMDAEFRH 658

RESULT 11

ID 09TUI0 PRELIMINARY; PRT; 770 AA.

AC 09TUI0; 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE AMYLOID PRECURSOR PROTEIN.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OX NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kimura A., Takahashi T.:  
 RT "Amyloid Precursor Protein 770.";  
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AB032550; BAA84580.1; -.  
 DR HSSP: P05067; 1AAP.  
 DR InterPro: IPR001868; A4\_APP.  
 DR InterPro: IPR002223; Kunitz\_BPTI.  
 DR Pfam: PF02177; A4\_EXTRA; 1.  
 DR Pfam: PF00014; Kunitz\_BPTI; 1.  
 DR PRINTS: PR00203; AMYLOIDA4.  
 DR PRINTS: PR00759; BASICPTASE.  
 DR SMART: SM00006; A4\_EXTRA; 1.  
 DR SMART: SM00131; KU; 1.  
 DR PROSITE: PS00319; A4\_EXTRA; 1.  
 DR PROSITE: PS00320; A4\_INTRA; 1.  
 DR PROSITE: PS00280; BPTI\_KUNITZ\_1; 1.  
 DR PROSITE: PS0279; BPTI\_KUNITZ\_2; 1.  
 KW Serine protease inhibitor.  
 SQ SEQUENCE 770 AA; 86961 MW; 5F7A1DCB2BCC583E CRC64;

Query Match 100.0%; Score 53; DB 6; Length 770;  
 Best Local Similarity 100.0%; Pred. NO. 0.024;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EVKMDAEFRH 10  
 |||||  
 DB 668 EVKMDAEFRH 677

RESULT 12

ID 098SG0 PRELIMINARY; PRT; 693 AA.

AC 098SG0; 01-JUN-2001 (TREMBlrel. 17, Created)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE BETA-AMYLOID PRECURSOR PROTEIN A.  
 GN APP.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Van den Hurk W.H.;  
 RL Thesis (2001), Department of Biological Sciences,  
 University of Nijmegen, Nijmegen, Netherlands.  
 DR EMBL: AJ298150; CAC37193.1; -.  
 DR HSSP: P05067; 1H23.  
 DR InterPro: IPR001868; A4\_APP.  
 DR Pfam: PF02177; A4\_EXTRA; 1.  
 DR PRINTS: PR00203; AMYLOIDA4.  
 DR SMART: SM00006; A4\_EXTRA; 1.  
 DR PROSITE: PS00319; A4\_EXTRA; 1.  
 DR PROSITE: PS00320; A4\_INTRA; 1.  
 KW Signal.  
 FT SIGNAL  
 FT SIGNAL  
 SQ SEQUENCE 693 AA; 78568 MW; CAF1DF655C1AB653 CRC64;

Query Match 88.7%; Score 47; DB 13; Length 693;  
 Best Local Similarity 80.0%; Pred. NO. 0.36;  
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 EVKMDAEFRH 10  
 |||||  
 DB 591 EVKMDSEFRH 600

RESULT 13

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098SF9          PRELIMINARY;      PRT;      695 AA.
ID 098SF9
AC 098SF9;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE BETA-AMYLOID PRECURSOR PROTEIN B.
GN APP.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Van den Hurk W.H.;
RL Thesis (2001), Department of Biological Sciences,
RL University of Nijmegen, Nijmegen, Netherlands.
DR EMBL: AJ298151; CAC37194.1; -.
DR HSSP: P05067.1H23.
DR InterPro: IPR001868; A4_APP.
DR Pfam: PF02177; A4_EXTRA; 1.
DR PRINTS: PR00203; AMYLOIDA.
DR SMART: SM00006; A4_EXTRA; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
KW SIGNAL.
FT SIGNAL.
SQ SEQUENCE 695 AA; 78603 MW; DC14EB02AFB0204A CRC64;

Query Match      88.7%; Score 47; DB 13; Length 695;
Best Local Similarity 80.0%; Pred. No. 0.36;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 EVKMDAEFRH 10
   |||||:|:|
Db 593 EVKMDSEYRH 602

RESULT 14
091963          PRELIMINARY;      PRT;      747 AA.
ID 091963
AC 091963;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE APP747.
GN APP747.
OS Xenopus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae.
OX NCBI_TaxID=8353;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93129227; PubMed=1282805;
RA Okada H., Okamoto H.;
RT "A Xenopus homologue of the human beta-amyloid precursor protein:
RT developmental regulation of its gene expression.";
RL Biochem. Biophys. Res. Commun. 189:1561-1568(1992).
DR EMBL: S52417; AAB24853.1; -.
DR HSSP: P05067.1H23.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR PRINTS: PR00203; AMYLOIDA.
DR PRINTS: PR00759; BASICPTASE.
DR SMART: SM00006; A4_EXTRA; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.

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DR PROSITE: PS00279; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor.
SQ SEQUENCE 747 AA; 84893 MW; A75E81885681D948 CRC64;

Query Match      88.7%; Score 47; DB 13; Length 747;
Best Local Similarity 80.0%; Pred. No. 0.39;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 EVKMDAEFRH 10
   |||||:|:|
Db 645 EVKMDSEYRH 654

RESULT 15
035463          PRELIMINARY;      PRT;      79 AA.
ID 035463
AC 035463;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE ALZHEIMER'S AMYLOID BETA PROTEIN (FRAGMENT).
GN BETA APP.
OS Cricetus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetulus.
OX NCBI_TaxID=10029;
RN [1]
RP SEQUENCE FROM N.A.
RA Sambamurti K., Pinnix I., Gandhi S.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF030413; AAB86608.1; -.
DR HSSP: P05067.1BA4.
FT NON_TER
FT NON_TER
SQ SEQUENCE 79 AA; 8538 MW; 37F2CC63BFF3F597 CRC64;

Query Match      86.8%; Score 46; DB 11; Length 79;
Best Local Similarity 90.0%; Pred. No. 0.059;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 EVKMDAEFRH 10
   |||||:|:|
Db 17 EVKMDSEYRH 26

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Search completed: October 29, 2002, 10:29:42  
 Job time : 19.1429 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 29, 2002, 10:23:56 : Search time 9 Seconds  
(without alignments)  
27.140 Million cell updates/sec

Title: US-09-580-018-5  
Perfect score: 53  
Sequence: 1 EVKMDAEFRH 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PTUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfilest1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	100.0	12	5	PCT-US94-07043A-2
2	53	100.0	16	5	PCT-US94-07043A-1
3	53	100.0	27	1	US-08-141-374-11
4	53	100.0	27	1	US-08-541-902-11
5	53	100.0	45	1	US-08-462-859A-5
6	53	100.0	45	1	US-08-123-659A-5
7	53	100.0	45	1	US-08-464-247A-5
8	53	100.0	45	1	US-08-464-248A-5
9	53	100.0	58	1	US-08-371-930-25
10	53	100.0	58	5	PCT-US94-01712-25
11	53	100.0	59	1	US-08-484-969-3
12	53	100.0	59	1	US-08-472-627-3
13	53	100.0	59	1	US-08-388-453-3
14	53	100.0	63	1	US-08-462-859A-3
15	53	100.0	63	1	US-08-462-859A-4
16	53	100.0	63	1	US-08-123-659A-4
17	53	100.0	63	1	US-08-123-659A-4
18	53	100.0	63	1	US-08-464-247A-3
19	53	100.0	63	1	US-08-464-247A-4
20	53	100.0	63	1	US-08-464-248A-3
21	53	100.0	63	1	US-08-464-248A-4
22	53	100.0	103	2	US-08-404-831-2
23	53	100.0	103	2	US-08-612-785B-2
24	53	100.0	103	2	US-08-475-579A-2
25	53	100.0	103	2	US-08-920-162A-2
26	53	100.0	103	3	US-08-339-708A-10
27	53	100.0	103	4	US-09-356-931-2

28	53	100.0	103	4	US-08-703-675C-2	Sequence 2, Appli
29	53	100.0	103	4	US-08-617-267C-2	Sequence 2, Appli
30	53	100.0	105	2	US-08-729-345-1	Sequence 1, Appli
31	53	100.0	117	2	US-08-729-345-3	Sequence 3, Appli
32	53	100.0	152	6	5187153-4	Patent No. 5187153
33	53	100.0	162	6	5220013-4	Patent No. 5220013
34	53	100.0	162	6	5223482-4	Patent No. 5223482
35	53	100.0	264	1	US-07-990-893-5	Sequence 5, Appli
36	53	100.0	487	1	US-08-462-859A-9	Sequence 9, Appli
37	53	100.0	487	1	US-08-123-659A-9	Sequence 9, Appli
38	53	100.0	487	1	US-08-464-247A-9	Sequence 9, Appli
39	53	100.0	487	1	US-08-464-248A-9	Sequence 9, Appli
40	53	100.0	492	1	US-08-462-859A-7	Sequence 7, Appli
41	53	100.0	492	1	US-08-123-659A-7	Sequence 7, Appli
42	53	100.0	492	1	US-08-464-247A-7	Sequence 7, Appli
43	53	100.0	492	1	US-08-464-248A-7	Sequence 7, Appli
44	53	100.0	537	1	US-08-453-552-4	Sequence 4, Appli
45	53	100.0	537	2	US-08-710-637-4	Sequence 4, Appli

## ALIGNMENTS

RESULT 1  
PCT-US94-07043A-2  
Sequence 2, Application PC/TUS9407043A  
GENERAL INFORMATION:  
APPLICANT: Tamburini, Paul P.; Benz, G nter; H bich,  
APPLICANT: Dieter; Dreyer, Robert N.; Koehnig, Gerhard  
TITLE OF INVENTION: CATHEPSIN D IS AN AMYLOIDGENIC  
TITLE OF INVENTION: PROTEASE IN ALZHEIMER S DISEASE  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Miles Inc.  
STREET: 400 Morgan Lane  
CITY: West Haven  
STATE: Connecticut  
COUNTRY: USA  
ZIP: 06516  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 800 kb storage  
COMPUTER: Sharp PC 4600  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/07043A  
FILING DATE: June 21, 1994  
CLASSIFICATION:  
APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/10889  
FILING DATE: November 12, 1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/995,660  
FILING DATE: December 16, 1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/880,914  
FILING DATE: May 11, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Pamela A. Simonon  
REGISTRATION NUMBER: 31,060  
REFERENCE/DOCKET NUMBER: MTI 224.3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (203) 937-2340  
TELEFAX: (203) 937-2795  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
PCT-US94-07043A-2  
Query Match 100.0%; Score 53; DB 5; Length 12;  
Best local Similarity 100.0%; Pred. No. 0.00016;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMDAEFRH 10  
 |||||  
 Db 3 EVKMDAEFRH 12

## RESULT 2

PCT-US94-07043A-1  
 ; Sequence 1, Application PC/TUS9407043A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Tamburini, Paul P.; Benz, G nter; H bich,  
 ; APPLICANT: Dieter; Dreyer, Robert N.; Koenig, Gerhard  
 ; TITLE OF INVENTION: CATHEPSIN D IS AN AMYLOIDGENIC  
 ; TITLE OF INVENTION: PROTEASE IN ALZHEIMER S DISEASE  
 ; NUMBER OF SEQUENCES: 11  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Miles Inc.  
 ; STREET: 400 Morgan Lane  
 ; CITY: West Haven  
 ; STATE: Connecticut  
 ; COUNTRY: USA  
 ; ZIP: 06516  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette, 3.50 inch, 800 kb storage  
 ; COMPUTER: Sharp PC 4600  
 ; OPERATING SYSTEM: MS-DOS  
 ; SOFTWARE: Wordperfect 5.1  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US94/07043A  
 ; FILING DATE: June 21, 1994  
 ; CLASSIFICATION:  
 ; PRIORITY APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US93/10889  
 ; FILING DATE: November 12, 1993  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 07/995,660  
 ; FILING DATE: December 16, 1992  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 07/880,914  
 ; FILING DATE: May 11, 1992  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Pamela A. Simonton  
 ; REGISTRATION NUMBER: 31,060  
 ; REFERENCE/DOCKET NUMBER: WTI 224.3  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (203) 937-2340  
 ; TELEFAX: (203) 937-2795  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 16 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; PCT-US94-07043A-1  
 ;  
 ; Query Match 100.0%; Score 53; DB 5; Length 16;  
 ; Best Local Similarity 100.0%; Pred. No. 0.00021;  
 ; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMDAEFRH 10  
 |||||  
 Db 3 EVKMDAEFRH 12

## RESULT 3

US-08-141-324-11  
 ; Sequence 11, Application US/08141324  
 ; Patent No. 5475097  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Travls, James  
 ; APPLICANT: Potempa, Jan S.  
 ; APPLICANT: Barr, Philip J.  
 ; APPLICANT: Pavloff, Nadine

APPLICANT: Pike, Robert N.  
 ; TITLE OF INVENTION: Lysine-specific Porphyromonas gingivalis  
 ; TITLE OF INVENTION: Protease  
 ; NUMBER OF SEQUENCES: 28  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Greenlee and Winner, P.C.  
 ; STREET: 5370 Manhattan Circle, Suite 201  
 ; CITY: Boulder  
 ; STATE: CO  
 ; COUNTRY: US

ZIP: 80303

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/141,324

FILING DATE: 21-OCT-1993

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Ferber, Donna M.

REGISTRATION NUMBER: 33,878

REFERENCE/DOCKET NUMBER: 44-93

TELECOMMUNICATION INFORMATION:

TELEPHONE: 303-499-8080

TELEFAX: 303-499-8089

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 27 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHEICAL: NO

ANTI-SENSE: NO

## Query Match

Best Local Similarity 100.0%; Score 53; DB 1; Length 27;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMDAEFRH 10  
 |||||  
 Db 5 EVKMDAEFRH 14

## RESULT 4

US-08-541-902-11  
 ; Sequence 11, Application US/08541902  
 ; Patent No. 5707620  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Travls, James  
 ; APPLICANT: Potempa, Jan S.  
 ; APPLICANT: Barr, Philip J.  
 ; APPLICANT: Pavloff, Nadine  
 ; APPLICANT: Pike, Robert N.  
 ; TITLE OF INVENTION: Lysine-specific Porphyromonas gingivalis  
 ; TITLE OF INVENTION: Protease  
 ; NUMBER OF SEQUENCES: 28  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Greenlee and Winner, P.C.  
 ; STREET: 5370 Manhattan Circle, Suite 201  
 ; CITY: Boulder  
 ; STATE: CO  
 ; COUNTRY: US  
 ; ZIP: 80303  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:



APPLICATION NUMBER: US/08/541,902  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/141,324  
FILING DATE: 21-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Felder, Donna M.  
REGISTRATION NUMBER: 33,878  
REFERENCE/DOCKET NUMBER: 44-93  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 303-499-8080  
TELEFAX: 303-499-8089  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-541-902-11

Query Match 100.0%; Score 53; DB 1; Length 27;  
Best Local Similarity 100.0%; Pred. No. 0.00037;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMDAEFRH 10  
Db 5 EVKMDAEFRH 14

RESULT 5  
US-08-462-859A-5  
Sequence 5, Application US/08462859A  
Patent No. 5652092  
GENERAL INFORMATION:  
APPLICANT: Jacobsen, J. S.  
TITLE OF INVENTION: NO. 5652092el Amyloid Precursor and Method of  
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation  
of B-Amyloid Peptide  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: American Cyanamid Company  
STREET: One Cyanamid Plaza  
CITY: Wayne  
STATE: New Jersey  
COUNTRY: United States  
ZIP: 07470-8426  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/462,859A  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Barnhard, Elizabeth M.  
REGISTRATION NUMBER: 31,088  
REFERENCE/DOCKET NUMBER: 31,844-04  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (201)831-3246  
TELEFAX: (201)831-3305  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 45 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear

MOLECULE TYPE: protein  
US-08-462-859A-5

Query Match 100.0%; Score 53; DB 1; Length 45;  
Best Local Similarity 100.0%; Pred. No. 0.00062;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMDAEFRH 10  
Db 6 EVKMDAEFRH 15

RESULT 6  
US-08-123-659A-5  
Sequence 5, Application US/08123659A  
Patent No. 5656477  
GENERAL INFORMATION:  
APPLICANT: Jacobsen, J. S.  
TITLE OF INVENTION: NO. 5656477el Amyloid Precursor and Method of  
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation  
of B-Amyloid Peptide  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Anne Rosenblum  
STREET: 163 Delaware Avenue, Suite 212  
CITY: Delmar  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 12054  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/123,659A  
FILING DATE: 20-SEP-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Rosenblum, Anne M.  
REGISTRATION NUMBER: 30,419  
REFERENCE/DOCKET NUMBER: 31,844-01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (518)475-0611  
TELEFAX: (518)475-0619  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 45 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-123-659A-5

Query Match 100.0%; Score 53; DB 1; Length 45;  
Best Local Similarity 100.0%; Pred. No. 0.00062;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMDAEFRH 10  
Db 6 EVKMDAEFRH 15

RESULT 7  
US-08-464-247A-5  
Sequence 5, Application US/08464247A  
Patent No. 5693478  
GENERAL INFORMATION:  
APPLICANT: Jacobsen, J. S.  
TITLE OF INVENTION: NO. 5693478el Amyloid Precursor and Method of  
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation  
of B-Amyloid Peptide

NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: American Cyanamid Company  
STREET: One Campus Drive  
CITY: Parsippany  
STATE: New Jersey  
COUNTRY: United States  
ZIP: 07054  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/464,247A  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Barnhard, Elizabeth M.  
REGISTRATION NUMBER: 31,088  
REFERENCE/DOCKET NUMBER: 31,844-03  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-683-2158  
TELEFAX: 201-683-4117  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 45 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-464-247A-5

Query Match 100.0%; Score 53; DB 1; Length 45;  
Best Local Similarity 100.0%; Pred. No. 0.00062;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMDAEFRH 10  
Db 6 EVKMDAEFRH 15

RESULT 8  
US-08-464-248A-5  
Sequence 5, Application US/08464248A  
Patent No. 5703209  
GENERAL INFORMATION:  
APPLICANT: Jacobsen, J. S.  
APPLICANT: Vittek, M. P.  
TITLE OF INVENTION: No. 5703209el Amyloid Precursor and Method of  
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation  
TITLE OF INVENTION: of B-Amyloid Peptide  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: American Cyanamid Company  
STREET: One Cyanamid Plaza  
CITY: Wayne  
STATE: New Jersey  
COUNTRY: United States  
ZIP: 07470-8426  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/464,248A  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Barnhard, Elizabeth M.  
REGISTRATION NUMBER: 31,088  
REFERENCE/DOCKET NUMBER: 31,844-02

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (201)831-3246  
TELEFAX: (201)831-3305  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 45 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-464-248A-5

Query Match 100.0%; Score 53; DB 1; Length 45;  
Best Local Similarity 100.0%; Pred. No. 0.00062;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMDAEFRH 10  
Db 6 EVKMDAEFRH 15

RESULT 9  
US-08-371-930-25  
Sequence 25, Application US/08371930  
Patent No. 5578451  
GENERAL INFORMATION:  
APPLICANT: Nishimoto, Ikuro  
TITLE OF INVENTION: ALZHEIMER'S DISEASE THERAPEUTICS  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
COMPUTER: IBM PS/2 Model 502 or 55SX  
OPERATING SYSTEM: MS-DOS (Version 5.0)  
SOFTWARE: Wordperfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/371,930  
FILING DATE:  
CLASSIFICATION: 436  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/019,208  
FILING DATE: February 18, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 00786/154001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 58  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-371-930-25

Query Match 100.0%; Score 53; DB 1; Length 58;  
Best Local Similarity 100.0%; Pred. No. 0.00061;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMDAEFRH 10  
Db 43 EVKMDAEFRH 52

RESULT 10  
PCT-US94-01712-25  
Sequence 25, Application PC/TUS9401712  
GENERAL INFORMATION:  
APPLICANT: Nishimoto, Ikuro  
TITLE OF INVENTION: ALZHEIMER'S DISEASE THERAPEUTICS  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM PS/2 Model 502 or 555x  
OPERATING SYSTEM: MS-DOS (Version 5.0)  
SOFTWARE: Wordperfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/01712  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/019,208  
FILING DATE: February 18, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 00786/154001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154  
INFORMATION FOR SEQ. ID NO.: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 58  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
PCT-US94-01712-25  
Query Match 100.0%; Score 53; DB 5; Length 58;  
Best Local Similarity 100.0%; Pred. No. 0.00081;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EVKMDAEFRH 10  
DB 43 EVKMDAEFRH 52

RESULT 11  
US-08-484-969-3  
Sequence 3, Application US/08484969  
Patent No. 5679531  
GENERAL INFORMATION:  
APPLICANT: Konig, Gerhard  
APPLICANT: Graham, Paul  
TITLE OF INVENTION: Monoclonal Antibody Specific for BA4  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Allegretti & Witcoff, Ltd.  
STREET: 10 South Wacker Drive Suite 3000  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,969  
FILING DATE:  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: McDonnell, John J  
REGISTRATION NUMBER: 26,949  
REFERENCE/DOCKET NUMBER: 95,216  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-715-1000  
TELEFAX: 312-715-1234  
INFORMATION FOR SEQ. ID NO.: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 59 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Cleavage-site  
LOCATION: 4..5  
OTHER INFORMATION: /label= Beta  
OTHER INFORMATION: /note= "Beta cleavage site in App"  
FEATURE:  
NAME/KEY: Cleavage-site  
LOCATION: 20..21  
OTHER INFORMATION: /label= Alpha  
OTHER INFORMATION: /note= "Alpha cleavage site in App, residues 16/17"  
FEATURE:  
NAME/KEY: Cleavage-site  
LOCATION: 46..47  
OTHER INFORMATION: /label= Gamma  
OTHER INFORMATION: /note= "Gamma cleavage site in App"  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 5..47  
OTHER INFORMATION: /label= BA4  
OTHER INFORMATION: /note= "BA4 peptide"  
FEATURE:  
NAME/KEY: Region  
LOCATION: 33..56  
OTHER INFORMATION: /label= Tm  
OTHER INFORMATION: /note= "Transmembrane region of App"  
FEATURE:  
NAME/KEY: Region  
LOCATION: 1..32  
OTHER INFORMATION: /label= Ex  
OTHER INFORMATION: /note= "N-terminal extracellular part of App"  
US-08-484-969-3  
Query Match 100.0%; Score 53; DB 1; Length 59;  
Best Local Similarity 100.0%; Pred. No. 0.00082;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EVKMDAEFRH 10  
DB 1 EVKMDAEFRH 10

RESULT 12  
US-08-472-627-3  
Sequence 3, Application US/08472627  
Patent No. 5693753  
GENERAL INFORMATION:  
APPLICANT: Konig, Gerhard  
APPLICANT: Graham, Paul  
TITLE OF INVENTION: Monoclonal Antibody Specific for BA4  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Allegretti & Witcoff, Ltd.  
STREET: 10 South Wacker Drive Suite 3000

CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/472,627  
FILING DATE:  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: McDowell, John J  
REGISTRATION NUMBER: 26,949  
REFERENCE/DOCKET NUMBER: 95,216  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-715-1234  
TELEFAX: 312-715-1000  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 59 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Cleavage-site  
LOCATION: 4..5  
OTHER INFORMATION: /label= Beta  
OTHER INFORMATION: /note= "Beta cleavage site in App"  
FEATURE:  
NAME/KEY: Cleavage-site  
LOCATION: 20..21  
OTHER INFORMATION: /label= Alpha  
OTHER INFORMATION: /note= "Alpha cleavage site in App, residues 16/17"  
FEATURE:  
NAME/KEY: Cleavage-site  
LOCATION: 46..47  
OTHER INFORMATION: /label= Gamma  
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NAME/KEY: Peptide  
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FEATURE:  
NAME/KEY: Region  
LOCATION: 33..56  
OTHER INFORMATION: /label= Tm  
OTHER INFORMATION: /note= "Transmembrane region of App"  
FEATURE:  
NAME/KEY: Region  
LOCATION: 1..32  
OTHER INFORMATION: /label= Ex  
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US-08-472-627-3  
Query Match 100.0%; Score 53; DB 1; Length 59;  
Best Local Similarity 100.0%; Pred. No. 0.00082;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 EVKMDAEFRH 10  
Db 1 EVKMDAEFRH 10

RESULT 13  
US-08-388-463-3  
Sequence 3, Application US/08388463  
Patent No. 5786180

GENERAL INFORMATION:  
APPLICANT: Konig, Gerhard  
TITLE OF INVENTION: Monoclonal Antibody Specific for BA4  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Allegretti & Witcoff, Ltd.  
STREET: 10 South Wacker Drive Suite 3000  
CITY: Chicago  
STATE: Illinois  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/388,463  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: McDowell, John J  
REGISTRATION NUMBER: 26,949  
REFERENCE/DOCKET NUMBER: 95,216  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-715-1000  
TELEFAX: 312-715-1234  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 59 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Cleavage-site  
LOCATION: 4..5  
OTHER INFORMATION: /label= Beta  
OTHER INFORMATION: /note= "Beta cleavage site in App"  
FEATURE:  
NAME/KEY: Cleavage-site  
LOCATION: 20..21  
OTHER INFORMATION: /label= Alpha  
OTHER INFORMATION: /note= "Alpha cleavage site in App, residues 16/17"  
FEATURE:  
NAME/KEY: Cleavage-site  
LOCATION: 46..47  
OTHER INFORMATION: /label= Gamma  
OTHER INFORMATION: /note= "Gamma cleavage site in App"  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 5..47  
OTHER INFORMATION: /label= BA4  
OTHER INFORMATION: /note= "BA4 peptide"  
FEATURE:  
NAME/KEY: Region  
LOCATION: 33..56  
OTHER INFORMATION: /label= Tm  
OTHER INFORMATION: /note= "Transmembrane region of App"  
FEATURE:  
NAME/KEY: Region  
LOCATION: 1..32  
OTHER INFORMATION: /label= Ex  
OTHER INFORMATION: /note= "N-terminal extracellular part of App"  
US-08-388-463-3  
Query Match 100.0%; Score 53; DB 1; Length 59;  
Best Local Similarity 100.0%; Pred. No. 0.00082;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EVKMDAEFRH 10  
|||||  
DB 1 EVKMDAEFRH 10

RESULT 14  
US-08-462-859A-3  
; Sequence 3, Application US/08462859A  
; Patent No. 5652092

GENERAL INFORMATION:

APPLICANT: Vittek, M. P. S.  
TITLE OF INVENTION: NO. 5652092el Amyloid Precursor and Method of  
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation  
TITLE OF INVENTION: of B-Amyloid Peptide  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: American Cyanamid Company  
STREET: One Cyanamid Plaza  
CITY: Wayne  
STATE: New Jersey  
COUNTRY: United States  
ZIP: 07470-8426

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/462,859A  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: Barnhard, Elizabeth M.  
REGISTRATION NUMBER: 31,088  
REFERENCE/DOCKET NUMBER: 31,844-04  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (201)831-3246  
TELEFAX: (201)831-3305

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:  
LENGTH: 63 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-462-859A-3

Query Match 100.0%; Score 53; DB 1; Length 63;

Best Local Similarity 100.0%; Pred. No. 0.00088;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EVKMDAEFRH 10  
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DB 6 EVKMDAEFRH 15

RESULT 15  
US-08-462-859A-4

; Sequence 4, Application US/08462859A  
; Patent No. 5652092

GENERAL INFORMATION:

APPLICANT: Jacobsen, J. S.  
TITLE OF INVENTION: NO. 5652092el Amyloid Precursor and Method of  
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation  
TITLE OF INVENTION: of B-Amyloid Peptide  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: American Cyanamid Company  
STREET: One Cyanamid Plaza  
CITY: Wayne  
STATE: New Jersey

COUNTRY: United States  
ZIP: 07470-8426

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/462,859A  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: Barnhard, Elizabeth M.  
REGISTRATION NUMBER: 31,088  
REFERENCE/DOCKET NUMBER: 31,844-04  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (201)831-3246  
TELEFAX: (201)831-3305

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:  
LENGTH: 63 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-462-859A-4

Query Match 100.0%; Score 53; DB 1; Length 63;

Best Local Similarity 100.0%; Pred. No. 0.00088;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EVKMDAEFRH 10  
|||||  
DB 6 EVKMDAEFRH 15

Search completed: October 29, 2002, 10:32:07  
Job time : 9 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: October 29, 2002, 10:22:21 ; Search time 23.1429 Seconds  
(without alignments)  
47.995 Million cell updates/sec

Title: US-09-580-018-6

Perfect score: 54  
Sequence: 1 VKMAEPRHD 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

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2: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:\*  
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5: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:\*  
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7: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:\*  
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22: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	10	22	AAAB46210
2	54	100.0	16	21	AAAB06315
3	54	100.0	16	21	AAAB06317
4	54	100.0	18	16	AAAR75696
5	54	100.0	18	22	AAAE00608
6	54	100.0	19	12	AAAR14135
7	54	100.0	20	21	AAAB69713
8	54	100.0	33	20	AAAB96002
9	54	100.0	39	21	AAAB69717
10	54	100.0	45	18	AAAW26512
11	54	100.0	45	18	AAAW26392

12 54 100.0 45 19 AAAB4748  
13 54 100.0 45 19 AAAB2977  
14 54 100.0 48 22 AAAB37523  
15 54 100.0 53 15 AAAR55695  
16 54 100.0 53 15 AAAR55696  
17 54 100.0 53 15 AAAR55697  
18 54 100.0 53 16 AAAR64168  
19 54 100.0 54 21 AAAB32126  
20 54 100.0 57 21 AAAB10910  
21 54 100.0 58 17 AAAR58937  
22 54 100.0 59 17 AAAB05375  
23 54 100.0 59 19 AAAB70863  
24 54 100.0 59 22 AAAB84425  
25 54 100.0 60 21 AAAB69701  
26 54 100.0 63 18 AAAB26511  
27 54 100.0 63 18 AAAB26391  
28 54 100.0 63 19 AAAB47477  
29 54 100.0 63 19 AAAB47476  
30 54 100.0 63 19 AAAB42975  
31 54 100.0 63 19 AAAB42976  
32 54 100.0 67 19 AAAB71377  
33 54 100.0 93 22 ABG19083  
34 54 100.0 103 16 AAAB74697  
35 54 100.0 103 20 AAAB51317  
36 54 100.0 103 20 AAAB69372  
37 54 100.0 103 21 AAAB56103  
38 54 100.0 103 22 AAAB2509  
39 54 100.0 104 19 AAAB51100  
40 54 100.0 112 17 AAAB3556  
41 54 100.0 115 20 AAAB97999  
42 54 100.0 117 19 AAAB51102  
43 54 100.0 162 9 AAAB8151  
44 54 100.0 162 12 AAAB10023  
45 54 100.0 162 14 AAAB37863

#### ALIGNMENTS

RESULT 1  
ID AAB46210 standard; peptide: 10 AA.  
AC AAB46210;

04-APR-2001 (first entry)

Human APP derived immunogenic peptide #6.

Human APP deposit; APP; Abeta; brain; human; clearing response; nootropic;  
Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;  
amyloid precursor protein; Alzheimer's disease.

Homo sapiens.

W0200072880-A2.

07-DEC-2000.

26-MAY-2000; 2000WO-US14810.

28-MAY-1999; 99US-0322289.

(NEUR-) NEURALAB LTD.

Schenk DB, Bard F, Vasquez NJ, Yednock T;

WPI; 2001-032104/04.

Preventing or treating a disease associated with amyloid deposits,  
especially Alzheimer's disease, comprises administering amyloid  
specific antibody -

PS Disclosure; Figure 19; 143pp; English.

CC This invention describes a novel method of preventing or treating a

CC disease associated with amyloid deposits of amyloid precursor protein

CC (APP) Abeta fragments in the brain of a patient, which comprises

CC administering to the patient: (a) an antibody that binds to Abeta, the

CC antibody binds to an amyloid deposit and induces a clearing response (Fc

CC receptor mediated phagocytosis) against it (b) a polypeptide containing

CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent

CC that induces an immunogenic response against residues 1-3 to 7-11 of

CC Abeta. The products of the invention have neurotropic and neuroprotective

CC activity. The method is also useful for monitoring a course of treatment

CC being administered to a patient e.g. active and passive immunization. The

CC methods are useful for prophylactic and therapeutic treatment of

CC Alzheimer's disease.

XX Sequence 10 AA:

QY Query Match 100.0%; Score 54; DB 22; Length 10;

Db Best Local Similarity 100.0%; Pred. No. 0.00024;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VKMDAEFRHD 10

Db 1 VKMDAEFRHD 10

RESULT 2

AAB06315

ID AAB06315 standard; peptide; 16 AA.

XX AAB06315;

AC AAB06315;

XX 03-OCT-2000 (first entry)

DT 03-OCT-2000 (first entry)

XX Human beta-amyloid precursor protein beta-secretase cleavage site.

DE Human beta-amyloid precursor protein; beta-APP; beta-secretase;

XX Human; beta-amyloid precursor protein; beta-APP; beta-secretase;

KW Subtilisin-kexin isoenzyme 1; SKI-1;

KM pro-brain-derived neurotrophic factor; proBDNF; antilipemic;

KW cytosolic; vasotropic; SKI-1 inhibitor; hypercholesterolaemia;

KM liver steatosis; Ras-dependent cancer; restenosis;

KW amyloid protein formation.

XX Homo sapiens.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Cleavage-site 8..9

XX WO200026348-A2.

PN WO200026348-A2.

XX 11-MAY-2000.

PD 11-MAY-2000.

XX 04-NOV-1999; 99WO-CA01058.

PF 04-NOV-1999; 99WO-CA01058.

XX 04-NOV-1998; 98CA-2249648.

PR 04-NOV-1998; 98CA-2249648.

XX (RECL-) INST RECH CLINIQUES MONTREAL.

PA (RECL-) INST RECH CLINIQUES MONTREAL.

XX Seidah N, Chretien M, Marcinkiewicz M, Laaksonen R, Davignon J;

PI Seidah N, Chretien M, Marcinkiewicz M, Laaksonen R, Davignon J;

XX WPI; 2000-365601/31.

DR WPI; 2000-365601/31.

XX Novel soluble proteic fragment of subtilisin-kexin isoenzyme for

PT producing a polypeptide useful for treating hypercholesterolemia, liver

PT steatosis and amyloidosis, comprises a specific amino acid sequence -

XX Example 4; Page 51; 119pp; English.

PS The present sequence is the beta-secretase site of human beta-amyloid

XX precursor protein (beta-APP). The sequence may be cleaved

CC by a mammalian subtilase, specifically subtilisin-kexin isoenzyme 1

CC (SKI-1), a type-I membrane-bound proteinase. Peptides which bind to and

CC are cleaved by SKI-1 may be used for monitoring SKI-1 activity, for

CC screening inhibitors of SKI-1 activity, or for screening enhancers of

CC SKI-1 activity. Proteic fragments of SKI-1 which bind to the SKI-1

CC catalytic site may be used as inhibitors of SKI-1 activity. They may be

CC used to treat diseases involving overexpression of SKI-1 or SKI-1

CC substrate. Such diseases include hypercholesterolaemia, high levels of

CC fatty acids, lipids or farnesyl pyrophosphate, liver steatosis,

CC Ras-dependent cancer, restenosis and amyloid protein formation.

XX Sequence 16 AA:

QY Query Match 100.0%; Score 54; DB 21; Length 16;

Db Best Local Similarity 100.0%; Pred. No. 0.0004;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VKMDAEFRHD 10

Db 6 VKMDAEFRHD 15

RESULT 3

AAB06317

ID AAB06317 standard; peptide; 16 AA.

XX AAB06317;

AC AAB06317;

XX 03-OCT-2000 (first entry)

DT 03-OCT-2000 (first entry)

XX Human beta-amyloid precursor protein beta-epsilont-secretase site.

DE Human beta-amyloid precursor protein beta-epsilont-secretase site.

XX Human; beta-amyloid precursor protein; beta-APP;

KW beta-epsilont-secretase; subtilisin-kexin isoenzyme 1; SKI-1;

KM pro-brain-derived neurotrophic factor; proBDNF; antilipemic;

KW cytosolic; vasotropic; SKI-1 inhibitor; hypercholesterolaemia;

KM liver steatosis; Ras-dependent cancer; restenosis;

KW amyloid protein formation.

XX Homo sapiens.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Cleavage-site 8..9

XX WO200026348-A2.

PN WO200026348-A2.

XX 11-MAY-2000.

PD 11-MAY-2000.

XX 04-NOV-1999; 99WO-CA01058.

PF 04-NOV-1999; 99WO-CA01058.

XX 04-NOV-1998; 98CA-2249648.

PR 04-NOV-1998; 98CA-2249648.

XX (RECL-) INST RECH CLINIQUES MONTREAL.

PA (RECL-) INST RECH CLINIQUES MONTREAL.

XX Seidah N, Chretien M, Marcinkiewicz M, Laaksonen R, Davignon J;

PI Seidah N, Chretien M, Marcinkiewicz M, Laaksonen R, Davignon J;

XX WPI; 2000-365601/31.

DR WPI; 2000-365601/31.

XX Novel soluble proteic fragment of subtilisin-kexin isoenzyme for

PT producing a polypeptide useful for treating hypercholesterolemia, liver

PT steatosis and amyloidosis, comprises a specific amino acid sequence -

XX Example 4; Page 51; 119pp; English.

PS The present sequence is the beta-epsilont-secretase site of human

XX beta-amyloid precursor protein (beta-APP). The sequence may be cleaved

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CC (SKI-1), a type-I membrane-bound proteinase. Peptides which bind to and

CC are cleaved by SKI-1 may be used for monitoring SKI-1 activity, for

CC screening inhibitors of SKI-1 activity, or for screening enhancers of

CC SKI-1 activity. Proteic fragments of SKI-1 which bind to the SKI-1

CC catalytic site may be used as inhibitors of SKI-1 activity. They may be

CC used to treat diseases involving overexpression of SKI-1 or SKI-1

CC substrate. Such diseases include hypercholesterolaemia, high levels of

CC fatty acids, lipids or farnesyl pyrophosphate, liver steatosis,

CC are cleaved by SKI-1 may be used for monitoring SKI-1 activity, for

CC screening inhibitors of SKI-1 activity, or for screening enhancers of

CC SKI-1 activity. Proteic fragments of SKI-1 which bind to the SKI-1

CC catalytic site may be used as inhibitors of SKI-1 activity. They may be

CC used to treat diseases involving overexpression of SKI-1 or SKI-1

CC substrate. Such diseases include hypercholesterolaemia, high levels of

CC fatty acids, lipids or farnesyl pyrophosphate, liver steatosis,

CC Ras-dependent cancer, restenosis and amyloid protein formation.

XX Sequence 16 AA:

QY Query Match 100.0%; Score 54; DB 21; Length 16;

Db Best Local Similarity 100.0%; Pred. No. 0.0004;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VKMDAEFRHD 10

Db 6 VKMDAEFRHD 15

RESULT 3

AAB06317

ID AAB06317 standard; peptide; 16 AA.

XX AAB06317;

AC AAB06317;

XX 03-OCT-2000 (first entry)

DT 03-OCT-2000 (first entry)

XX Human beta-amyloid precursor protein beta-epsilont-secretase site.

DE Human beta-amyloid precursor protein beta-epsilont-secretase site.

XX Human; beta-amyloid precursor protein; beta-APP;

KW beta-epsilont-secretase; subtilisin-kexin isoenzyme 1; SKI-1;

KM pro-brain-derived neurotrophic factor; proBDNF; antilipemic;

KW cytosolic; vasotropic; SKI-1 inhibitor; hypercholesterolaemia;

KM liver steatosis; Ras-dependent cancer; restenosis;

KW amyloid protein formation.

XX Homo sapiens.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Cleavage-site 8..9

XX WO200026348-A2.

PN WO200026348-A2.

XX 11-MAY-2000.

PD 11-MAY-2000.

XX 04-NOV-1999; 99WO-CA01058.

PF 04-NOV-1999; 99WO-CA01058.

XX 04-NOV-1998; 98CA-2249648.

PR 04-NOV-1998; 98CA-2249648.

XX (RECL-) INST RECH CLINIQUES MONTREAL.

PA (RECL-) INST RECH CLINIQUES MONTREAL.

XX Seidah N, Chretien M, Marcinkiewicz M, Laaksonen R, Davignon J;

PI Seidah N, Chretien M, Marcinkiewicz M, Laaksonen R, Davignon J;

XX WPI; 2000-365601/31.

DR WPI; 2000-365601/31.

XX Novel soluble proteic fragment of subtilisin-kexin isoenzyme for

PT producing a polypeptide useful for treating hypercholesterolemia, liver

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XX Example 4; Page 51; 119pp; English.

PS The present sequence is the beta-epsilont-secretase site of human

XX beta-amyloid precursor protein (beta-APP). The sequence may be cleaved

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CC (SKI-1), a type-I membrane-bound proteinase. Peptides which bind to and

CC are cleaved by SKI-1 may be used for monitoring SKI-1 activity, for

CC screening inhibitors of SKI-1 activity, or for screening enhancers of

CC SKI-1 activity. Proteic fragments of SKI-1 which bind to the SKI-1

CC catalytic site may be used as inhibitors of SKI-1 activity. They may be

CC used to treat diseases involving overexpression of SKI-1 or SKI-1

CC substrate. Such diseases include hypercholesterolaemia, high levels of

CC fatty acids, lipids or farnesyl pyrophosphate, liver steatosis,





OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Cleavage-site 4..5  
 FT /note="chymase and multicatalytic protease site"  
 XX  
 XX  
 PN MO9113904-A.  
 XX  
 PD 19-SEP-1991.  
 XX  
 PF 04-MAR-1991; 91WO-US01474.  
 XX  
 PR 05-MAR-1990; 90US-0489290.  
 XX  
 PA (CEPH-) CEPHALON INC.  
 XX  
 PI Siman R, Nelson RB, Kauer J, Potter H;  
 XX  
 DR WPI; 1991-295576/40.  
 XX  
 PT New chymotrypsin-like serine protease(s) - and their inhibitors  
 PT are used to treat Alzheimer's disease  
 XX  
 PS Claim 41: Page 63; 86pp; English.  
 XX  
 CC This peptide is designed based on the sequence of beta-APP A4  
 CC cleavage site. Cleavage by proteases in the brain releases beta-  
 CC amyloid protein, the deposition of which is a feature of Alzheimer's  
 CC disease neuropathology. The peptide is used to screen for candidate  
 CC proteases which cleave between the Met and Asp residues. Two new  
 CC proteases have been isolated having this cleavage specificity.  
 CC Chymase was isolated from rat brains and multicatalytic protease was  
 CC isolated from human cerebral cortex. See also AAR14136-9.  
 XX  
 SQ Sequence 19 AA:  
 Query Match 100.0%; Score 54; DB 12; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 0.00048;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VKMDAEFRHD 10  
 |||||||||  
 Db 2 VKMDAEFRHD 11  
 RESULT 7  
 AAY69713  
 ID AAY69713 standard; peptide; 20 AA.  
 XX  
 AC AAY69713;  
 XX  
 DT 11-APR-2000 (first entry)  
 XX  
 DE Beta-APP alpha-secretase substrate [KM]-APP(-10,+10).  
 XX  
 KW Noctropic; neuroprotective; beta-amyloid precursor protein; metabolism;  
 KW cleavage site; beta-secretase; neurodegenerative disease;  
 KW Alzheimer's disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN MO9964587-A1.  
 XX  
 PD 16-DEC-1999.  
 XX  
 PF 04-JUN-1999; 99WO-FR01326.  
 XX  
 PR 05-JUN-1998; 98FR-0007068.  
 PR 31-MAR-1999; 99US-0122599.  
 XX  
 PA (RHON) RHONE-POULENC RORER SA.  
 PA (UYPA-) UNIV CURIE PARIS VI P & M.  
 XX

PI Rholam M, Munoz-Gimenez N, Moutaouakil M, Cohen P, Bertrand P;  
 XX  
 DR WPI; 2000-097537/08.  
 XX  
 PT Polypeptide with beta-secretase activity, specific for wild-type  
 PT amyloid precursor protein, useful in treating Alzheimer's disease -  
 XX  
 PS Example 3; Page 24; 44pp; French.  
 XX  
 CC Peptides AAY69702-Y69718 represent synthetic peptide substrates for a  
 CC novel polypeptide with beta-secretase activity that can cleave  
 CC specifically the natural beta-amyloid precursor protein (BAPP). Normal  
 CC cleavage of the protein occurs between amino acids Met596-Asp597 and  
 CC Val636-Ile637 (positions 4-5 and 44-45 of AAY69701). The novel  
 CC polypeptide is used to identify agents that interact specifically with  
 CC it. These agents regulate metabolism of APP, particularly they slow down  
 CC or reduce production of beta-amyloid, so can be used to treat  
 CC neurodegenerative diseases, particularly Alzheimer's disease.  
 XX  
 SQ Sequence 20 AA:  
 Query Match 100.0%; Score 54; DB 21; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 0.00051;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VKMDAEFRHD 10  
 |||||||||  
 Db 8 VKMDAEFRHD 17  
 RESULT 8  
 AAW98002  
 ID AAW98002 standard; Protein; 33 AA.  
 XX  
 AC AAW98002;  
 XX  
 DT 21-JUN-1999 (first entry)  
 XX  
 DE Amyloid precursor protein (aa656-678) with Swedish mutation.  
 XX  
 KW Amyloid precursor protein; APP; human; gene targeting;  
 KW homologous recombination; transgenic mouse; transgenic animal;  
 KW animal model; Alzheimer's disease.  
 XX  
 OS Mus musculus.  
 XX  
 PN WO9909150-A1.  
 XX  
 PD 25-FEB-1999.  
 XX  
 PF 18-AUG-1997; 97WO-US14507.  
 XX  
 PR 18-AUG-1997; 97WO-US14507.  
 XX  
 PA (FARB) BAYER CORP.  
 XX  
 PI Wirak DO;  
 XX  
 DR WPI; 1999-181029/15.  
 XX  
 PT Modification of target nucleic acids - by homologous recombination,  
 PT used particularly for introducing a humanised amyloid precursor  
 PT protein gene into rodents for producing models of Alzheimer's  
 PT disease  
 XX  
 PS Disclosure; Page 145; 203pp; English.  
 XX  
 CC This polypeptide comprises residues 656-678 of a murine amyloid  
 CC precursor protein (APP). The invention provides a novel gene  
 CC targeting strategy that facilitates the introduction of one or  
 CC more specific mutations into any gene in a single double reciprocal  
 CC homologous recombination step. The method has been used  
 CC particularly for introducing a humanised APP gene into rodents for

CC producing animal models of Alzheimer's disease (AD). 4 Independent  
CC lines of transgenic mice (lines ES5007, ES5103, ES5401 and ES5403)  
CC have been created using the gene targeting technique applied to  
CC embryonic stem cells. In each line, the mouse APP gene was modified  
CC to encode a mouse/human hybrid (m/hAPP) where amino acid residues  
CC 666-770 of APP770 were hybrid by human cDNA sequences instead of  
CC mouse genomic exons (exons 16-18). Within these residues, only 3  
CC amino acid differences exist between the mouse and human proteins,  
CC i.e. Gly-676 to Arg, Phe-681 to Thr and Arg-684 to His. The  
CC exon-cDNA fusion gene therefore encodes an APP containing a  
CC humanised beta-amyloid domain. Swedish- and/or London-PAD APP  
CC mutations have also been introduced (see also AAW97997-W98001).

Sequence 33 AA;

Query Match 100.0%; Score 54; DB 20; Length 33;  
Best Local Similarity 100.0%; Pred. No. 0.00086;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VKMDAEFRHD 10  
Db 14 VKMDAEFRHD 23

## RESULT 9

AAV69717  
ID AAV69717 standard; peptide; 39 AA.

AC AAV69717;

DT 11-APR-2000 (first entry)

DE Beta-APP alpha-secretase substrate [KM]-APP(-20,+20).

KM Neurotrophic; neuroprotective; beta-amyloid precursor protein; metabolism;  
KM cleavage site; beta-secretase; neurodegenerative disease;

KW Alzheimer's disease.

OS Homo sapiens.

XX MO9964587-A1.

PD 16-DEC-1999.

PF 04-JUN-1999; 99MO-FR01326.

PR 05-JUN-1998; 98PR-0007068.

PR 31-MAR-1999; 99US-0122599.

PA (RHON ) RHONE-POULENC RORER SA.

PA (UYPA-) UNIV CURIE PARIS VI P 6 M.

PI Rholam M, Munoz-Simenez N, Moutaouakil M, Cohen P, Bertrand P;

DR WPI; 2000-097537/08.

XX Polypeptide with beta-secretase activity, specific for wild-type  
PT amyloid precursor protein, useful in treating Alzheimer's disease -  
XX  
XX  
XX Example 3; Page 24; 44pp; French.

XX Peptides AAV69702-Y69718 represent synthetic peptide substrates for a  
CC novel polypeptide with beta-secretase activity that can cleave  
CC specifically the natural beta-amyloid precursor protein (bAPP). Normal  
CC cleavage of the protein occurs between amino acids Met596-Asp597 and  
CC Val636-Ile637 (positions 4-5 and 44-45 of AAV69701). The novel  
CC polypeptide is used to identify agents that interact specifically with  
CC it. These agents regulate metabolism of APP, particularly they slow down  
CC or reduce production of beta-amyloid, so can be used to treat  
CC neurodegenerative diseases, particularly Alzheimer's disease.

Sequence 39 AA;

Query Match 100.0%; Score 54; DB 21; Length 39;  
Best Local Similarity 100.0%; Pred. No. 0.001;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VKMDAEFRHD 10  
Db 17 VKMDAEFRHD 26

## RESULT 10

AAW26512  
ID AAW26512 standard; peptide; 45 AA.

AC AAW26512;

DT 06-JAN-1998 (first entry)

DE Amyloid precursor protein fragment APP-REP 751 (BAP del11-28).

KM Amyloid precursor protein; APP; beta-amyloid protein; BAP;  
KM substrate; muten; secretase; Alzheimer's disease; human.

OS Chimeric Homo sapiens.

OS Chimeric synthetic.

FH Key Location/Qualifiers

FT Cleavage-site 7..8 /note= "secretase cleavage site"

FT Peptide 10..33 /label= BAP(del11-28)

FT Domain 20..42 /note= "truncated beta-amyloid protein"

XX US5656477-A.

PD 12-AUG-1997.

PF 01-MAY-1992; 92US-0877675.

PR 20-SEP-1993; 93US-0123659.

PR 01-MAY-1992; 92US-0877675.

PA (AMCY ) AMERICAN CYANAMID CO.

PI Jacobsen JS, Vitek MP;

DR WPI; 1997-414594/38.

XX Nucleic acid encoding amyloid precursor muten(s) - comprising  
PT reporter gene and coding sequence, for identifying compounds which  
PT modify the activity of proteolytic enzymes which cleave APP  
XX  
XX Disclosure; Fig 5A; 84pp; English.

XX This peptide sequence shows the region of amyloid precursor protein  
CC (APP) that includes a truncated beta-amyloid protein (BAP) lacking  
CC the native secretase cleavage/recognition site. In an attempt to  
CC engineer an APP non-cleavable substrate for secretase, an  
CC APP-reporter (APP-REP) protein that carries the BAP deletion has  
CC been expressed in recombinant host cells. Deletion of these 18  
CC amino acids, however, still resulted in the secretion of an  
CC N-terminal APP-reporter fragment into the cytoplasm. Non-  
CC cleavable APP substrates can be used to detect other putative  
CC abnormal APP processing events. They can also be used to  
CC investigate cellular post-translational modifications to APP in  
CC order to determine the potential influence on normal secretase and  
CC abnormal BAP 'clipping' activities.

Sequence 45 AA;

Query Match 100.0%; Score 54; DB 18; Length 45;  
Best Local Similarity 100.0%; Pred. No. 0.0012;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 VKMDAEFRHD 10  
|||||  
Db 7 VKMDAEFRHD 16

RESULT 11  
AAW26392  
ID AAW26392 standard; Peptide: 45 AA.  
AC AAW26392;  
XX

DT 15-DEC-1997 (first entry)  
XX

DE Amyloid precursor protein fragment APP-RPP 751 (BAP del11-28).  
XX

KW Amyloid precursor protein; APP; beta-amyloid protein; BAP;  
KW substrate; muten; secretase; Alzheimer's disease; human.  
XX

OS Chimeric Homo sapiens;  
OS Chimeric synthetic.  
XX

PH Key Location/Qualifiers  
FT Cleavage-site 7..8 /note= "secretase cleavage site"  
FT Peptide 10..33 /label= BAP(del11-28)  
FT /note= "truncated beta-amyloid protein"  
FT Domain 20..42 /label= Transmembrane  
XX

PN US5652092-A.  
XX

PD 29-JUL-1997.  
XX

PF 01-MAY-1992; 92US-0877675.  
XX

PR 20-SEP-1993; 93US-0123659.  
PR 01-MAY-1992; 92US-0877675.  
PR 05-JUN-1995; 95US-0462859.  
XX

PA (AMCY ) AMERICAN CYANAMID CO.  
XX

PI Jacobsen JS, Vitek MP;  
XX

DR WPI; 1997-392937/36.  
XX

PT Screening for compounds which reduce beta-amyloid protein formation  
PT - using cells which express a construct encoding a marker and an  
PT amyloid precursor muten derived from APP isoforms  
XX

PS Disclosure; Fig 5A; 84pp; English.  
XX

CC This peptide sequence shows the region of amyloid precursor protein  
CC (APP) that includes a truncated beta-amyloid protein (BAP) lacking  
CC the native secretase cleavage/recognition site. In an attempt to  
CC engineer an APP non-cleavable substrate for secretase, an  
CC APP-reporter (APP-RPP) protein that carries the BAP deletion has  
CC been expressed in recombinant host cells. Deletion of these 18  
CC amino acids, however, still resulted in the secretion of an  
CC N-terminal APP-reporter fragment into the cytoplasm. Non-  
CC cleavable APP substrates can be used to detect other putative  
CC abnormal APP processing events. They can also be used to  
CC investigate cellular post-translational modifications to APP in  
CC order to determine the potential influence on normal secretase and  
CC abnormal BAP 'clipping' activities.  
XX

SO Sequence 45 AA;  
XX

Query Match 100.0%; Score 54; DB 18; Length 45;  
Best Local Similarity 100.0%; Pred. No. 0.0012;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VKMDAEFRHD 10  
|||||  
Db 7 VKMDAEFRHD 16

RESULT 12  
AAW44748  
ID AAW44748 standard; Protein: 45 AA.  
AC AAW44748;  
XX

DT 01-JUN-1998 (first entry)  
XX

DE APP-RPP 751 [BAP delta(11-28)] peptide.  
XX

KW Amyloid precursor protein; APP; APP 751 isoform; deletion; substrate P;  
KW epitope; Met-enkephalin; detection; secretase; beta-amyloid protein; BAP;  
KW Alzheimer's disease; cleavage.  
XX

OS Homo sapiens.  
OS Synthetic.  
XX

PH Key Location/Qualifiers  
FT Cleavage-site 7..8 /note= "putative secretase cleavage site"  
FT Misc-difference 19..20 /note= "residues 11-28 of the wild type BAP sequence  
FT /note= "are deleted from between these positions"  
XX

PN US5693478-A.  
XX

PD 02-DEC-1997.  
XX

PF 05-JUN-1995; 95US-0464247.  
XX

PR 20-SEP-1993; 93US-0123659.  
PR 01-MAY-1992; 92US-0877675.  
PR 05-JUN-1995; 95US-0464247.  
XX

PA (AMCY ) AMERICAN CYANAMID CO.  
XX

PI Jacobsen JS, Vitek MP;  
XX

DR WPI; 1998-031744/03.  
XX

PT Amyloid precursor muten reporter molecule assay containing antibody  
PT recognised marker - used to study pathways associated with  
PT Alzheimer's disease  
XX

PS Disclosure; Fig 5A; 84pp; English.  
XX

CC This sequence represent the beta-amyloid protein sequence from the  
CC construct APP-REP751 [BAP delta(11-28)]. The mutant sequence contains  
CC a deletion of the wild type BAP residues 11-28. This causes a  
CC shortening of the BAP sequence. This may affect cleavage of the BAP by  
CC the "secretase" dependent on whether the "secretase" recognises the  
CC cleavage site by a positional effect or by sequence. The mutant sequence  
CC can be used in a method to study secretase and beta-amyloid protein  
CC (BAP)-generating pathways associated with Alzheimer's disease by  
CC studying proteolytic cleavage of the reporter polypeptides (e.g.  
CC AAW4744 and AAW4745).  
XX

SO Sequence 45 AA;  
XX

Query Match 100.0%; Score 54; DB 19; Length 45;  
Best Local Similarity 100.0%; Pred. No. 0.0012;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VKMDAEFRHD 10  
|||||  
Db 7 VKMDAEFRHD 16

RESULT 13  
AAM42977  
ID AAM42977 standard; peptide; 45 AA.  
XX  
AC  
XX AAM42977;  
AC  
XX  
DT 01-MAY-1998 (first entry)  
XX  
XX  
DE Deletion beta-amyloid peptide (BAP) derived from APP-REP 751.  
XX  
KW Beta-amyloid peptide; BAP; extracellular BAP plaque;  
KW cerebrovascular deposit; Alzheimers disease; Downs syndrome;  
KW amyloid precursor protein; APP; secretase; BAP aggregation;  
KW abnormal proteolytic cleavage.  
XX  
OS Homo sapiens.  
XX  
FH Key  
FT Domain  
FT 20..43  
FT /note= "putative transmembrane domain"  
XX  
PN US5703209-A.  
XX  
PD 30-DEC-1997.  
XX  
PP 05-JUN-1995; 95US-0464248.  
XX  
PR 20-SEP-1993; 93US-0123659.  
PR 01-MAY-1992; 92US-0877675.  
XX  
PA (AMCY ) AMERICAN CYANAMID CO.  
XX  
PI Jacobsen JS, Vittek MP.  
XX  
DR WPI; 1998-076482/07.  
XX  
PT Amyloid precursor protein fusion polypeptides - comprising APP  
PT fragment and marker, useful for research and drug screening  
XX  
XX  
PS Disclosure; Fig 5A; 84pp; English.  
XX  
CC The present sequence represents a beta-amyloid peptide (BAP), with  
CC a deletion amino acids 11-28 (numbered according to AAM42976). Abnormal  
CC accumulation of extracellular BAP in plaques and cerebrovascular  
CC deposits is characteristic in brains of individuals suffering from  
CC Alzheimers disease and Downs syndrome. BAP is a poorly soluble,  
CC self-aggregating protein which is derived from a larger amyloid precursor  
CC protein (APP). APP is expressed as an integral membrane protein, and is  
CC cleaved by secretase, between BAP 16lys and 17leu. Cleavage at this site  
CC precludes amyloidogenesis and results in the release of the  
CC amino-terminal APP fragment. Three major isoforms of APP exist: APP-695,  
CC APP-751 and APP-770. These isoforms are derived by alternative splicing.  
CC APP-APP 751 is a deletion construct of APP-751, which has a deletion of  
CC 276 amino acids to within 15 amino acids of the BAP domain. APP can be  
CC used as a substrate for studying abnormal proteolytic cleavage which  
CC results in the release of BAP, and also to screen for drugs that will  
CC inhibit such cleavage.  
XX  
SQ Sequence 45 AA:  
Query Match 100.0%; Score 54; DB 19; Length 45;  
Best Local Similarity 100.0%; Pred. No. 0.0012;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX  
AC AAB37523;  
XX  
DT 01-MAR-2001 (first entry)  
XX  
XX Amyloid precursor protein APP residues 669-716.  
DE  
XX Amyloid precursor protein; APP; Alzheimer's disease; Abeta.  
KW  
XX Unidentified.  
OS  
XX  
PN W0200066181-A1.  
XX  
PD 09-NOV-2000.  
XX  
PP 01-MAY-2000; 2000MO-US11715.  
XX  
PR 29-APR-1999; 99US-0131579.  
XX  
PA (GBHO ) GEN HOSPITAL CORP.  
XX  
PI Bush AI, Huang X, Atwood CS, Tanzi RE;  
XX  
DR WPI; 2001-015918/02.  
XX  
PT Screening for agents useful in treating Alzheimer's disease by adding  
PT the agent to an Abeta-containing sample and detecting inhibition of  
PT oxygen-dependent hydrogen peroxide formation by the agent .  
XX  
PS Disclosure; Fig 6; 98pp; English.  
XX  
CC The present invention relates to methods for identifying agents which  
CC can be used in the treatment or Alzheimer's disease. These agents are  
CC identified for their ability to inhibit oxygen-dependent hydrogen  
CC peroxide formation but their inability to inhibit superoxide-dependent  
CC hydrogen peroxide formation. This means that they decrease the  
CC neurotoxicity of Abeta, the protein which is thought to cause Alzheimer's  
CC disease.  
XX  
SQ Sequence 48 AA:  
Query Match 100.0%; Score 54; DB 22; Length 48;  
Best Local Similarity 100.0%; Pred. No. 0.0013;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 VKMDAEFRHD 10  
DB 1 VKMDAEFRHD 10  
RESULT 15  
AAR55695  
ID AAR55695 standard; Protein; 53 AA.  
XX  
AC AAR55695;  
XX  
DT 29-DEC-1994 (first entry)  
XX  
XX Sequence of unidentified protein sequence ID number 20.  
DE  
XX Amyloid precursor protein; APP; plaque; beta/A4; Alzheimers;  
KW transgene; ss.  
XX  
OS Synthetic.  
XX  
PN W09412627-A.  
XX  
PD 09-JUN-1994.  
XX  
PP 24-NOV-1993; 93WO-US11480.  
XX  
PR 25-NOV-1992; 92US-0989850.  
PR 09-NOV-1993; 93US-0149222.

```
XX (CEPH-) CEPHALON INC.
PA
XX
XX Howland DS, Scott RW;
PI
XX
XX WPI; 1994-200256/24.
DR
XX
XX Transgenic animal model for Alzheimer's disease - contains
PT transgene encoding amyloid protein under transcriptional control
PT of synapsin gene promoter
XX
XX
XX Example: Page 54; 94pp; English.
PS
XX
XX There was no apparent reference to sequence ID numbers 20, 21 or 22
CC in the specification. The specification describes a transgenic
CC animal model for Alzheimer's disease. A transgenic animal
CC harbouring a transgene coding for an amyloid protein under the
CC control of a promoter is claimed. The amyloid protein can be
CC APP695, APP751 or APP770. The coding sequence may contain a
CC mutation, including the hereditary cerebral haemorrhage with
CC amyloidosis - Dutch type (HCHWA-DT) and familial Alzheimer's
CC disease (FAD). Perhaps SQ IDs 20-22 corresp. to wt. HCHWA-DT
CC and FAD?
CC
XX
XX SQ Sequence 53 AA;
XX
XX Query Match 100.0%; Score 54; DB 15; Length 53;
XX Best Local Similarity 100.0%; Pred. No. 0.0014;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VKMDAEFRHD 10
Db 2 VKMDAEFRHD 11
1111111111
```

Search completed: October 29, 2002, 10:26:44  
Job time : 23.1429 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compen Ltd.

OM protein - protein search, using sw model

Run on: October 29, 2002, 10:23:36 ; Search time 10.4286 Seconds  
(without alignments)  
92.140 Million cell updates/sec

Title: US-09-580-018-6

Perfect score: 54

Sequence: 1 VKMDAEFRHD 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	57	2 E60045	Alzheimer's disease
2	54	100.0	57	2 F60045	Alzheimer's disease
3	54	100.0	57	2 G60045	Alzheimer's disease
4	54	100.0	57	2 D60045	Alzheimer's disease
5	54	100.0	57	2 A60045	Alzheimer's disease
6	54	100.0	57	2 B60045	Alzheimer's disease
7	54	100.0	82	2 P00438	Alzheimer's disease
8	54	100.0	695	1 A49795	Alzheimer's disease
9	54	100.0	770	1 QRH044	Alzheimer's disease
10	48	88.9	747	2 JH0773	Alzheimer's disease
11	47	87.0	33	2 S23094	Alzheimer's disease
12	47	87.0	695	2 A27485	Alzheimer's disease
13	47	87.0	695	2 S00550	Alzheimer's disease
14	40	74.1	42	2 PN0512	Alzheimer's disease
15	37	68.5	478	2 C70179	Alzheimer's disease
16	36	66.7	543	2 T48239	Alzheimer's disease
17	36	66.7	578	2 D82053	Alzheimer's disease
18	35	64.8	428	2 B83420	Alzheimer's disease
19	35	64.8	503	2 T24985	Alzheimer's disease
20	35	64.8	511	2 A56750	Alzheimer's disease
21	35	64.8	647	2 T26240	Alzheimer's disease
22	35	64.8	774	2 A61565	Alzheimer's disease
23	35	64.8	900	2 E83189	Alzheimer's disease
24	35	64.8	1001	2 T17365	Alzheimer's disease
25	34	63.0	79	2 D83411	Alzheimer's disease
26	34	63.0	142	2 E89026	Alzheimer's disease
27	34	63.0	213	2 F87669	Alzheimer's disease
28	34	63.0	226	2 T29404	Alzheimer's disease
29	34	63.0	246	2 AG1140	Alzheimer's disease

30	34	63.0	255	2 G90509	dolichol-phosphate
31	34	63.0	376	2 B84277	hypothetical prote
32	34	63.0	400	2 S70187	44.7k vira protein
33	34	63.0	423	2 C84991	elongation factor
34	34	63.0	426	2 B69876	acetylornithine de
35	34	63.0	763	2 JC4376	beta-glucosidase (
36	34	63.0	1237	2 AE1915	hypothetical prote
37	34	63.0	1256	2 AB2042	hypothetical prote
38	33.5	62.0	293	2 T26934	hypothetical prote
39	33	61.1	177	2 AB3649	hypothetical prote
40	33	61.1	316	2 T46000	hypothetical prote
41	33	61.1	322	2 A69963	hypothetical prote
42	33	61.1	336	2 AF2085	transcription regu
43	33	61.1	392	2 T49471	mucin (muc3) relat
44	33	61.1	427	2 C83591	N-carbamoyl-beta-a
45	33	61.1	811	2 T48468	disease resistance

#### ALIGNMENTS

##### RESULT 1

E60045 Alzheimer's disease amyloid beta/A4 protein precursor - sheep (fragment)

C:Species: Ovis sp. (sheep)

C>Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 28-Jul-1995

C:Accession: E60045

R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d

A:Reference number: A60045; MUID:92017079

A:Accession: E60045

A:Molecule type: mRNA

A:Residues: 1-57 <JOH>

A:Cross-references: EMBL:X56130

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas

C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 54; DB 2; Length 57;

Best Local Similarity 100.0%; Pred. No. 0.00047;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 VKMDAEFRHD 10  
Db 3 VKMDAEFRHD 12

##### RESULT 2

F60045 Alzheimer's disease amyloid beta/A4 protein precursor - pig (fragment)

C:Species: Sus scrofa domestica (domestic pig)

C>Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 13-Aug-1999

C:Accession: F60045

R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d

A:Reference number: A60045; MUID:92017079

A:Accession: F60045

A:Molecule type: mRNA

A:Residues: 1-57 <JOH>

A:Cross-references: EMBL:X56127; NID:91895; PIDN:CAA39592.1; PID:91896

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas

C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 54; DB 2; Length 57;

Best Local Similarity 100.0%; Pred. No. 0.00047;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 VKMDAEFRHD 10  
Db 3 VKMDAEFRHD 12

```
RESULT 3
G60045
Alzheimer's disease amyloid beta/A4 protein precursor - guinea pig (fragment)
C:Species: Cavia porcellus (guinea pig)
C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: G60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079
A:Accession: G60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56126
C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match          100.0%; Score 54; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.00047;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKMDAEFRHD 10
    |||||||
DB 3 VKMDAEFRHD 12

RESULT 4
D60045
Alzheimer's disease amyloid beta/A4 protein precursor - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: D60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079
A:Accession: D60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56124
C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match          100.0%; Score 54; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.00047;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKMDAEFRHD 10
    |||||||
DB 3 VKMDAEFRHD 12

RESULT 5
A60045
Alzheimer's disease amyloid beta/A4 protein precursor - dog (fragment)
C:Species: Canis lupus familiaris (dog)
C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: A60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079
A:Accession: A60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56125
C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match          100.0%; Score 54; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.00047;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 VKMDAEFRHD 10
    |||||||
DB 3 VKMDAEFRHD 12

RESULT 6
B60045
Alzheimer's disease amyloid beta/A4 protein precursor - polar bear (fragment)
C:Species: Ursus maritimus (polar bear)
C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
C:Accession: B60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d
A:Reference number: A60045; MUID:92017079
A:Accession: B60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56128; NID:92165; PIDN:CAA39593.1; PID:92166
C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match          100.0%; Score 54; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.00047;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKMDAEFRHD 10
    |||||||
DB 3 VKMDAEFRHD 12

RESULT 7
PQ0438
Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995
C:Accession: PQ0438; C60045
R:Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.E.
Biochem. Biophys. Res. Commun. 188, 905-911, 1992
A:Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precurs
A:Reference number: PQ0438; MUID:93075180
A:Accession: PQ0438
A:Molecule type: DNA
A:Residues: 1-82 <DAV>
A:Cross-references: GB:M83558; GB:M83657
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d
A:Reference number: A60045; MUID:92017079
A:Accession: C60045
A:Molecule type: mRNA
A:Residues: 12-68 <JOH>
A:Cross-references: EMBL:X56129
C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match          100.0%; Score 54; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 0.00071;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKMDAEFRHD 10
    |||||||
DB 14 VKMDAEFRHD 23

RESULT 8
A49795
Alzheimer's disease amyloid beta protein precursor - crab-eating macaque
C:Species: Macaca fascicularis (crab-eating macaque)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A49795
R:Podlisky, M.B.; Tolan, D.R.; Selkoe, D.J.
Am. J. Pathol. 138, 1423-1435, 1991
```



A:Title: Homology of the amyloid beta protein precursor in monkey and human supports a  
A:Reference number: A49795; MUID:91273117  
A:Accession: A49795  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-695 <PD>  
A:Cross-references: GB:M58727; NID:9342062; PIDN:AAA36829.1; PID:9342063  
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase  
C:Keywords: alternative splicing

Query Match 100.0%; Score 54; DB 1; Length 695;  
Best Local Similarity 100.0%; Pred. No. 0.0076;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKMDAEPFRHD 10  
Db 594 VKMDAEPFRHD 603

RESULT 9  
ORHUA  
Alzheimer's disease amyloid beta protein precursor [validated] - human  
N:Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor Xla inhibi  
N:Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vasculat  
C:protein precursor splice form APP(770)  
C:Species: Homo sapiens (man)  
C>Date: 30-Jun-1987 #sequence revision 28-Jul-1995 #text change 15-Sep-2000  
C:Accession: S02260; S05194; A32277; A33260; A35486; I39452; I39451; I39453; I59562; A4  
4688; A28583; A29302; A60806; J10038; S06121; A60355; A59011; A38384; S29076; S38252; S3  
Nucleic Acids Res. 17, 517-522, 1989  
A:Title: The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded b  
A:Reference number: S02260; MUID:89128427  
A:Accession: S02260  
A:Molecule type: DNA  
A:Residues: 1-288, 'V', 365-770 <LEM1>  
A:Cross-references: EMBL:X13466  
A>Note: alternative splice form APP(695)  
R:Lemaire, H.G.  
submitted to the EMBL Data Library, November 1988  
A:Reference number: S05194  
A:Accession: S05194  
A:Molecule type: DNA  
A:Residues: 1-14, 'VW', 17-288, 'V', 365-770 <LEM2>  
A:Cross-references: EMBL:X13466; NID:935598; PIDN:CAA31830.1; PID:9871360  
A>Note: alternative splice form APP(695)  
R:La Fauci, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.  
Biochem. Biophys. Res. Commun. 159, 297-304, 1989  
A:Title: Characterization of the 5'-end region and the first two exons of the beta-prote  
A:Reference number: A32277; MUID:89165870  
A:Accession: A32277  
A:Molecule type: DNA  
A:Residues: 1-75 <IAF>  
A:Cross-references: GB:M24546; GB:M24547; NID:9341202; PIDN:AA31654.1; PID:9516074  
R:Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.  
Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989  
A:Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows similarit  
A:Reference number: A33260; MUID:89392030  
A:Accession: A33260  
A:Molecule type: DNA  
A:Residues: 656-737 <TOH>  
A:Cross-references: NID:9178863; PIDN:AA51768.1; PID:9178865  
R:Prelli, F.; Levy, E.; van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B.  
Biochem. Biophys. Res. Commun. 170, 301-307, 1990  
A:Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid of  
A:Reference number: A35486; MUID:90321244  
A:Accession: A35486  
A:Molecule type: DNA  
A:Residues: 672-710 <PRE1>  
A>Note: 693-Gln was found in DNA isolated from HCHMA-D patients  
R:Yoshikawa, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.  
Gene 87, 257-263, 1990  
A:Title: Genomic organization of the human amyloid beta-protein precursor gene.

A:Reference number: I39451; MUID:90236318  
A:Accession: I39452  
A>Status: nucleic acid sequence not shown; translation not shown; translated from GB/  
A:Molecule type: DNA  
A:Residues: 1-770 <IOS1>  
A:Cross-references: GB:M33112; NID:9178613; PIDN:AA59502.1; PID:9178616  
A:Accession: I39451  
A>Status: nucleic acid sequence not shown; translation not shown; translated from GB/  
A:Molecule type: DNA  
A:Residues: 1-530, 'QWLMFVLPAPFWEAKVGR' <IOS2>  
A:Cross-references: GB:M34875; NID:9178608; PIDN:AA59501.1; PID:9178615  
R:Yoshikawa, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.  
Gene 102, 291-292, 1991  
A:Reference number: A59020; MUID:91340168  
A:Contents: annotation: erratum  
A>Note: revised physical map for reference I39451  
R:Levy, E.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van Du  
Science 248, 1124-1126, 1990  
A:Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemo  
A:Reference number: I39453; MUID:90260663  
A:Accession: I39453  
A>Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 656-737 <LEV>  
A:Cross-references: GB:M37896; NID:9178618; PIDN:AA51727.1; PID:9178620  
R:Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.  
Science 254, 97-99, 1991  
A:Title: A mutation in the amyloid precursor protein associated with hereditary Alzhe  
A:Reference number: I59562; MUID:92022553  
A:Accession: I59562  
A>Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 689-716, 'F', 718-737 <MUP>  
A:Cross-references: GB:S57665; NID:9236720; PIDN:AA31991.1; PID:9236721  
R:Kamino, K.; Orr, H.T.; Payant, H.; Wilsman, E.M.; Alonso, M.E.; Pulst, S.M.; Anders  
arakis, S.E.; Korenberg, J.R.; Sharma, V.; Kukulski, W.; Larson, E.; Heston, L.L.; Mart  
Am. J. Hum. Genet. 51, 998-1014, 1992  
A:Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for t  
A:Reference number: A44017; MUID:93053937  
A:Accession: A44017  
A:Molecule type: DNA  
A:Residues: 687-692, 'G', 694-718 <KAM1>  
A:Cross-references: GB:S45135; NID:9257377; PIDN:AA323645.1; PID:9257378  
A:Experimental source: familial Alzheimer disease family SB  
A>Note: sequence extracted from NCBI backbone (NCBI:P.115374)  
A:Accession: B44017  
A:Molecule type: DNA  
A:Residues: 687-718 <KAM2>  
A:Cross-references: GB:S45136; NID:9257379; PIDN:AA323646.1; PID:9257380  
A:Experimental source: familial Alzheimer disease family LIT  
A>Note: sequence extracted from NCBI backbone (NCBI:P.115376)  
R:Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.  
Nature 325, 733-736, 1987  
A:Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-sur  
A:Reference number: A03134; MUID:87144572  
A:Accession: A03134  
A:Molecule type: mRNA  
A:Residues: 1-288, 'V', 365-770 <KAN>  
A:Cross-references: GB:Y00264; NID:928525; PIDN:CAA68374.1; PID:928526  
A>Note: alternative splice form APP(695)  
R:Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.  
Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987  
A:Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascula  
A:Reference number: A29030; MUID:87231971  
A:Accession: A29030  
A:Molecule type: mRNA  
A:Residues: 284-288, 'V', 365-646, 'E', 648-770 <ROB>  
A:Cross-references: GB:M16765; NID:9178539; PIDN:AA51722.1; PID:9178540  
A>Note: the authors translated the codon GAG for residue 647 as Asp  
R:Goldhaber, D.; Ierman, M.I.; McBride, O.W.; Saffioti, U.; Gajdusek, D.C.  
Science 235, 877-880, 1987

A:Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid  
 A:Reference number: A47584; MUID:87120328  
 A:Accession: A47584  
 A:Molecule type: mRNA  
 A:Residues: 674-756, 'S', 758-770 <GOL>  
 A:Cross-references: GB:M15533; NID:g178706; PIDN:AAA5540.1; PID:g178707  
 A:Experimental source: brain  
 R:Tanzil, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van Ke  
 Science 235, 880-884, 1987  
 A:Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near th  
 A:Reference number: A47585; MUID:87120329  
 A:Accession: A47585  
 A:Molecule type: mRNA  
 A:Residues: 674-703 <TRAN1>  
 A:Cross-references: GB:M15532; NID:g177957; PIDN:AAA51564.1; PID:g177958  
 R:Dykes, T.; Weidemann, A.; Mulhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Muelle  
 EMBO J. 7, 949-957, 1988  
 A:Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 prec  
 A:Reference number: S02638; MUID:88122637  
 A:Accession: S02638  
 A:Molecule type: mRNA  
 A:Residues: 672-678 <DYR>  
 R:Tanzil, R.E.; McClatchey, A.I.; Lampertli, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Nerve  
 Nature 331, 528-530, 1988  
 A:Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associat  
 A:Reference number: S00707; MUID:88122640  
 A:Accession: S00707  
 A:Molecule type: mRNA  
 A:Residues: 286-344, 'I', 365-366 <TAN2>  
 A:Cross-references: EMBL:X06982; NID:928817; PIDN:CAA30042.1; PID:g929612  
 A:Experimental source: promyelocytic leukemia cell line HL60  
 A:Note: alternative splice form App(751)  
 R:Porte, P.; Gonzalez-Demhitt, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.; De  
 Nature 331, 525-527, 1988  
 A:Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibit  
 A:Reference number: S00925; MUID:88122639  
 A:Accession: S00925  
 A:Molecule type: mRNA  
 A:Residues: 1-344, 'I', 365-770 <PO2>  
 A:Cross-references: GB:X06989; EMBL:Y00297; NID:928720; PIDN:CAA30050.1; PID:g28721  
 A:Note: alternative splice form App(751)  
 R:Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.  
 Nature 331, 530-532, 1988  
 A:Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibitor  
 A:Reference number: A38949; MUID:88122641  
 A:Accession: A38949  
 A:Molecule type: mRNA  
 A:Residues: 287-367 <KIT>  
 A:Cross-references: GB:X06981; NID:g28816; PIDN:CAA30041.1; PID:g929611  
 A:Experimental source: glioblastoma cell line  
 A:Note: alternative splice form App(770)  
 R:Vitek, M.P.; Rasooli, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ashton  
 Brain Res. Mol. Brain Res. 4, 121-131, 1988  
 A:Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of three F  
 A:Reference number: A30320  
 A:Accession: A30320  
 A:Molecule type: mRNA  
 A:Status: not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 284-288, 'V', 365-770 <VIT1>  
 A:Accession: C30320  
 A:Status: not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 606-770 <VIT3>  
 R:Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta, C.A  
 Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988  
 A:Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease br  
 A:Reference number: A31087; MUID:88124954  
 A:Accession: A31087  
 A:Molecule type: mRNA

A:Residues: 507-770 <ZAI>  
 A:Cross-references: GB:M18734; NID:g178572; PIDN:AAA51726.1; PID:g178573  
 A:Note: the authors translated the codon GAA for residue 599 as Gly, ACC for residue  
 8 as Val, GTG for residue 609 as Asn, AAT for residue 610 as Gly, and GGT for residue  
 A:Note: the cited Genbank accession number, J03594, is not in release 101.0  
 R:Masters, C.L.; Mulhaup, G.; Simms, G.; Potgiesser, J.; Martins, R.N.; Beyreuther,  
 Query Match 100.0%; Score 54; DB 1; Length 770;  
 Best Local Similarity 100.0%; Pred. No. 0.0086;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VKMDAERRHD 10  
 |||||  
 Db 669 VKMDAERRHD 678  
 RESULT 10  
 JH0773  
 Alzheimer's disease amyloid beta protein precursor - African clawed frog  
 C:Species: Xenopus laevis (African clawed frog)  
 C:Date: 10-Jun-1993 #sequence\_revision 10-Jun-1993 #text\_change 13-Aug-1999  
 C:Accession: JH0773  
 R:Okado, H.; Okamoto, H.  
 Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992  
 A:Title: A Xenopus homologue of the human beta-amyloid precursor protein: development  
 A:Reference number: JH0773; MUID:93129227  
 A:Accession: JH0773  
 A:Molecule type: mRNA  
 A:Residues: 1-747 <OKA>  
 A:Cross-references: GB:S52417; NID:9263150; PIDN:AAB24853.1; PID:g263151  
 A:Experimental source: larva  
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas  
 C:Keywords: alternative splicing; amyloid  
 F:287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>  
 Query Match 88.9%; Score 48; DB 2; Length 747;  
 Best Local Similarity 80.0%; Pred. No. 0.14;  
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VKMDAERRHD 10  
 |||||  
 Db 646 VKMDSEYRHD 655  
 RESULT 11  
 S23094  
 beta-amyloid protein precursor - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 03-May-1996  
 C:Accession: S23094  
 R:Kojima, S.; Omori, M.  
 FEBS Lett. 304, 57-60, 1992  
 A:Title: Two-way cleavage of beta-amyloid protein precursor by multicatalytic protein  
 A:Reference number: S23094; MUID:92316198  
 A:Accession: S23094  
 A:Molecule type: protein  
 A:Residues: 1-33 <KOJ>  
 C:superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas  
 Query Match 87.0%; Score 47; DB 2; Length 33;  
 Best Local Similarity 90.0%; Pred. No. 0.0068;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 VKMDAERRHD 10  
 |||||  
 Db 3 VKMDAERGH 12  
 RESULT 12  
 A27485  
 Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse  
 N:Alternate names: proteinase nexin II  
 C:Species: Mus musculus (house mouse)

C>Date: 31-Mar-1989 #sequence\_revision 31-Mar-1989 #text\_change 13-Aug-1999  
 C:Accession: A27485; S19727; I49485  
 R:Yamada, T.; Sasaki, H.; Furuya, H.; Miyata, T.; Goto, I.; Sasaki, Y.  
 Biochem. Biophys. Res. Commun. 149, 665-671, 1987  
 A:Title: Complementary DNA for the mouse homolog of the human amyloid beta protein precursor  
 A:Reference number: A27485; MUID:88106489  
 A:Accession: A27485  
 A:Molecule type: mRNA  
 A:Residues: 1-695 <YAM>  
 A:Cross-references: GB:M18373; NID:g191568; PIDN:AAA7139.1; PID:g309085  
 A:Experimental source: brain  
 Ride, Strooper, B.; van Leuven, F.; van den Berghe, H.  
 Biochim. Biophys. Acta 1129, 141-143, 1991  
 A:Title: The amyloid beta protein precursor or proteinase nexin II from mouse is closer  
 A:Reference number: S19727; MUID:92096458  
 A:Accession: S19727  
 A:Molecule type: mRNA  
 A:Residues: 1-210, 'G', 212-220, 'S', 222-396, 'A', 398-402, 'T', 404-448, 'A', 450-695 <STR>  
 A:Cross-references: EMBL:X59379  
 R:Zumi, R.; Yamada, T.; Yoshikata, S.; Sasaki, H.; Hattori, M.; Sasaki, Y.  
 Gene 112, 189-195, 1992  
 A:Title: Positive and negative regulatory elements for the expression of the Alzheimer's  
 A:Reference number: I49485; MUID:92209998  
 A:Accession: I49485  
 A>Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-19 <RES>  
 A:Cross-references: GB:D10603; NID:g220328; PIDN:BA01456.1; PID:g220329  
 C:Genetics:  
 A:Map position: 16C3  
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1  
 C:Keywords: alternative splicing; amyloid; transmembrane protein

Query Match 87.0%; Score 47; DB 2; Length 695;  
 Best Local Similarity 90.0%; Pred. No. 0.2;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 VKMDAEPFRHD 10  
 |||||  
 Db 594 VKMDAEPFRHD 603

RESULT 13  
 S00550  
 Alzheimer's disease amyloid beta protein precursor - rat  
 N:Alternate names: beta-A4 amyloid protein  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 13-Aug-1999  
 C:Accession: S00550; A41245; A39820; S46251  
 R:Shivers, B.D.; Hildich, C.; Multhaup, G.; Salbaum, M.; Beyreuther, K.; Seeburg, P.H.  
 EMBO J. 7, 1365-1370, 1988  
 A:Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brain  
 A:Reference number: S00550; MUID:88312583  
 A:Accession: S00550  
 A:Molecule type: mRNA  
 A:Residues: 1-695 <SHI>  
 A:Cross-references: EMBL:X07648; NID:g55616; PIDN:CAA30488.1; PID:g55617  
 R:Schubert, D.; Schroeder, R.; Lacortiere, M.; Salton, T.; Cole, G.  
 Science 241, 223-226, 1988  
 A:Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan core  
 A:Reference number: A41245; MUID:88264430  
 A:Accession: A41245  
 A:Molecule type: protein  
 A:Residues: 18-37, 'X', 39-40, 'X', 42-44 <SCH>  
 A>Note: evidence for heparan sulfate attachment  
 R:Hesse, L.; Behr, D.; Masters, C.L.; Multhaup, G.  
 FEBS Lett. 349, 109-116, 1994  
 A:Title: The beta-A4 amyloid precursor protein binding to copper.  
 A:Reference number: S46251; MUID:94320627  
 A:Contents: annotation; copper binding sites  
 A>Note: rat peptides were isolated but not sequenced  
 R:Proemka, A.; Styles, J.; Mehta, P.; Kim, K.S.; Miller, D.L.  
 J. Biol. Chem. 266, 8464-8469, 1991

A:Title: Purification and tissue level of the beta-amyloid peptide precursor of rat b  
 A:Reference number: A39820; MUID:91217087  
 A:Accession: A39820  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 18-32 <POT>  
 A:Experimental source: brain  
 C:Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques is  
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase  
 C:Keywords: alternative splicing; amyloid; glycoprotein; transmembrane protein  
 F:625-648/Domain: transmembrane #status predicted <TM>

Query Match 87.0%; Score 47; DB 2; Length 695;  
 Best Local Similarity 90.0%; Pred. No. 0.2;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 VKMDAEPFRHD 10  
 |||||  
 Db 594 VKMDAEPFRHD 603

RESULT 14  
 PN0512  
 beta-amyloid protein - guinea pig (fragment)  
 C:Species: Cavia porcellus (guinea pig)  
 C>Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 17-Mar-1999  
 C:Accession: PN0512  
 R:Shimohigashi, Y.; Matsumoto, H.; Takano, Y.; Salto, R.; Iwata, T.; Kamiya, H.; Ohno  
 Biochem. Biophys. Res. Commun. 193, 624-630, 1993  
 A:Title: Receptor-mediated specific biological activity of a beta-amyloid protein fra  
 A:Reference number: PN0512; MUID:93290653  
 A:Accession: PN0512  
 A:Molecule type: protein  
 A:Residues: 1-42 <SHI>  
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase  
 C:Keywords: alternative splicing; amyloid

Query Match 74.1%; Score 40; DB 2; Length 42;  
 Best Local Similarity 100.0%; Pred. No. 0.23;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 DAEPFRHD 10  
 |||||  
 Db 1 DAEPFRHD 7

RESULT 15  
 C70179  
 Probable glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) - Lyme disease spirochete  
 C:Species: Borrelia burgdorferi (Lyme disease spirochete)  
 C>Date: 13-Feb-1998 #sequence\_revision 13-Feb-1998 #text\_change 11-Jun-1999  
 C:Accession: C70179  
 R:Fraser, C.M.; Castjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; Wh  
 son, D.; Peterson, J.; Kellavag, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vu  
 ; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.  
 Nature 390, 580-586, 1997  
 A:Authors: Venter, J.C.  
 A:Title: Genomic sequence of a Lyme disease spirochete, Borrelia burgdorferi.  
 A:Reference number: A70100; MUID:98065943  
 A:Accession: C70179  
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-478 <KUE>  
 A:Cross-references: GB:AE001165; GB:AE000783; NID:g2688561; PIDN:AAB91531.1; PID:g268  
 A:Experimental source: strain B31  
 C:Superfamily: glucose-6-phosphate dehydrogenase  
 C:Keywords: oxidoreductase

Query Match 68.5%; Score 37; DB 2; Length 478;  
 Best Local Similarity 60.0%; Pred. No. 14;  
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 VKMDAEPFRHD 10

Tue Oct 29 11:23:38 2002

us-09-580-018-6.rpr

Page 6

Db : | : | | | |  
248 IKFDSERHD 257

Search completed: October 29, 2002, 10:31:04  
Job time : 12.4286 secs

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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 29, 2002, 10:22:36 ; Search time 5 Seconds

(without alignments)  
77.439 Million cell updates/sec

Title: US-09-580-018-6  
Perfect score: 54  
Sequence: 1 VKMDAEFRHD 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	54	100.0	57	A4_PIG	Q29023 sus scrofa
2	54	100.0	57	A4_URNSA	Q29149 ursus marit
3	54	100.0	58	A4_CANFA	Q28280 canis famill
4	54	100.0	58	A4_RABIT	Q28748 oryctolagus
5	54	100.0	58	A4_SHEEP	Q28757 ovis aries
6	54	100.0	59	A4_BOVIN	Q28053 bos taurus
7	54	100.0	751	A4_SAISC	Q95241 salmistr sci
8	54	100.0	770	A4_HUMAN	P05067 homo sapien
9	47	87.0	770	A4_MOUSE	P12033 mus musculu
10	47	87.0	770	A4_MOUSE	P08592 rattus norv
11	37	68.5	478	G6PD_BORBU	P01581 borrelia bu
12	35	64.8	511	COPD_BOVIN	P53619 bos taurus
13	35	64.8	511	COPD_HUMAN	P48444 homo sapien
14	35	64.8	900	GLND_PSPAF	Q92980 pseudomonas
15	34	63.0	394	A4_RAT	Q31257 buchiera ap
16	33	61.1	322	FTOUA_BACSU	P54538 bacillus su
17	33	61.1	922	C133_DROME	Q09493 drosophila
18	33	61.1	927	C133_DROME	Q09822 schizosacch
19	32	59.3	107	T2AH_DROME	Q9W5B9 drosophila
20	32	59.3	132	RNPA_MICLU	P21172 micrococcu
21	32	59.3	198	TNFA_MOUSE	P43468 mus musculu
22	32	59.3	213	NULD_DROME	P52845 drosophila
23	32	59.3	269	T2S1_STRFI	O52512 streptomyce
24	32	59.3	304	MDH_HALMA	Q07841 halocarcula
25	32	59.3	328	P2Y3_MEIGA	O93361 melalegria g
26	32	59.3	402	RDS1_SCHPO	P53693 schizosacch
27	32	59.3	431	PDR8_SYNPO	P74383 schizosacch
28	32	59.3	500	STCL_EMBNI	Q00704 emeritella
29	32	59.3	502	YGCU_ECOLI	Q46901 escherichia
30	32	59.3	780	TREB_YEAST	P35172 saccharomyc
31	32	59.3	930	DPO1_HAENI	P43741 haemophilus
32	32	59.3	1579	SSK2_YEAST	P53599 saccharomyc
33	31	57.4	77	ACP_BACSU	P80643 bacillus su

34	31	57.4	190	1	GP38_BPSPI	O48394 bacterioph
35	31	57.4	210	1	PEM_MOUSE	P52651 mus musculu
36	31	57.4	351	1	VAOD_HUMAN	P12953 homo sapien
37	31	57.4	351	1	VAOD_MOUSE	P51863 mus musculu
38	31	57.4	453	1	YK8_YEAST	P34252 saccharomyc
39	31	57.4	481	1	THRC_CORGL	P23669 corynebacte
40	31	57.4	497	1	PSD3_SCHPO	Q42897 schizosacch
41	31	57.4	1101	1	KOE5_YEAST	Q08217 saccharomyc
42	31	57.4	1178	1	MNNA_YEAST	P36044 saccharomyc
43	31	57.4	1451	1	A2M2_MOUSE	P28666 mus musculu
44	31	57.4	1476	1	A2M1_MOUSE	P28655 mus musculu
45	31	57.4	1477	1	A113_RAT	P14046 rattus norv

## ALIGNMENTS

```

RESULT 1
A4_PIG
AC Q29023; STANDARD; PRT; 57 AA.
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-APP) (A-beta)] (Fragment).
GN APP.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
ON NCBI_TaxID=9823;
RX MEDLINE=92017079; PubMed=1656157;
RA Jonstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis."
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@sib-sib.ch).
CC
DR EMBL: X56127; CAA39592.1; -.
DR HSP: P05067; IBA4.
DR InterPro: IPR001868; A4_APP.
DR PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR PROSITE: PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.
FT NON_TER 1
FT CHAIN 6 48
FT DOMAIN <1 33
FT TRANSEM 34 57
FT NON_TER 57
SQ
SEQUENCE 57 AA: 6172 MW; 84209D88EBA82DEA CRC64;
Query Match 100.0%; Score 54; DB 1; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.00024;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 VKMDAEFRHD 10
|||||

```

Db 3 VKMDAEFRHD 12

RESULT 2

A4\_URSMA STANDARD: PRT: 57 AA.

AC 029149;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE Alzheimer's disease amyloid A4 protein homolog [contains: Beta-amyloid protein (Beta-APP) (A-beta)] (Fragment).

GN APP.

OS Ursus maritimus (Polar bear) (Thalarcos maritimus).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.

NCBI\_TaxID=29073;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RA MEDLINE=92017079; PubMed=1656157;

RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.; "Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis."

RT peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis."

RL Brain Res. Mol. Brain Res. 10:299-305(1991).

CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN G(O) (BY SIMILARITY).

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.

CC -----

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CC -----

DR EMBL: X56128; CAA39593.1; -

DR HSSP: P05067; IBA4.

DR InterPro: IPR001868; A4\_APP.

DR PROSITE: PS00319; A4\_EXTRA; PARTIAL.

DR PROSITE: PS00320; A4\_INTRA; PARTIAL.

KW Glycoprotein; Amyloid; Neurone; Transmembrane.

FT NON\_TER 1 48

FT CHAIN 6 48

FT DOMAIN <1 33

FT TRANSMEM 34 57

FT NON\_TER 57 57

FT POTENTIAL.

FT EXTRACELLULAR (POTENTIAL).

FT SEQUENCE 57 AA: 6172 MW: 84209D88BA82DFA CRC64;

Query Match 100.0%; Score 54; DB 1; Length 57;

Best Local Similarity 100.0%; Pred. NO. 0.00024;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 VKMDAEFRHD 10

Db 3 VKMDAEFRHD 12

RESULT 3

A4\_CANFA STANDARD: PRT: 58 AA.

AC 028280;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE Alzheimer's disease amyloid A4 protein homolog [contains: Beta-amyloid protein (Beta-APP) (A-beta)] (Fragment).

GN APP.

OS Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

NCBI\_TaxID=9615;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Kidney;

RA MEDLINE=92017079; PubMed=1656157;

RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.; "Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis."

RT peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis."

RL Brain Res. Mol. Brain Res. 10:299-305(1991).

CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN G(O) (BY SIMILARITY).

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.

CC -----

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CC -----

DR EMBL: X56125; CAA39590.1; -

DR HSSP: P05067; IBA4.

DR InterPro: IPR001868; A4\_APP.

DR PROSITE: PS00319; A4\_EXTRA; PARTIAL.

DR PROSITE: PS00320; A4\_INTRA; PARTIAL.

KW Glycoprotein; Amyloid; Neurone; Transmembrane.

FT NON\_TER 1 49

FT CHAIN 7 49

FT DOMAIN <1 34

FT TRANSMEM 35 58

FT NON\_TER 58 58

FT POTENTIAL.

FT EXTRACELLULAR (POTENTIAL).

FT SEQUENCE 58 AA: 6285 MW: 8469D488A2E12DFA CRC64;

Query Match 100.0%; Score 54; DB 1; Length 58;

Best Local Similarity 100.0%; Pred. NO. 0.00024;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 VKMDAEFRHD 10

Db 4 VKMDAEFRHD 13

RESULT 4

A4\_RABIT STANDARD: PRT: 58 AA.

AC 028748;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Alzheimer's disease amyloid A4 protein homolog [contains: Beta-amyloid protein (Beta-APP) (A-beta)] (Fragment).

GN APP.

OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

NCBI\_TaxID=9986;

OX [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RA MEDLINE=92017079; PubMed=1656157;

RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.; "Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis."

RT peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis."

RL Brain Res. Mol. Brain Res. 10:299-305(1991).

CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN

```

CC G(O) (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
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CC -----
DR EMBL: X56129; CAA39594.1; -.
DR HSSP: P05067; 1BA4.
DR InterPro: IPR001868; A4_APP.
DR PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR PROSITE: PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.
FT NON_TER 1 1
FT CHAIN 1 48 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 34 57 POTENTIAL.
FT DOMAIN 58 >58 CYTOPLASMIC (POTENTIAL).
FT NON_TER 58 58
SQ SEQUENCE 58 AA; 6300 MW; FA34209D88BA82D CRC64;

Query Match 100.0%; Score 54; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.00024;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKMDAEFRHD 10
Db 3 VKMDAEFRHD 12

RESULT 5
A4_SHEEP STANDARD; PRT; 58 AA.
ID A4_SHEEP Q28757;
AC Q28757;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-Ap) (A-beta)] (Fragment).
GN APP.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
-1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
G(O) (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
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DR EMBL: X56130; CAA39595.1; -.
DR HSSP: P05067; 1AML.
DR InterPro: IPR001868; A4_APP.
DR PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR PROSITE: PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.
FT NON_TER 1 1
FT CHAIN 1 48 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 34 57 POTENTIAL.
FT DOMAIN 58 >58 CYTOPLASMIC (POTENTIAL).
FT NON_TER 58 58
SQ SEQUENCE 58 AA; 6300 MW; FA34209D88BA82D CRC64;

Query Match 100.0%; Score 54; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.00024;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKMDAEFRHD 10
Db 3 VKMDAEFRHD 12

RESULT 6
A4_BOVIN STANDARD; PRT; 59 AA.
ID A4_BOVIN Q28053;
AC Q28053;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-Ap) (A-beta)] (Fragment).
GN APP.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
-1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
G(O) (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X56124; CAA39589.1; -.
DR EMBL: X56126; CAA39591.1; -.
DR HSSP: P05067; 1BA4.
DR InterPro: IPR001868; A4_APP.
DR PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR PROSITE: PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.
FT NON_TER 1 1
FT CHAIN 1 49 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 34 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 35 58 POTENTIAL.
FT DOMAIN 59 >59 CYTOPLASMIC (POTENTIAL).

```

FT NON\_TER 59 59  
SQ SEQUENCE 59 AA; 6414 MW; F43469D488A2E12D CRC64;  
Query Match 100.0%; Score 54; DB 1; Length 59;  
Best Local Similarity 100.0%; Pred. No. 0.00024;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 VKMADEFHRD 10  
| | | | | | | | | |  
Db 4 VKMADEFHRD 13  
RESULT 7  
A4\_SAISC STANDARD; PRT; 751 AA.  
ID A4\_SAISC  
AC 095241;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Alzheimer's disease amyloid A4 protein precursor [contains: Beta-amyloid protein (Beta-Ap) (A-beta)].  
GN APP.  
OS Saimiri sciureus (Common squirrel monkey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri. NCBI\_TaxID=9521.  
RX TISSUE=Liver, and Kidney;  
RC MEDLINE=96108492; PubMed=8532114;  
RA Levy E., Amorim A., Frangione B., Walker L.C.;  
RT "beta-amyloid precursor protein gene in squirrel monkeys with cerebellar amyloid angiopathy";  
RT Neurobiol. Aging 16:805-808(1995).  
CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN G(O).  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE NXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF PHOSPHORYLATION (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.  
CC -1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.  
CC -----  
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CC -----  
DR EMBL; S81024; AAD14347.1; .  
DR HSSP; P05067; IAP.  
DR InterPro: IPR001868; A4\_APP.  
DR InterPro: IPR002223; Kunitz\_BPTI.  
DR Pfam: PF02177; A4\_EXTRA; 1.  
DR PRINTS; PR00203; AMYLOIDA4.  
DR PRINTS; PR00759; BASICPTASE.  
DR SMART; SM00006; A4\_EXTRA; 1.  
DR SMART; SM00131; KU; 1.  
DR PROSITE; PS00319; A4\_EXTRA; 1.  
DR PROSITE; PS00320; A4\_INTRA; 1.  
DR PROSITE; PS00280; BPTI\_KUNITZ\_1; 1.  
DR PROSITE; PS00279; BPTI\_KUNITZ\_2; 1.  
KM Glycoprotein. Amyloid. Neurone; Transmembrane; Alternative splicing; Signal; Serine protease inhibitor.  
FT SIGNAL 1 17 BY SIMILARITY.  
FT CHAIN 18 751 A4 PROTEIN.  
FT CHAIN 653 695 BETA-AMYLOID PROTEIN (POTENTIAL).  
FT

FT DOMAIN 18 680 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 681 704 POTENTIAL.  
FT DOMAIN 705 751 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 287 345 BPTI/KUNITZ INHIBITOR.  
FT SITE 740 743 CLATHRIN-BINDING (BY SIMILARITY).  
FT ACT\_SITE 301 302 REACTIVE BOND.  
FT DISULFID 291 341 BY SIMILARITY.  
FT DISULFID 300 324 BY SIMILARITY.  
FT DISULFID 316 337 BY SIMILARITY.  
FT CARBOHYD 523 523 N-LINKED (GLCNAC. . .) (PROBABLE).  
FT CARBOHYD 552 552 N-LINKED (GLCNAC. . .) (PROBABLE).  
SQ SEQUENCE 751 AA; 84893 MW; 6C3EA31089569049 CRC64;  
Query Match 100.0%; Score 54; DB 1; Length 751;  
Best Local Similarity 100.0%; Pred. No. 0.0035;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 VKMADEFHRD 10  
| | | | | | | | | |  
Db 650 VKMADEFHRD 659  
RESULT 8  
A4\_HUMAN STANDARD; PRT; 770 AA.  
ID A4\_HUMAN  
AC P05067; P09000; Q16011;  
DT 13-AUG-1987 (Rel. 05, Created)  
DT 01-NOV-1991 (Rel. 20, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Alzheimer's disease amyloid A4 protein precursor (Protease nexin-II) (PN-II) (APP) [contains: Beta-amyloid protein (Beta-Ap) (A-beta)].  
GN APP OR A4 OR CVAP OR ADL.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. NCBI\_TaxID=9606;  
RX TISSUE=Brain;  
RC MEDLINE=87144572; PubMed=2881207;  
RA Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L., Grzeschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.;  
RT "The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surface receptor";  
RT Nature 325:733-736(1987).  
RL Nature 331:525-527(1988).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88122639; PubMed=2893289;  
RA Ponte P., Gonzalez-Dewhitt P., Schilling J., Miller J., Hsu D., Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F., Cordell B.;  
RT "A new A4 amyloid mRNA contains a domain homologous to serine protease inhibitors";  
RT Nature 331:525-527(1988).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89128427; PubMed=2783775;  
RA Lemaire H.-G., Salbaum J.M., Multhaup G., Kang J., Bayney R.M., Unterbeck A., Beyreuther K., Mueller-Hill B.;  
RT "The preA4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded by 16 exons";  
RL Nucleic Acids Res. 17:517-522(1989).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97263807; PubMed=9108164;  
RA Hattori M., Tsukahara F., Furuhata Y., Tanahashi H., Hirose M., Saito M., Tsukuni S., Sakaki Y.;  
RT "A novel method for making nested deletions and its application for sequencing of a 300 kb region of human APP locus";  
RL Nucleic Acids Res. 25:1802-1808(1997).  
RN [5]  
RP SEQUENCE OF 286-345 AND 365-366 FROM N.A.  
RX MEDLINE=88122640; PubMed=2893290;  
RX



RA Tanzi R.E., McClatchey A.I., Lamperti E.D., Villa-Komaroff L.,  
RA Gusella J.F., Neve R.L.;  
RT "Protease inhibitor domain encoded by an amyloid protein precursor  
RT mRNA associated with Alzheimer's disease.";  
RL Nature 331:528-530(1988).  
RN  
RP SEQUENCE OF 287-367 FROM N.A.  
RX MEDLINE=88122641; PubMed=2893291;  
RA Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.;  
RT "Novel precursor of Alzheimer's disease amyloid protein shows  
RT protease inhibitory activity.";  
RL Nature 331:530-532(1988).  
RN  
RN SEQUENCE OF 284-289 AND 365-770 FROM N.A.  
RX MEDLINE=87231971; PubMed=3035574;  
RA Robakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;  
RT "Molecular cloning and characterization of a cDNA encoding the  
RT cerebrovascular and the neuritic plaque amyloid peptides.";  
RL Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).  
RN  
RN SEQUENCE OF 507-770 FROM N.A.  
RX MEDLINE=88124954; PubMed=2893379;  
RA Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,  
RA Marotta C.A.;  
RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer  
RT disease brain: coding and noncoding regions of the fetal precursor  
RT mRNA are expressed in the cortex.";  
RL Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).  
RN  
RN SEQUENCE OF 672-681.  
RX MEDLINE=88035004; PubMed=3312495;  
RA Pardollge W.M., Vinters H.V., Yang J., Eisenberg J., Choi T.B.,  
RA Tourtellotte W.W., Huebner V., Shively J.E.;  
RT "Amyloid angiopathy of Alzheimer's disease: amino acid composition  
RT and partial sequence of a 4,200-dalton peptide isolated from cortical  
RT microvessels.";  
RL J. Neurochem. 49:1394-1401(1987).  
RN  
RN SEQUENCE OF 739-770 FROM N.A.  
RX MEDLINE=90236318; PubMed=2110105;  
RA Yoshikai S.-I., Sasaki H., Doh-Ura K., Furuya H., Sakaki Y.;  
RT "Genomic organization of the human amyloid beta-protein precursor  
RT gene.";  
RL Gene 87:257-263(1990).  
RN  
RN SEQUENCE OF 1-10 FROM N.A.  
RP TISSUE-LIVER;  
RC MEDLINE=89016647; PubMed=3140222;  
RA Schon E.A., Mita S., Sadlock J., Herbert J.;  
RT "A cDNA specifying the human amyloid beta precursor protein (ABP)  
RT encodes a 95-kDa polypeptide.";  
RL Nucleic Acids Res. 16:9351-9351(1988).  
RN  
RN SEQUENCE OF 18-50.  
RX MEDLINE=87250462; PubMed=3597385;  
RA Van Nostrand W.E., Cunningham D.D.;  
RT "Purification of protease nexin II from human fibroblasts.";  
RL J. Biol. Chem. 262:8508-8514(1987).  
RN  
RN IDENTITY OF APP WITH NEXIN-II.  
RX MEDLINE=89384866; PubMed=2506449;  
RA Oltersdorf T., Fritz L.C., Schenk D.B., Lieberburg I.,  
RA Johnson-Wood K.L., Beattie E.C., Ward P.J., Blachek R.W., Dovey H.F.,  
RA Sinha S.;  
RT "The secreted form of the Alzheimer's amyloid precursor protein with  
RT the kunitz domain is protease nexin-II.";  
RL Nature 341:144-147(1989).  
RN  
RN PROTEASE-SPECIFICITY OF INHIBITOR DOMAIN.  
RX MEDLINE=90211252; PubMed=1969731;  
RA Kido H., Fukutomi A., Schilling J., Wang Y., Corbelli B., Kitunuma N.;  
RT "Protease-specificity of kunitz inhibitor domain of Alzheimer's  
RT disease amyloid protein precursor.";

RL Biochem. Biophys. Res. Commun. 167:716-721(1990).  
RN  
RN COMPLEX WITH G(O).  
RX MEDLINE=93188965; PubMed=8446172;  
RA Nishimoto I., Okamoto T., Matsuura Y., Takahashi S., Okamoto T.,  
RA Murayama Y., Ogata E.;  
RT "Alzheimer amyloid protein precursor complexes with brain GTP-binding  
RT protein G(O).";  
RL Nature 362:75-79(1993).  
RN  
RN X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 28-133.  
RX MEDLINE=99215582; PubMed=10201399;  
RA Rossjohn J., Cappai R., Fell S.C., Henry A., McKinsty W.J.,  
RA Galatis D., Heese L., Multhaup G., Beyreuther K., Masters C.L.,  
RA Parker M.W.;  
RT "Crystal structure of the N-terminal growth factor-like domain of  
RT Alzheimer amyloid precursor protein.";  
RL Nat. Struct. Biol. 6:327-331(1999).  
RN  
RN X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF 287-344.  
RX MEDLINE=91104913; PubMed=2125487;  
RA Hynes T.R., Randal M., Kennedy L.A., Eigenbrodt C., Kosiakof A.A.;  
RT "X-ray crystal structure of the protease inhibitor domain of  
RT Alzheimer's amyloid beta-protein precursor.";  
RL Biochemistry 29:10018-10022(1990).  
RN  
RN STRUCTURE BY NMR OF 289-344.  
RX MEDLINE=92031488; PubMed=1718421;  
RA Heald S.L., Tilton R.F., Jr., Hammond L.S., Lee A., Bayney R.M.,  
RA Kamaek M.E., Ramabhadran T.V., Dreyer R.N., Davis G., Unterbeck A.,  
RA Tamburini P.P.;  
RT "Sequential NMR resonance assignment and structure determination of  
RT the kunitz-type inhibitor domain of the Alzheimer's beta-amyloid  
RT precursor protein.";  
RL Biochemistry 30:10467-10476(1991).  
RN  
RN STRUCTURE BY NMR OF 672-699.  
RX MEDLINE=94281210; PubMed=7516706;  
RA Talafous J., Marchowski K.J., Klopman G., Zagorski M.G.;  
RT "Solution structure of residues 1-28 of the amyloid beta-peptide.";  
RL Biochemistry 33:7788-7796(1994).  
RN  
RN STRUCTURE BY NMR OF 696-706.  
RX MEDLINE=97128622; PubMed=8973180;  
RA Kohno T., Kobayashi K., Maeda T., Sato K., Takashima A.;  
RT "Three-dimensional structures of the amyloid beta peptide (25-35) in  
RT membrane-mimicking environment.";  
RL Biochemistry 35:16094-16104(1996).  
RN  
RN STRUCTURE BY NMR OF 672-711.  
RX MEDLINE=98359783; PubMed=9693002;  
RA Coles M., Bicknell W., Watson A.A., Fairlie D.P., Craik D.J.;  
RT "Solution structure of amyloid beta-peptide(1-40) in a water-miscelle  
RT environment. Is the membrane-spanning domain where we think it is?";  
RL Biochemistry 37:11064-11077(1998).  
RN  
RN STRUCTURE BY NMR OF 672-699.  
RX MEDLINE=20400066; PubMed=10940222;  
RA Poulsen S.-A., Watson A.A., Craik D.J.;  
RT "Solution structures in aqueous SDS micelles of two amyloid beta  
RT peptides of Abeta(1-28) mutated at the alpha-secretase cleavage  
RT site.";  
RL J. Struct. Biol. 130:142-152(2000).  
RN  
RN STRUCTURE BY NMR OF 681-706.  
RX MEDLINE=20400065; PubMed=10940221;  
RA Zhang S., Iwata K., Lachenmann M.J., Peng J.W., Li S., Stimson E.R.,  
RA Lu Y., Felix A.M., Maggio J.E., Lee J.P.;  
RT "The Alzheimer's peptide a beta adopts a collapsed coil structure in  
RT water.";  
RL J. Struct. Biol. 130:130-141(2000).  
RN  
RN SIGNAL SEQUENCE CLEAVAGE SITE, AND TOPOLOGY.



DB 669 VKMDAEFGHD 678

RESULT 10

A4\_RAT STANDARD: PRT: 770 AA.

AC P08592;

DT 01-ANG-1988 (Rel. 08, Created)

DT 01-DEC-1992 (Rel. 24, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Alzheimer's disease amyloid A4 protein homolog precursor

DE (Amyloidogenic glycoprotein) (AG).

GN APP

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI\_Taxid=10116;

RP [1]

RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.

RC TISSUE=Brain;

RC MEDLINE=88312583; PubMed=2900758;

RA Shivers B.D., Hilbich C., Multaup G., Salbaum J.M., Beyreuther K., Seeburg P.H.;

RT "Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brain suggests a role in cell contact.";

RT EMBO J. 7:1365-1370(1988).

RN [2]

RP SEQUENCE OF 289-364 FROM N.A.

RC TISSUE=Liver;

RC MEDLINE=89183625; PubMed=2648331;

RA Kang J., Mueller-Hill B.;

RT "The sequence of the two extra exons in rat preA4.";

RC Nucleic Acids Res. 17:2130-2130(1989).

CC -1- SUBCELLULAR LOCATION: Type I membrane protein.

CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS; APP(395), APP(563), APP(695), APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.

CC -1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION WITH X11 ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF PHOSPHORYLATION (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.

CC -1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.

CC -----

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CC -----

CC EMBL; X07648; CA30488.1; -

CC EMBL; X14066; CAA3229.1; -

CC PIR; S00550; S00550.

CC PIR; S03607; S03607.

CC HSSP; F05067; IAP.

CC InterPro; IPR001868; A4\_APP.

CC InterPro; IPR002223; Kunitz\_BPTI.

CC Pfam; PF02177; A4\_EXTRA.1.

CC Pfam; PF00014; Kunitz\_BPTI.1.

CC PRINTS; PR00203; AMYLOD4.

CC PRINTS; PR00759; BASICPASE.

CC SMART; SM00006; A4\_EXTRA.1.

CC SMART; SM00131; KU.1.

CC PROSITE; PS00319; A4\_EXTRA.1.

CC PROSITE; PS00320; A4\_INTRA.1.

CC PROSITE; PS00280; BPTI\_KUNITZ\_1.

CC PROSITE; PS02729; BPTI\_KUNITZ\_2.1.

CC Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;

KW Alternative splicing; Serine protease inhibitor.

FT SIGNAL 1 17 BY SIMILARITY.

FT CHAIN 18 770 ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN

FT DOMAIN 18 699 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 700 723 POTENTIAL.

FT DOMAIN 724 770 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 673 715 EQUIVALENT OF BETA-AMYLOID PROTEIN.

FT SITE 287 345 BPTI/KUNITZ INHIBITOR.

FT SITE 759 762 CLATHRIN-BINDING (BY SIMILARITY).

FT DISULFID 291 341 BY SIMILARITY.

FT DISULFID 300 324 BY SIMILARITY.

FT DISULFID 316 337 BY SIMILARITY.

FT CARBOHYD 542 542 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 571 571 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT VARSPIC 289 289 E -> V (IN ISOFORM APP(695)).

FT VARSPIC 290 364 MISSING (IN ISOFORM APP(695)).

SO SEQUENCE 770 AA; 86704 MW; C26C9DBB2D929A7 CRC64;

Query Match 87.0%; Score 47; DB 1; Length 770;

Best Local Similarity 90.0%; Pred. No. 0.092;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 VKMDAEFGHD 10

DB 669 VKMDAEFGHD 678

RESULT 11

G6PD\_BORBU

ID G6PD\_BORBU STANDARD: PRT: 478 AA.

AC O51581;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) (G6PD).

GN ZNF OR B06636.

OS Borrelia burgdorferi (Lyme disease spirochete).

OC Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.

OX NCBI\_Taxid=139;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 35210 / B31;

RC MEDLINE=98065943; PubMed=9403685;

RA Fraser C.M., Casjens S., Huang W.M., Dodson R., Hickey E.K., Gwin M., Lathigra R., White O., Ketchum K.A.;

RA Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D., Peterson J., Kellavage A.R., Quackenbush J., Salzberg S., Hanson M., van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J., Uterback T., Watney L., McDonald L., Artiach P., Bowman C., Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B., Smith H.O., Venter J.C.;

RA "Genomic sequence of a Lyme disease spirochete, Borrelia burgdorferi.";

RT Nature 390:580-586(1997).

RT NATURE 390:580-586(1997).

CC -1- CATALYTIC ACTIVITY: D-glucose 6-phosphate + NADP(+) = D-glucono-1,5-lactone 6-phosphate + NADPH.

CC -1- PATHWAY: FIRST STEP IN PENTOSE PHOSPHATE PATHWAY.

CC -1- SIMILARITY: BELONGS TO THE GLUCOSE-6-PHOSPHATE DEHYDROGENASE FAMILY.

CC -----

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CC -----

CC EMBL; AE001165; AAB91531.1; -

CC HSSP; P11411; IDPG.

CC TIGR; B06636; -

CC InterPro; IPR001282; G6PD.

CC Pfam; PF00479; G6PD.1.

DR Pfam; PF02781; G6PD\_C.1.

DR PRINTS: PR00079; G6PDHHRGNASE.  
 DR PRODOM: PD001129; G6PD; 1.  
 DR PROSITE: PS00069; G6P\_DEHYDROGENASE; 1.  
 KW Oxidoreductase: NADP: Glucose metabolism: Complete proteome.  
 FT ACT\_SITE 176 176 BY SIMILARITY.  
 SO SEQUENCE 478 AA; 56113 MW; 4DDCE2861161C8A CRC64;

Query Match 68.5%; Score 37; DB 1; Length 478;  
 Best Local Similarity 60.0%; Pred. No. 5.6;  
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 VKMDAERHD 10  
 : : : : :  
 Db 248 IKFDESEFHD 257

RESULT 12  
 ID COPD\_BOVIN STANDARD; PRT; 511 AA.  
 AC P53619;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Coatomer delta subunit (Delta-coat protein) (Delta-COP).  
 GN COPD.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 CC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE OF 2-511 FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=97011152; PubMed=8858162;  
 RA Falstich D., Auerbach S., Orci L., Ravazzola M., Wegehingel S.,  
 RA Lottspeich F., Stenbeck G., Harter C., Wieland F.T., Tschochner H.;  
 RT "Architecture of coatomer: molecular characterization of delta-COP  
 RT and protein interactions within the complex.";  
 RL J. Cell Biol. 135:53-61(1996).  
 CC -1- FUNCTION: THE COATOMER IS A CYTOSOLIC PROTEIN COMPLEX THAT BINDS  
 CC TO DILYSINE MOTIFS AND REVERSIBLY ASSOCIATES WITH GOLGI NON-  
 CC CLATHRIN-COATED VESICLES, WHICH FURTHER MEDIATE BIOSYNTHETIC  
 CC PROTEIN TRANSPORT FROM THE ER, VIA THE GOLGI UP TO THE TRANS GOLGI  
 CC NETWORK. COATOMER COMPLEX IS REQUIRED FOR BUDDING FROM GOLGI  
 CC MEMBRANES, AND IS ESSENTIAL FOR THE RETROGRADE GOLGI-TO-ER  
 CC TRANSPORT OF DILYSINE-TAGGED PROTEINS. IN MAMMALS, THE COATOMER  
 CC CAN ONLY BE RECRUITED BY MEMBRANES ASSOCIATED TO ADP-RIBOSYLATION  
 CC FACTORS (ARFS), WHICH ARE SMALL GTP-BINDING PROTEINS. THE COMPLEX  
 CC ALSO INFLUENCES THE GOLGI STRUCTURAL INTEGRITY, AS WELL AS THE  
 CC PROCESSING, ACTIVITY, AND ENDOCYTIC RECYCLING OF LDL RECEPTORS (BY  
 CC SIMILARITY).  
 CC -1- SUBUNIT: OLIGOMERIC COMPLEX THAT CONSISTS OF AT LEAST THE ALPHA,  
 CC BETA, BETA', GAMMA, DELTA, EPSILON AND ZETA SUBUNITS.  
 CC -1- SUBCELLULAR LOCATION: THE COATOMER IS CYTOPLASMIC OR POLYMERIZED  
 CC ON THE CYTOPLASMIC SIDE OF THE GOLGI, AS WELL AS ON THE  
 CC VESICLES/BUDS ORIGINATING FROM IT (BY SIMILARITY).  
 CC -1- TISSUE SPECIFICITY: UBICITOUSLY EXPRESSED.  
 CC -1- SIMILARITY: BELONGS TO THE ADAPTOR COMPLEXES MEDIUM SUBUNITS  
 CC FAMILY. COPD SUBFAMILY.

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 CC -----  
 DR EMBL: X94265; CAA63941.1; -;  
 DR InterPro: IPR001992; Adap\_comp\_sub.  
 DR Pfam: PF00928; Adap\_comp\_sub; 1.  
 KW Transport; Protein transport; Golgi stack; Membrane.  
 SO SEQUENCE 511 AA; 57274 MW; 6A285798F252C7F CRC64;

Query Match 64.8%; Score 35; DB 1; Length 511;  
 Best Local Similarity 55.6%; Pred. No. 15;  
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 KMDAERHD 10  
 : : : : :  
 Db 424 EIDGEXRHD 432

RESULT 13  
 ID COPD\_HUMAN STANDARD; PRT; 511 AA.  
 AC P48444;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Coatomer delta subunit (Delta-coat protein) (Delta-COP) (Archain).  
 GN COPD OR ARCN1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95301274; PubMed=7782067;  
 RA Radice P., Pensotti V., Jones C., Perry H., Pierotti M.A.,  
 RA Tunaciliffe A.;  
 RT "The human archain gene, ARCN1, has highly conserved homologs in rice  
 RT and Drosophila.";  
 RL Genomics 26:101-106(1995).  
 CC -1- FUNCTION: THE COATOMER IS A CYTOSOLIC PROTEIN COMPLEX THAT BINDS  
 CC TO DILYSINE MOTIFS AND REVERSIBLY ASSOCIATES WITH GOLGI NON-  
 CC CLATHRIN-COATED VESICLES, WHICH FURTHER MEDIATE BIOSYNTHETIC  
 CC PROTEIN TRANSPORT FROM THE ER, VIA THE GOLGI UP TO THE TRANS GOLGI  
 CC NETWORK. COATOMER COMPLEX IS REQUIRED FOR BUDDING FROM GOLGI  
 CC MEMBRANES, AND IS ESSENTIAL FOR THE RETROGRADE GOLGI-TO-ER  
 CC TRANSPORT OF DILYSINE-TAGGED PROTEINS. IN MAMMALS, THE COATOMER  
 CC CAN ONLY BE RECRUITED BY MEMBRANES ASSOCIATED TO ADP-RIBOSYLATION  
 CC FACTORS (ARFS), WHICH ARE SMALL GTP-BINDING PROTEINS. THE COMPLEX  
 CC ALSO INFLUENCES THE GOLGI STRUCTURAL INTEGRITY, AS WELL AS THE  
 CC PROCESSING, ACTIVITY, AND ENDOCYTIC RECYCLING OF LDL RECEPTORS (BY  
 CC SIMILARITY).  
 CC -1- SUBUNIT: OLIGOMERIC COMPLEX THAT CONSISTS OF AT LEAST THE ALPHA,  
 CC BETA, BETA', GAMMA, DELTA, EPSILON AND ZETA SUBUNITS.  
 CC -1- SUBCELLULAR LOCATION: THE COATOMER IS CYTOPLASMIC OR POLYMERIZED  
 CC ON THE CYTOPLASMIC SIDE OF THE GOLGI, AS WELL AS ON THE  
 CC VESICLES/BUDS ORIGINATING FROM IT (BY SIMILARITY).  
 CC -1- TISSUE SPECIFICITY: UBICITOUSLY EXPRESSED.  
 CC -1- SIMILARITY: BELONGS TO THE ADAPTOR COMPLEXES MEDIUM SUBUNITS  
 CC FAMILY. COPD SUBFAMILY.

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 CC -----  
 DR EMBL: X81197; CAA57071.1; -;  
 DR EMBL: X81196; CAA57072.1; ALT\_INIT.  
 DR MIM: 600820; -;  
 DR InterPro: IPR001992; Adap\_comp\_sub.  
 DR Pfam: PF00928; Adap\_comp\_sub; 1.  
 KW Transport; Protein transport; Golgi stack; Membrane; Polymorphism.  
 FT VARIANT 186 186 F->L (IN DBSNP:682327).  
 FT /FTID=VAR\_011786.  
 FT VARIANT 309 309 K->N (IN DBSNP:1063124).  
 FT /FTID=VAR\_011789.  
 SO SEQUENCE 511 AA; 57210 MW; 4ED1F7D2D12A7E75 CRC64;

Query Match 64.8%; Score 35; DB 1; Length 511;

Best Local Similarity 55.6%; Pred. No. 15;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 KMDAERRD 10  
Db 424 IDDEFRHD 432

## RESULT 14

GLND\_PSEAE STANDARD; PRT; 900 AA.

AC Q929H0.  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE [Protein-PilI uridylyltransferase (EC 2.7.7.59) (Pti uridylyl-  
transferase) (uridylyl removing enzyme) (Urase).  
GN GLND OR PA3658.  
OS Pseudomonas aeruginosa.  
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
OC Pseudomonas.  
OX NCBI\_TaxID=287;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 15692 / PA01;  
RA Nishimoto H.;  
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.

## RESULT 15

GLND\_PSEAE STANDARD; PRT; 394 AA.

AC Q31297.  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Elongation factor Tu (EF-Tu).  
GN TUF OR B0526.  
OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum  
symbiotic bacterium).  
OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.  
OX NCBI\_TaxID=118099;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=TOKYO 1998;  
RA MEDLINE=20445173; PubMed=10993077;  
RA Shigenobu S., Matanabe H., Hattori M., Sakaki Y., Ishikawa H.;  
RT "Genome sequence of the endocellular bacterial symbiont of aphids  
Buchnera sp. APS."  
RL Mature 407:81-86(2000).  
RN [2]  
RP SEQUENCE OF 20-384 FROM N.A.  
RX MEDLINE=98242088; PubMed=9580987;  
RA Brynne E.U., Kurland C.G., Moran N.A., Andersson S.G.;  
RT "Evolutionary rates for tuf genes in endosymbionts of aphids."  
RL Mol. Biol. Evol. 15:574-582(1998).  
CC -1- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING OF  
AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN  
BIOSYNTHESIS.  
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -1- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.  
CC EF-TU/EF-1A SUBFAMILY.

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CC -----

CC EMBL: AB024601; BAA75913.1; ALT\_FRAME.  
CC EMBL: AE004785; AAG07046.1; -.  
CC InterPro: IPR002912; ACT.  
CC InterPro: IPR002819; HD.  
CC InterPro: IPR003607; HDC.  
CC InterPro: IPR002934; NTP\_transf.  
CC Pfam: PF01842; ACT; 2.  
CC Pfam: PF01842; HD; 1.  
CC Pfam: PF01909; NTP\_transf\_2; 1.  
CC SMART: SM00471; HDC; 1.  
CC Transferrase: Nucleotidyltransferase; Complete proteome.  
CC TRANSFERASE: Nucleotidyltransferase; Complete proteome.  
CC CONFLICT 811 811 L->V (IN REF. 1).  
CC SOURCE 900 AA: 103404 MW; 7C71F31EC284E836 CRC64;

CC Query Match 64.8%; Score 35; DB 1; Length 900;  
CC Best Local Similarity 75.0%; Pred. No. 27;  
CC Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 KMDAERRD 10  
Db 400 IDDEFRHD 407

RESULT 15  
EFTU\_BUCAI STANDARD; PRT; 394 AA.

AC Q31297.  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Elongation factor Tu (EF-Tu).  
GN TUF OR B0526.  
OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum  
symbiotic bacterium).  
OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.  
OX NCBI\_TaxID=118099;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=TOKYO 1998;  
RA MEDLINE=20445173; PubMed=10993077;  
RA Shigenobu S., Matanabe H., Hattori M., Sakaki Y., Ishikawa H.;  
RT "Genome sequence of the endocellular bacterial symbiont of aphids  
Buchnera sp. APS."  
RL Mature 407:81-86(2000).  
RN [2]  
RP SEQUENCE OF 20-384 FROM N.A.  
RX MEDLINE=98242088; PubMed=9580987;  
RA Brynne E.U., Kurland C.G., Moran N.A., Andersson S.G.;  
RT "Evolutionary rates for tuf genes in endosymbionts of aphids."  
RL Mol. Biol. Evol. 15:574-582(1998).  
CC -1- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING OF  
AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN  
BIOSYNTHESIS.  
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -1- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.  
CC EF-TU/EF-1A SUBFAMILY.

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CC -----

CC EMBL: AF001119; BAB13219.1; ALT\_INIT.  
CC EMBL: Y12307; CAI72974.1; -.  
CC HSP: P02990; LEU.  
CC InterPro: IPR000795; GTP\_EFTU.  
CC Pfam: PF00009; GTP\_EFTU; 1.  
CC PRINTS: PS00315; EFCTOR\_GTP; 1.  
CC Elongation factor; Protein biosynthesis; GTP-binding;  
CC Complete proteome.  
CC NP\_BIND 19 26 GTP (BY SIMILARITY).  
CC NP\_BIND 81 85 GTP (BY SIMILARITY).  
CC NP\_BIND 136 139 GTP (BY SIMILARITY).  
CC CONFLICT 89 89 I->M (IN REF. 2).  
CC SOURCE 394 AA: 43465 MW; 09B73EADCA0DF5F6 CRC64;

CC Query Match 63.0%; Score 34; DB 1; Length 394;  
CC Best Local Similarity 66.7%; Pred. No. 18;  
CC Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 VKMDAERRH 9  
Db 68 VETDIFRRH 76

Tue Oct 29 11:23:38 2002

us-09-580-018-6.rsp

Page 10

Search completed: October 29, 2002, 10:27:31  
Job time : 6 secs

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OM protein - protein search, using sw model

Run on: October 29, 2002, 10:23:11 ; Search time 18 seconds

(without alignments)  
96.108 Million cell updates/sec

Title: US-09-580-018-6  
Perfect score: 54  
Sequence: 1 VKMAEFRRD 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: SPREMBL\_19:\*  
2: sp.archaea:\*  
3: sp.fungi:\*  
4: sp.human:\*  
5: sp.invertebrate:\*  
6: sp.mammal:\*  
7: sp.mhc:\*  
8: sp.organelle:\*  
9: sp.phage:\*  
10: sp.plant:\*  
11: sp.rodent:\*  
12: sp.virus:\*  
13: sp.vertibrate:\*  
14: sp.unclassified:\*  
15: sp.virus:\*  
16: sp.bacteriap:\*  
17: sp.archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	82	4	P78438
2	54	100.0	82	4	016014
3	54	100.0	82	4	016019
4	54	100.0	82	4	016020
5	54	100.0	534	13	093296
6	54	100.0	569	13	09FVL1
7	54	100.0	695	6	095KN7
8	54	100.0	695	11	060496
9	54	100.0	695	13	09DGB8
10	54	100.0	751	13	09DGB7
11	54	100.0	770	6	09TUI0
12	48	88.9	693	13	098SG0
13	48	88.9	695	13	098SF9
14	48	88.9	747	13	091963
15	47	87.0	79	11	035463
16	47	87.0	607	11	099K32

17	47	87.0	695	11	P97487	P97487 mus musculus
18	41	75.9	423	2	O52379	O52379 raietonia s
19	41	75.9	423	2	O45693	O45693 burkholderi
20	40	74.1	19	4	O9UCB8	O9UCB8 homo sapien
21	40	74.1	28	4	O9UCD1	O9UCD1 homo sapien
22	40	74.1	30	4	O9UCB9	O9UCB9 homo sapien
23	40	74.1	33	4	O9UCB3	O9UCB3 homo sapien
24	37	68.5	210	2	O93MK6	O93MK6 vibrio vuln
25	37	68.5	329	17	O9HGI1	O9HGI1 halobacteri
26	36	66.7	543	10	O9L2L4	O9L2L4 arabidopsis
27	36	66.7	578	16	O9KNV0	O9KNV0 vibrio chol
28	36	66.7	755	5	O9VFE30	O9VFE30 drosophila
29	35	64.8	347	12	O9LEB6	O9LEB6 chilo tride
30	35	64.8	428	16	O9L2D4	O9L2D4 pseudomonas
31	35	64.8	454	5	O9UA07	O9UA07 caenorhabdi
32	35	64.8	462	5	O9Y198	O9Y198 caenorhabdi
33	35	64.8	473	11	O91VG7	O91VG7 mus musculu
34	35	64.8	475	5	O9U343	O9U343 caenorhabdi
35	35	64.8	503	5	O21424	O21424 caenorhabdi
36	35	64.8	511	11	O91W48	O91W48 mus musculu
37	35	64.8	634	5	O9U9Y8	O9U9Y8 caenorhabdi
38	35	64.8	647	5	O62395	O62395 caenorhabdi
39	35	64.8	774	16	O92CV7	O92CV7 listeria in
40	35	64.8	1001	4	O9H2K7	O9H2K7 homo sapien
41	35	64.8	1001	4	O96L75	O96L75 homo sapien
42	35	64.8	1001	11	O08664	O08664 rattus norv
43	35	64.8	1005	4	O9P2I6	O9P2I6 homo sapien
44	34	63.0	79	16	O52658	O52658 pseudomonas
45	34	63.0	105	10	O9LJL9	O9LJL9 pyrus pyrif

## ALIGNMENTS

RESULT 1  
P78438 PRELIMINARY; PRT; 82 AA.  
AC P78438;  
DT 01-MAY-1997 (TRENBERL. 03, Created)  
DT 01-MAY-1997 (TRENBERL. 03, Last sequence update)  
DT 01-MAR-2001 (TRENBERL. 16, Last annotation update)  
DE AMYLOID PROTEIN (BETA-AMYLOID PROTEIN) (FRAGMENT).  
GN App.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=8932030; PubMed=2675837;  
RA Johnstone E.M., Chaney M.O., Moore R.E., Ward K.E., Norris F.H.,  
RA Little S.P.;  
RT "Alzheimer's disease amyloid peptide is encoded by two exons and shows  
RT similarity to soybean trypsin inhibitor.";  
RL Biochem. Biophys. Res. Commun. 163:1248-1255(1989).  
RN [2]  
RP SEQUENCE OF 19-48 FROM N.A.  
RX MEDLINE=87120329; PubMed=2949367;  
RA Tanzi R.E., Gusella J.F., Watkins P.C., Bruns G.A., George-Hyslop P.,  
RA Van Keuren M.L., Patterson D., Pagan S., Kurnit D.M., Neye R.L.;  
RT "Amyloid beta protein gene: CDNA, mRNA distribution, and genetic  
RT linkage near the Alzheimer locus.";  
RL Science 235:880-884(1987).  
RN [3]  
RP SEQUENCE OF 32-63 FROM N.A.  
RX MEDLINE=93035397; PubMed=1415269;  
RA Kamino K., Orr H.T., Payami H., Wilmsman E.M., Alonso M.E., Pulst S.M.,  
RA Anderson L., O'dahl S., Nemens E., White J.A.;  
RT "Linkage and mutational analysis of familial Alzheimer disease  
RT kindreds for the APP gene region.";  
RL Am. J. Hum. Genet. 51:998-1014(1992).  
DR EMBL; M29270; AAA51768.1; -.  
DR EMBL; M29269; AAA51768.1; JOINED.

DR EMBL: M15532: AAA51564.1: -.  
 DR EMBL: S45136: AAB23646.1: -.  
 DR HSSP: P05067: 1BA4.  
 FT NON\_TER 1  
 SQ SEQUENCE 82 AA: 8994 MW: 8DA9EA2B813A070E CRC64:

Query Match 100.0%; Score 54; DB 4; Length 82;  
 Best Local Similarity 100.0%; Pred. No. 0.0019;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKMDAEFRHD 10  
 DB 14 VKMDAEFRHD 23

## RESULT 2

Q16014 PRELIMINARY; PRT; 82 AA.

AC Q16014; (TREMBLREL. 01, Created)  
 DT 01-NOV-1996 (TREMBLREL. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLREL. 19, Last annotation update)  
 DE BETA-AMYLOID PEPTIDE (FRAGMENT).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93236601; PubMed=8476439;  
 RA Denman R.B., Rosenzweig R., Miller D.L.;  
 RT "A system for studying the effect(s) of familial Alzheimer disease  
 mutations on the processing of the beta-amyloid peptide precursor.";  
 RL Biochem. Biophys. Res. Commun. 192:96-103(1993).  
 DR EMBL: S60721: AAB26263.2: -.  
 DR HSSP: P05067: 1BA4.  
 FT NON\_TER 1  
 FT NON\_TER 82  
 SQ SEQUENCE 82 AA: 8972 MW: F534AA5B3EA9230A CRC64;

Query Match 100.0%; Score 54; DB 4; Length 82;  
 Best Local Similarity 100.0%; Pred. No. 0.0019;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKMDAEFRHD 10  
 DB 15 VKMDAEFRHD 24

## RESULT 3

Q16019 PRELIMINARY; PRT; 82 AA.

AC Q16019; (TREMBLREL. 01, Created)  
 DT 01-NOV-1996 (TREMBLREL. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLREL. 19, Last annotation update)  
 DE BETA-AMYLOID PEPTIDE (FRAGMENT).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93236601; PubMed=8476439;  
 RA Denman R.B., Rosenzweig R., Miller D.L.;  
 RT "A system for studying the effect(s) of familial Alzheimer disease  
 mutations on the processing of the beta-amyloid peptide precursor.";  
 RL Biochem. Biophys. Res. Commun. 192:96-103(1993).  
 DR EMBL: S61380: AAB26264.2: -.  
 DR HSSP: P05067: 1BA4.  
 FT NON\_TER 1  
 FT NON\_TER 82

SQ SEQUENCE 82 AA: 8938 MW: F534AA50E579230A CRC64;

Query Match 100.0%; Score 54; DB 4; Length 82;  
 Best Local Similarity 100.0%; Pred. No. 0.0019;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKMDAEFRHD 10  
 DB 15 VKMDAEFRHD 24

## RESULT 4

Q16020 PRELIMINARY; PRT; 82 AA.

AC Q16020; (TREMBLREL. 01, Created)  
 DT 01-NOV-1996 (TREMBLREL. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLREL. 19, Last annotation update)  
 DE BETA-AMYLOID PEPTIDE (FRAGMENT).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93236601; PubMed=8476439;  
 RA Denman R.B., Rosenzweig R., Miller D.L.;  
 RT "A system for studying the effect(s) of familial Alzheimer disease  
 mutations on the processing of the beta-amyloid peptide precursor.";  
 RL Biochem. Biophys. Res. Commun. 192:96-103(1993).  
 DR EMBL: S61383: AAB26265.2: -.  
 DR HSSP: P05067: 1BA4.  
 FT NON\_TER 1  
 FT NON\_TER 82  
 SQ SEQUENCE 82 AA: 8882 MW: F534AA5AE5D9230A CRC64;

Query Match 100.0%; Score 54; DB 4; Length 82;  
 Best Local Similarity 100.0%; Pred. No. 0.0019;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKMDAEFRHD 10  
 DB 15 VKMDAEFRHD 24

## RESULT 5

Q93296 PRELIMINARY; PRT; 534 AA.

AC Q93296; (TREMBLREL. 08, Created)  
 DT 01-NOV-1998 (TREMBLREL. 08, Last sequence update)  
 DT 01-DEC-2001 (TREMBLREL. 19, Last annotation update)  
 DE AMYLOID PROTEIN (FRAGMENT).  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98337885; PubMed=9671674;  
 RA Barnes N.Y., Li L., Yoshikawa K., Schwartz L.M., Oppenheim R.W.,  
 RA Milligan C.E.;  
 RT "Increased production of amyloid precursor protein provides a  
 substrate for caspase-3 in dying motoneurons.";  
 RL J. Neurosci. 18:5869-5880(1998).  
 DR EMBL: AF042098: AAC25052.1: -.  
 DR HSSP: P05067: 1BA4.  
 DR InterPro: IPR001868; A4\_APP.  
 DR PRINTS: PR00203; AMYLOID4.  
 DR PROSITE: PS00319; A4\_EXTRA; 1.  
 DR PROSITE: PS00320; A4\_INTRA; 1.



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FT NON_TER 1
SQ SEQUENCE 534 AA; 60597 MW; FB53ECC2E66D4C92 CRC64;
Query Match 100.0%; Score 54; DB 13; Length 534;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VKMDAEFRHD 10
DB 433 VKMDAEFRHD 442

RESULT 6
O95KNT PRELIMINARY; PRT; 569 AA.
ID O95KNT
AC O95KNT
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE AMYLOID PROTEIN (FRAGMENT).
GN APP.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauromorpha; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Coulson E.J., Paliaga K., Beyreuther K., Masters C.L.;
RT "What the evolution of the amyloid protein precursor supergene family
RT tells us about its function."
RL Neurochem. Int. 0:0-0(2000).
DR EMBL: AF030341; AAF12698.1; -.
DR HSSP: P05067; 1BA4.
DR InterPro: IPR001868; A4_APP.
DR Pfam: PF02177; A4_EXTRA; 1.
DR PRINTS: PR00203; AMYLOIDA.
DR SMART: SM00006; A4_EXTRA; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
FT NON_TER 1
SQ SEQUENCE 569 AA; 64753 MW; 0AB8B851863A19D CRC64;
Query Match 100.0%; Score 54; DB 13; Length 569;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VKMDAEFRHD 10
DB 469 VKMDAEFRHD 478

RESULT 7
O95KNT PRELIMINARY; PRT; 695 AA.
ID O95KNT
AC O95KNT
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE AMYLOID B-PROTEIN PRECURSOR.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CEREBELLUM;
RX Podlany M.B., Tolian D.R., Selkoe D.J.;
RA "Homology of the amyloid beta protein precursor in monkey and human
RT supports a primate model for beta amyloidosis in Alzheimer's

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RT disease."
RL Am. J. Pathol. 138:1423-1435(1991).
DR EMBL: M58727; AAA36829.1; -.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 597 636
SQ SEQUENCE 695 AA; 78663 MW; 4F6EA0139F969D56 CRC64;
Query Match 100.0%; Score 54; DB 6; Length 695;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VKMDAEFRHD 10
DB 594 VKMDAEFRHD 603

RESULT 8
O60496 PRELIMINARY; PRT; 695 AA.
ID O60496
AC O60496
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE PUTATIVE AMYLOID PRECURSOR PROTEIN.
OS Cavia sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.
OX NCBI_TaxID=10143;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Beck M., Mueller D., Bigl V.;
RT "Amyloid precursor protein in Guinea pigs - complete cDNA sequence and
RT alternative splicing."
RL Biochim. Biophys. Acta 1351:17-21(1997).
DR EMBL: X97631; CA66230.1; -.
DR HSSP: P05067; 1BA4.
DR InterPro: IPR001868; A4_APP.
DR Pfam: PF02177; A4_EXTRA; 1.
DR PRINTS: PR00203; AMYLOIDA.
DR SMART: SM00006; A4_EXTRA; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
SQ SEQUENCE 695 AA; 78701 MW; 5196A0C4017F16AB CRC64;
Query Match 100.0%; Score 54; DB 11; Length 695;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VKMDAEFRHD 10
DB 594 VKMDAEFRHD 603

RESULT 9
O9DGJ8 PRELIMINARY; PRT; 695 AA.
ID O9DGJ8
AC O9DGJ8
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE BETA-AMYLOID PRECURSOR PROTEIN 695 ISOFORM.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauromorpha; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Sarasa M., Rodolase A., Sorribas V.;
RT "Cloning of full-length chicken beta-amyloid precursor protein
RT isoforms."

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RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF289218; AAC00593.1; -  
DR HSSP: P05067; 1BA4.  
DR InterPro: IPR001868; A4\_APP.  
DR Pfam: PF02177; A4\_EXTRA; 1.  
DR PRINTS: PR00203; AMYLOIDA4.  
DR SMART: SM00006; A4\_EXTRA; 1.  
DR PROSITE: PS00319; A4\_EXTRA; 1.  
SQ SEQUENCE 695 AA; 78565 MW; F201ED02AEC86D95 CRC64;  
  
Query Match 100.0%; Score 54; DB 13; Length 695;  
Best Local Similarity 100.0%; Pred. No. 0.018; Mismatches 0; Indels 0; Gaps 0;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 VKMDAEFRHD 10  
Db 594 VKMDAEFRHD 603  
|||||  
  
RESULT 10  
Q9DGJ7 PRELIMINARY; PRT; 751 AA.  
AC Q9DGJ7; (TREMUREL, 16, Created)  
DT 01-MAR-2001 (TREMUREL, 16, Last sequence update)  
DT 01-MAR-2001 (TREMUREL, 19, Last annotation update)  
DE BETA-AMYLOID PRECURSOR PROTEIN 751 ISOFORM.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Sarasa M., Rodolose A., Sorribas V.;  
RT "Cloning of full-length chicken beta-amyloid precursor protein  
isoforms."  
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF289219; AAC00594.1; -  
DR HSSP: P05067; 1BA4.  
DR InterPro: IPR001868; A4\_APP.  
DR InterPro: IPR002223; Kunitz\_BPTI.  
DR Pfam: PF02177; A4\_EXTRA; 1.  
DR Pfam: PF00014; Kunitz\_BPTI; 1.  
DR PRINTS: PR00203; AMYLOIDA4.  
DR PRINTS: PR00759; BASICPTASE.  
DR SMART: SM00006; A4\_EXTRA; 1.  
DR SMART: SM00131; KU; 1.  
DR PROSITE: PS00280; BPTI\_KUNITZ\_1; 1.  
DR PROSITE: PS50279; BPTI\_KUNITZ\_2; 1.  
KW Serine protease inhibitor.  
SQ SEQUENCE 751 AA; 84705 MW; E78E9413A8033D84 CRC64;  
  
Query Match 100.0%; Score 54; DB 13; Length 751;  
Best Local Similarity 100.0%; Pred. No. 0.02; Mismatches 0; Indels 0; Gaps 0;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 VKMDAEFRHD 10  
Db 650 VKMDAEFRHD 659  
|||||  
  
RESULT 11  
Q9TUI0 PRELIMINARY; PRT; 770 AA.  
AC Q9TUI0; (TREMUREL, 13, Created)  
DT 01-MAY-2000 (TREMUREL, 13, Last sequence update)  
DT 01-MAY-2000 (TREMUREL, 19, Last annotation update)  
DE AMYLOID PRECURSOR PROTEIN.  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OX NCBI\_TaxID=9823;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Kimura A., Takahashi T.;  
RT "Amyloid Precursor Protein 770."  
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AB032550; BAA84580.1; -  
DR HSSP: P05067; 1AAP.  
DR InterPro: IPR001868; A4\_APP.  
DR InterPro: IPR002223; Kunitz\_BPTI.  
DR Pfam: PF02177; A4\_EXTRA; 1.  
DR Pfam: PF00014; Kunitz\_BPTI; 1.  
DR PRINTS: PR00203; AMYLOIDA4.  
DR PRINTS: PR00759; BASICPTASE.  
DR SMART: SM00006; A4\_EXTRA; 1.  
DR SMART: SM00131; KU; 1.  
DR PROSITE: PS00319; A4\_EXTRA; 1.  
DR PROSITE: PS00320; A4\_INTRA; 1.  
DR PROSITE: PS00280; BPTI\_KUNITZ\_1; 1.  
DR PROSITE: PS50279; BPTI\_KUNITZ\_2; 1.  
KW Serine protease inhibitor.  
SQ SEQUENCE 770 AA; 86961 MW; 5F7A1DCB2BC583E CRC64;  
  
Query Match 100.0%; Score 54; DB 6; Length 770;  
Best Local Similarity 100.0%; Pred. No. 0.02; Mismatches 0; Indels 0; Gaps 0;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 VKMDAEFRHD 10  
Db 669 VKMDAEFRHD 678  
|||||  
  
RESULT 12  
Q98SG0 PRELIMINARY; PRT; 693 AA.  
ID Q98SG0;  
AC Q98SG0; (TREMUREL, 17, Created)  
DT 01-JUN-2001 (TREMUREL, 17, Last sequence update)  
DT 01-JUN-2001 (TREMUREL, 19, Last annotation update)  
DE BETA-AMYLOID PRECURSOR PROTEIN A.  
GN APP.  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Van den Hurk W.H.;  
RL Thesis (2001), Department of Biological Sciences,  
University of Nijmegen, Nijmegen, Netherlands.  
DR EMBL: AJ298150; CAC37193.1; -  
DR HSSP: P05067; 1H23.  
DR InterPro: IPR001868; A4\_APP.  
DR InterPro: IPR002223; Kunitz\_BPTI.  
DR Pfam: PF02177; A4\_EXTRA; 1.  
DR PRINTS: PR00203; AMYLOIDA4.  
DR SMART: SM00006; A4\_EXTRA; 1.  
DR PROSITE: PS00319; A4\_EXTRA; 1.  
DR PROSITE: PS00320; A4\_INTRA; 1.  
KW Signal.  
FT SIGNAL 1 18 POTENTIAL.  
SQ SEQUENCE 693 AA; 78568 MW; CAF1DF655C1AB653 CRC64;  
  
Query Match 88.9%; Score 48; DB 13; Length 693;  
Best Local Similarity 80.0%; Pred. No. 0.29; Mismatches 0; Indels 0; Gaps 0;  
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 VKMDAEFRHD 10  
Db 592 VKMDSEYRHD 601  
|||||  
  
RESULT 13

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Q98SF9          PRELIMINARY;      PRT;      695 AA.
ID  Q98SF9;
AC  Q98SF9;
DT  01-JUN-2001 (TREMBLrel. 17, Created)
DT  01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE  01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE  BETA-AMYLROID PRECURSOR PROTEIN B.
GN  APP.
OS  Xenopus laevis (African clawed frog).
OC  Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC  Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC  Xenopodinae; Xenopus.
OX  NCBI_TaxID=8355;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Van den Hurk W.H.;
RL  Thesis (2001). Department of Biological Sciences,
    University of Nijmegen, Nijmegen, Netherlands.
DR  HSP; A0298151; CAC37194.1; -.
DR  HSP; P05067; I1H3.
DR  InterPro: IPR001868; A4_APP.
DR  Pfam: PF02177; A4_EXTRA; 1.
DR  PRINTS: PR00203; AMYLOIDA4.
DR  SMART; SM00066; A4_EXTRA; 1.
DR  PROSITE; PS00319; A4_EXTRA; 1.
DR  PROSITE; PS00320; A4_INTRA; 1.
KW  Signal.
FT  SIGNAL.
SQ  SEQUENCE 695 AA; 78803 MW; DC4EB02AFB0204A CRC64;

Query Match
Best Local Similarity 88.9%; Score 48; DB 13; Length 695;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY  1 VKMDAEFRHD 10
    |||:|:|
DB  594 VKMDSYRHD 603

RESULT 14
Q91963          PRELIMINARY;      PRT;      747 AA.
ID  Q91963;
AC  Q91963;
DT  01-NOV-1996 (TREMBLrel. 01, Created)
DT  01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE  01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE  APP747.
GN  APP747.
OS  Xenopus.
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC  Xenopodinae.
OX  NCBI_TaxID=8353;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  MEDLINE=93129227; PubMed=1282805;
    Okado H., Okamoto H.;
RT  "A Xenopus homologue of the human beta-amyloid precursor protein:
    RT  developmental regulation of its gene expression";
    Biochem Biophys Res Commun. 189:1561-1568(1992).
DR  EMBL; S52417; AAB24853.1; -.
DR  HSP; P05067; I1H3.
DR  InterPro: IPR001868; A4_APP.
DR  Pfam: PF02177; A4_EXTRA; 1.
DR  InterPro: IPR002223; Kunitz_BPTI.
DR  Pfam: PF00014; Kunitz_BPTI; 1.
DR  PRINTS: PR00203; AMYLOIDA4.
DR  PRINTS: PR00759; BASICPTASE.
DR  SMART; SM00066; A4_EXTRA; 1.
DR  SMART; SM00131; KU; 1.
DR  PROSITE; PS00319; A4_EXTRA; 1.
DR  PROSITE; PS00320; A4_INTRA; 1.
DR  PROSITE; PS00280; BPTI_KUNITZ_1; 1.

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DR  PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW  Serine protease inhibitor.
SQ  SEQUENCE 747 AA; 84893 MW; A75E81885681D948 CRC64;

Query Match
Best Local Similarity 88.9%; Score 48; DB 13; Length 747;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY  1 VKMDAEFRHD 10
    |||:|:|
DB  646 VKMDSYRHD 655

RESULT 15
Q35463          PRELIMINARY;      PRT;      79 AA.
ID  Q35463;
AC  Q35463;
DT  01-JAN-1998 (TREMBLrel. 05, Created)
DT  01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DE  01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE  ALZHEIMER'S AMYLOID BETA PROTEIN (FRAGMENT).
GN  BETA APP.
OS  Cricetus griseus (Chinese hamster).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC  Cricetulus.
OX  NCBI_TaxID=10029;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Sambamurti K., Pimlx I., Gandhi S.;
RL  Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AF030413; AAB86608.1; -.
DR  HSP; P05067; I1H4.
FT  NON_TER 1 79
FT  NON_TER 79 79
SQ  SEQUENCE 79 AA; 8538 MW; 37F2C6C3BFF3F597 CRC64;

Query Match
Best Local Similarity 87.0%; Score 47; DB 11; Length 79;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  1 VKMDAEFRHD 10
    |||:|:|
DB  18 VKMDAEFRGHD 27

Search completed: October 29, 2002, 10:29:43
Job time : 19.1429 secs

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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 29, 2002, 10:23:56 ; Search time 9 Seconds  
(without alignments)  
27.140 Million cell updates/sec

Title: US-09-580-018-6

Perfect score: 54

Sequence: 1 YXMAEFRRMD 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

Issued\_Patents\_AA:\*  
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3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PCRTUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/Backfilest1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	54	100.0	16	5	PCT-US94-07043A-1
2	54	100.0	18	2	US-08-149-975A-3
3	54	100.0	27	1	US-08-141-32A-11
4	54	100.0	27	1	US-08-541-902-11
5	54	100.0	45	1	US-08-462-859A-5
6	54	100.0	45	1	US-08-123-659A-5
7	54	100.0	45	1	US-08-464-247A-5
8	54	100.0	45	1	US-08-464-248A-5
9	54	100.0	53	4	US-09-173-887-5
10	54	100.0	58	1	US-08-371-930-25
11	54	100.0	58	5	PCT-US94-01712-25
12	54	100.0	59	1	US-08-484-969-3
13	54	100.0	59	1	US-08-472-627-3
14	54	100.0	59	1	US-08-388-463-3
15	54	100.0	63	1	US-08-462-859A-3
16	54	100.0	63	1	US-08-462-859A-4
17	54	100.0	63	1	US-08-123-659A-3
18	54	100.0	63	1	US-08-123-659A-4
19	54	100.0	63	1	US-08-464-247A-3
20	54	100.0	63	1	US-08-464-247A-4
21	54	100.0	63	1	US-08-464-248A-3
22	54	100.0	63	1	US-08-464-248A-4
23	54	100.0	103	2	US-08-404-831-2
24	54	100.0	103	2	US-08-612-785B-2
25	54	100.0	103	2	US-08-475-579A-2
26	54	100.0	103	2	US-08-920-162A-2
27	54	100.0	103	3	US-08-339-708A-10

28	54	100.0	103	4	US-09-356-931-2	Sequence 2, Appl1
29	54	100.0	103	4	US-08-703-675C-2	Sequence 2, Appl1
30	54	100.0	103	4	US-08-617-267C-2	Sequence 2, Appl1
31	54	100.0	105	2	US-08-729-345-1	Sequence 1, Appl1
32	54	100.0	117	2	US-08-729-345-3	Sequence 3, Appl1
33	54	100.0	152	6	5187153-4	Patent No. 5187153
34	54	100.0	162	6	5220013-4	Patent No. 5220013
35	54	100.0	162	6	5223482-4	Patent No. 5223482
36	54	100.0	264	1	US-07-990-893-5	Sequence 5, Appl1
37	54	100.0	487	1	US-08-462-859A-9	Sequence 9, Appl1
38	54	100.0	487	1	US-08-123-659A-9	Sequence 9, Appl1
39	54	100.0	487	1	US-08-464-247A-9	Sequence 9, Appl1
40	54	100.0	487	1	US-08-464-248A-9	Sequence 9, Appl1
41	54	100.0	492	1	US-08-462-859A-7	Sequence 7, Appl1
42	54	100.0	492	1	US-08-123-659A-7	Sequence 7, Appl1
43	54	100.0	492	1	US-08-464-247A-7	Sequence 7, Appl1
44	54	100.0	492	1	US-08-464-248A-7	Sequence 7, Appl1
45	54	100.0	537	1	US-08-453-552-4	Sequence 4, Appl1

#### ALIGNMENTS

RESULT 1  
PCT-US94-07043A-1  
Sequence 1, Application PC/TUS9407043A  
GENERAL INFORMATION:  
APPLICANT: Tamburini, Paul P.; Benz, G nter; H bich,  
APPLICANT: Dieter; Dreyer, Robert N.; Koenig, Gerhard  
TITLE OF INVENTION: CATHEPSIN D IS AN AMYLOIDGENIC  
TITLE OF INVENTION: PROTEASE IN ALZHEIMER S DISEASE  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Miles Inc.  
STREET: 400 Morgan Lane  
CITY: West Haven  
STATE: Connecticut  
COUNTRY: USA  
ZIP: 06516  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 800 kb storage  
COMPUTER: Sharp PC 4600  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/07043A  
FILING DATE: June 21, 1994  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/10889  
FILING DATE: November 12, 1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/995,660  
FILING DATE: December 16, 1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/880,914  
FILING DATE: May 11, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Pamela A. Simonton  
REGISTRATION NUMBER: 31,060  
REFERENCE/DOCKET NUMBER: MTI 224.3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (203) 937-2340  
TELEFAX: (203) 937-2795  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
PCT-US94-07043A-1  
Query Match 100.0%; Score 54; DB 5; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0.00011;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKMDAEFRHD 10  
|||||  
Db 4 VKMDAEFRHD 13

## RESULT 2

US-08-149-975A-3

; Sequence 3, Application US/08149975A  
; Patent No. 5849600

GENERAL INFORMATION:

APPLICANT: Nixon, Ralph

APPLICANT: Honda, Toshiyuki

TITLE OF INVENTION: DIAGNOSTIC ASSAYS FOR ALZHEIMER'S

TITLE OF INVENTION: DISEASE

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish &amp; Richardson P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/149,975A

FILING DATE: 11-NOV-1993

CLASSIFICATION: 436

ATTORNEY/AGENT INFORMATION:

NAME: Clark, Paul T.

REGISTRATION NUMBER: 30,162

REFERENCE/DOCKET NUMBER: 04843/016001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/542-5070

TELEFAX: 617/542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-149-975A-3

QY 1 VKMDAEFRHD 10

Db 1 VKMDAEFRHD 10

Query Match 100.0%; Score 54; DB 2; Length 18;

Best local Similarity 100.0%; Pred. No. 0.00013;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## RESULT 3

US-08-141-324-11

; Sequence 11, Application US/08141324  
; Patent No. 5475097

GENERAL INFORMATION:

APPLICANT: Travis, James

APPLICANT: Potempa, Jan S.

APPLICANT: Barr, Philip J.

APPLICANT: Pavloff, Nadine

APPLICANT: Pike, Robert N.

TITLE OF INVENTION: Lysine-specific Porphyromonas gingivalis

TITLE OF INVENTION: Protease

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSEE: Greenlee and Winner, P.C.  
STREET: 5370 Manhattan Circle, Suite 201  
CITY: Boulder  
STATE: CO  
COUNTRY: US  
ZIP: 80303

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/141,324

FILING DATE: 21-OCT-1993

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Ferber, Donna M.

REGISTRATION NUMBER: 33,878

REFERENCE/DOCKET NUMBER: 44-93

TELECOMMUNICATION INFORMATION:

TELEPHONE: 303-499-8080

TELEFAX: 303-499-8089

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 27 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-08-141-324-11

QY 1 VKMDAEFRHD 10

Db 6 VKMDAEFRHD 15

Query Match 100.0%; Score 54; DB 1; Length 27;

Best local Similarity 100.0%; Pred. No. 0.0002;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## RESULT 4

US-08-541-902-11

; Sequence 11, Application US/08541902  
; Patent No. 5707620

GENERAL INFORMATION:

APPLICANT: Travis, James

APPLICANT: Potempa, Jan S.

APPLICANT: Barr, Philip J.

APPLICANT: Pavloff, Nadine

APPLICANT: Pike, Robert N.

TITLE OF INVENTION: Lysine-specific Porphyromonas gingivalis

TITLE OF INVENTION: Protease

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSEE: Greenlee and Winner, P.C.

STREET: 5370 Manhattan Circle, Suite 201

CITY: Boulder

STATE: CO

COUNTRY: US

ZIP: 80303

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/541,902

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/141,324

FILED DATE: 21-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Feibel, Donna M.  
REGISTRATION NUMBER: 33,878  
REFERENCE/DOCKET NUMBER: 44-93  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 303-499-8080  
TELEFAX: 303-499-8089  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-541-902-11

Query Match  
Best Local Similarity 100.0%; Score 54; DB 1; Length 27;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKMDAEFRHD 10  
Db 6 VKMDAEFRHD 15

RESULT 5  
US-08-462-859A-5  
Sequence 5, Application US/08462859A  
Patent No. 5652092  
GENERAL INFORMATION:  
APPLICANT: Jacobsen, J. S.  
APPLICANT: Vittek, M. P.  
TITLE OF INVENTION: No. 5652092e1 Amyloid Precursor and Method of  
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation  
TITLE OF INVENTION: of B-Amyloid Peptide  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: American Cyanamid Company  
STREET: One Cyanamid Plaza  
CITY: Wayne  
STATE: New Jersey  
COUNTRY: United States  
ZIP: 07470-8426  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/462,859A  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Barnhard, Elizabeth M.  
REGISTRATION NUMBER: 31,088  
REFERENCE/DOCKET NUMBER: 31,844-04  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (201)831-3246  
TELEFAX: (201)831-3305  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 45 amino acids  
TYPE: amino acid  
STRANDEDNESS: linear  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-462-859A-5

Query Match  
Best Local Similarity 100.0%; Score 54; DB 1; Length 45;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKMDAEFRHD 10  
Db 7 VKMDAEFRHD 16

RESULT 6  
US-08-123-659A-5  
Sequence 5, Application US/08123659A  
Patent No. 5656477  
GENERAL INFORMATION:  
APPLICANT: Jacobsen, J. S.  
APPLICANT: Vittek, M. P.  
TITLE OF INVENTION: No. 5656477e1 Amyloid Precursor and Method of  
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation  
TITLE OF INVENTION: of B-Amyloid Peptide  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Anne Rosenblum  
STREET: 163 Delaware Avenue, Suite 212  
CITY: Delmar  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 12054  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/123,659A  
FILING DATE: 20-SEP-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Rosenblum, Anne M.  
REGISTRATION NUMBER: 30,419  
REFERENCE/DOCKET NUMBER: 31,844-01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (518)475-0611  
TELEFAX: (518)475-0619  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 45 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-123-659A-5

Query Match  
Best Local Similarity 100.0%; Score 54; DB 1; Length 45;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKMDAEFRHD 10  
Db 7 VKMDAEFRHD 16

RESULT 7  
US-08-464-247A-5  
Sequence 5, Application US/08464247A  
Patent No. 5693478  
GENERAL INFORMATION:  
APPLICANT: Jacobsen, J. S.  
APPLICANT: Vittek, M. P.  
TITLE OF INVENTION: No. 5693478e1 Amyloid Precursor and Method of  
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation  
TITLE OF INVENTION: of B-Amyloid Peptide  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: American Cyanamid Company  
STREET: One Campus Drive  
CITY: Parsippany

STATE: New Jersey  
COUNTRY: United States  
ZIP: 07054  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: US/08/464,247A  
APPLICATION NUMBER: US/08/464,247A  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Barnhard, Elizabeth M.  
REGISTRATION NUMBER: 31,088  
REFERENCE/DOCKET NUMBER: 31,844-03  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-683-2158  
TELEFAX: 201-683-4117  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 45 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-464-247A-5

Query Match 100.0%; Score 54; DB 1; Length 45;  
Best Local Similarity 100.0%; Pred. No. 0.00033;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKMDAEFRHD 10  
DB 7 VKMDAEFRHD 16

RESULT 8  
US-08-464-248A-5  
Sequence 5, Application US/08464248A  
Patent No. 5703209  
GENERAL INFORMATION:  
APPLICANT: Jacobsen, J. S.  
APPLICANT: Vittek, M. P.  
TITLE OF INVENTION: No. 5703209el Amyloid Precursor and Method of  
TITLE OF INVENTION: Using Same to Access Agents Which Down Regulate Formation  
TITLE OF INVENTION: of B-Amyloid Peptide  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: American Cyanamid Company  
STREET: One Cyanamid Plaza  
CITY: Wayne  
STATE: New Jersey  
COUNTRY: United States  
ZIP: 07470-8426  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/464,248A  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Barnhard, Elizabeth M.  
REGISTRATION NUMBER: 31,088  
REFERENCE/DOCKET NUMBER: 31,844-02  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (201)831-3246  
TELEFAX: (201)831-3305  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:

LENGTH: 45 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-464-248A-5

Query Match 100.0%; Score 54; DB 1; Length 45;  
Best Local Similarity 100.0%; Pred. No. 0.00033;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKMDAEFRHD 10  
DB 7 VKMDAEFRHD 16

RESULT 9  
US-09-173-887-5  
Sequence 5, Application US/09173887  
Patent No. 6245884  
GENERAL INFORMATION:  
APPLICANT: Hook, Vivian Y.H.  
TITLE OF INVENTION: SECRETASES RELATED TO ALZHEIMER'S DEMENTIA  
FILE REFERENCE: P-AS 3337  
CURRENT APPLICATION NUMBER: US/09/173,887  
CURRENT FILING DATE: 1998-10-16  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 5  
LENGTH: 53  
TYPE: PRT  
ORGANISM: mammalian  
US-09-173-887-5

Query Match 100.0%; Score 54; DB 4; Length 53;  
Best Local Similarity 100.0%; Pred. No. 0.0004;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKMDAEFRHD 10  
DB 1 VKMDAEFRHD 10

RESULT 10  
US-08-371-930-25  
Sequence 25, Application US/08371930  
Patent No. 5578451  
GENERAL INFORMATION:  
APPLICANT: Nishimoto, Ikuro  
TITLE OF INVENTION: ALZHEIMER'S DISEASE THERAPEUTICS  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
COMPUTER: IBM PS/2 Model 502 or 55SX  
OPERATING SYSTEM: MS-DOS (Version 5.0)  
SOFTWARE: Wordperfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/371,930  
FILING DATE:  
CLASSIFICATION: 436  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/019,208  
FILING DATE: February 18, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162



REFERENCE/DOCKET NUMBER: 00786/154001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 58  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-371-930-25

Query Match 100.0%; Score 54; DB 1; Length 58;  
Best Local Similarity 100.0%; Pred. No. 0.00044;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKMDAEFRHD 10  
DB 44 VKMDAEFRHD 53

RESULT 11  
PCT-US94-01712-25  
Sequence 25, Application PC/TUS9401712  
GENERAL INFORMATION:  
APPLICANT: Nishimoto, Ikuro  
TITLE OF INVENTION: ALZHEIMER'S DISEASE THERAPEUTICS  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM PS/2 Model 502 or 55SX  
OPERATING SYSTEM: MS-DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/01712  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/019,208  
FILING DATE: February 18, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 00786/154001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 58  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
PCT-US94-01712-25

Query Match 100.0%; Score 54; DB 5; Length 58;  
Best Local Similarity 100.0%; Pred. No. 0.00044;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKMDAEFRHD 10  
DB 44 VKMDAEFRHD 53

RESULT 12  
US-08-484-969-3  
Sequence 3, Application US/08484969  
Patent No. 5679531  
GENERAL INFORMATION:  
APPLICANT: Konig, Gerhard  
APPLICANT: Graham, Paul  
TITLE OF INVENTION: Monoclonal Antibody Specific for BA4  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Allgeirel & Witcoff, Ltd.  
STREET: 10 South Wacker Drive Suite 3000  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,969  
FILING DATE:  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: McDonnell, John J  
REGISTRATION NUMBER: 26,949  
REFERENCE/DOCKET NUMBER: 95,216  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-715-1000  
TELEFAX: 312-715-1234  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 59 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Cleavage-site  
LOCATION: 4..5  
OTHER INFORMATION: /label= Beta  
OTHER INFORMATION: /note= "Beta cleavage site in App"  
FEATURE:  
NAME/KEY: Cleavage-site  
LOCATION: 20..21  
OTHER INFORMATION: /label= Alpha  
OTHER INFORMATION: /note= "Alpha cleavage site in App, residues 16/17  
FEATURE:  
NAME/KEY: Cleavage-site  
LOCATION: 46..47  
OTHER INFORMATION: /label= Gamma  
OTHER INFORMATION: /note= "Gamma cleavage site in App"  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 5..47  
OTHER INFORMATION: /label= BA4  
OTHER INFORMATION: /note= "BA4 peptide"  
FEATURE:  
NAME/KEY: Region  
LOCATION: 33..56  
OTHER INFORMATION: /label= Tm  
OTHER INFORMATION: /note= "Transmembrane region of App"  
FEATURE:  
NAME/KEY: Region  
LOCATION: 1..32  
OTHER INFORMATION: /label= Ex  
OTHER INFORMATION: /note= "N-terminal extracellular part of App"  
US-08-484-969-3

Query Match 100.0%; Score 54; DB 1; Length 59;  
Best Local Similarity 100.0%; Pred. No. 0.00044;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 VKMDAEFRHD 10  
Db 2 VKMDAEFRHD 11

RESULT 13  
US-08-472-627-3  
; Sequence 3, Application US/08472627  
; Patent No. 5693753  
; GENERAL INFORMATION:  
; APPLICANT: Konig, Gerhard  
; APPLICANT: Graham, Paul  
; TITLE OF INVENTION: Monoclonal Antibody Specific for BA4  
; TITLE OF INVENTION: Peptide  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Allegretti & Witcoff, Ltd.  
; STREET: 10 South Wacker Drive Suite 3000  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/472,627  
; FILING DATE:  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McDonnell, John J  
; REGISTRATION NUMBER: 26,949  
; REFERENCE/DOCKET NUMBER: 95,216  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312-715-1000  
; TELEFAX: 312-715-1234  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 59 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Cleavage-site  
; LOCATION: 4.5  
; OTHER INFORMATION: /label= Beta  
; OTHER INFORMATION: /note= "Beta cleavage site in App"  
; FEATURE:  
; NAME/KEY: Cleavage-site  
; LOCATION: 20..21  
; OTHER INFORMATION: /label= Alpha  
; OTHER INFORMATION: /note= "Alpha cleavage site in App, residues 16/17  
; OTHER INFORMATION: of BA4."  
; FEATURE:  
; NAME/KEY: Cleavage-site  
; LOCATION: 46..47  
; OTHER INFORMATION: /label= Gamma  
; OTHER INFORMATION: /note= "Gamma cleavage site in App"  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 5..47  
; OTHER INFORMATION: /label= BA4  
; OTHER INFORMATION: /note= "BA4 peptide"  
; FEATURE:  
; NAME/KEY: Region  
; LOCATION: 33..56

OTHER INFORMATION: /label= Tm  
OTHER INFORMATION: /note= "Transmembrane region of App"  
FEATURE:  
NAME/KEY: Region  
LOCATION: 1..32  
OTHER INFORMATION: /label= Ex  
OTHER INFORMATION: /note= "N-terminal extracellular part of App"  
US-08-472-627-3

Query Match 100.0%; Score 54; DB 1; Length 59;  
Best Local Similarity 100.0%; Pred. No. 0.00044;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 VKMDAEFRHD 10  
Db 2 VKMDAEFRHD 11

RESULT 14  
US-08-388-463-3  
; Sequence 3, Application US/08388463  
; Patent No. 5786180  
; GENERAL INFORMATION:  
; APPLICANT: Konig, Gerhard  
; APPLICANT: Graham, Paul  
; TITLE OF INVENTION: Monoclonal Antibody Specific for BA4  
; TITLE OF INVENTION: Peptide  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Allegretti & Witcoff, Ltd.  
; STREET: 10 South Wacker Drive Suite 3000  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/388,463  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McDonnell, John J  
; REGISTRATION NUMBER: 26,949  
; REFERENCE/DOCKET NUMBER: 95,216  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312-715-1000  
; TELEFAX: 312-715-1234  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 59 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Cleavage-site  
; LOCATION: 4..5  
; OTHER INFORMATION: /label= Beta  
; OTHER INFORMATION: /note= "Beta cleavage site in App"  
; FEATURE:  
; NAME/KEY: Cleavage-site  
; LOCATION: 20..21  
; OTHER INFORMATION: /label= Alpha  
; OTHER INFORMATION: /note= "Alpha cleavage site in App, residues 16/17  
; OTHER INFORMATION: of BA4."  
; FEATURE:  
; NAME/KEY: Cleavage-site  
; LOCATION: 46..47  
; OTHER INFORMATION: /label= Gamma

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: OTHER INFORMATION: /note= "Gamma cleavage site in App"
: FEATURE:
: NAME/KEY: Peptide
: LOCATION: 5..47
: OTHER INFORMATION: /label= BA4
: OTHER INFORMATION: /note= "BA4 peptide"
: FEATURE:
: NAME/KEY: Region
: LOCATION: 33..56
: OTHER INFORMATION: /label= Tm
: OTHER INFORMATION: /note= "Transmembrane region of App"
: FEATURE:
: NAME/KEY: Region
: LOCATION: 1..32
: OTHER INFORMATION: /label= Ex
: OTHER INFORMATION: /note= "N-terminal extracellular part of App"
: US-08-388-463-3

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Best Local Similarity 100.0%; Score 54; DB 1; Length 59;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKMDAEFRHD 10
Db 2 VKMDAEFRHD 11

RESULT 15
US-08-462-859A-3
: Sequence 3, Application US/08462859A
: Patent No. 5652092
: GENERAL INFORMATION:
: APPLICANT: Jacobsen, J. S.
: TITLE OF INVENTION: No. 5652092e1 Amyloid Precursor and Method of
: TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
: TITLE OF INVENTION: of B Amyloid Peptide
: NUMBER OF SEQUENCES: 19
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: American Cyanamid Company
: STREET: One Cyanamid Plaza
: CITY: Wayne
: STATE: New Jersey
: COUNTRY: United States
: ZIP: 07470-8426
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentln Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/462,859A
: FILING DATE: 05-JUN-1995
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Barnhard, Elizabeth M.
: REGISTRATION NUMBER: 31,088
: REFERENCE/DOCKET NUMBER: 31,844-04
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (201)831-3246
: TELEFAX: (201)831-3305
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 63 amino acids
: TYPE: amino acid
: STRANDEDNESS:
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-462-859A-3

Query Match
Best Local Similarity 100.0%; Score 54; DB 1; Length 63;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 VKMDAEFRHD 10
Db 7 VKMDAEFRHD 16
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Search completed: October 29, 2002, 10:32:08
Job time : 10 secs
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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 29, 2002, 10:22:21 ; Search time 23.1429 Seconds  
(without alignments)  
47.995 Million cell updates/sec

Title: US-09-580-018-7  
Perfect score: 54  
Sequence: 1 KMDAEPFRHDS 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A.Geneseq\_032802:\*

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22: /SIDS1/gcgdata//geneseq//geneseqp-emb1/AA2001.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	54	100.0	10	22	AA846211
2	54	100.0	16	21	AA806315
3	54	100.0	16	21	AA806317
4	54	100.0	18	16	AA875696
5	54	100.0	18	22	AA800608
6	54	100.0	19	12	AA814135
7	54	100.0	20	21	AA859713
8	54	100.0	33	20	AA898002
9	54	100.0	39	21	AA869717
10	54	100.0	45	18	AA826512
11	54	100.0	45	18	AA826392

12	54	100.0	45	19	AA844748
13	54	100.0	45	19	AA842977
14	54	100.0	48	22	AA837523
15	54	100.0	50	22	AA865957
16	54	100.0	53	15	AA835695
17	54	100.0	53	15	AA855696
18	54	100.0	53	15	AA855697
19	54	100.0	53	16	AA864168
20	54	100.0	54	21	AA832126
21	54	100.0	57	21	AA810910
22	54	100.0	58	15	AA858937
23	54	100.0	59	17	AA805375
24	54	100.0	59	19	AA870863
25	54	100.0	59	22	AA884425
26	54	100.0	60	21	AA869701
27	54	100.0	63	18	AA826511
28	54	100.0	63	18	AA826391
29	54	100.0	63	19	AA844747
30	54	100.0	63	19	AA844746
31	54	100.0	63	19	AA842975
32	54	100.0	63	19	AA842976
33	54	100.0	67	19	AA871377
34	54	100.0	70	22	AA809373
35	54	100.0	70	22	AA805015
36	54	100.0	93	22	AA819083
37	54	100.0	103	16	AA874697
38	54	100.0	103	19	AA851317
39	54	100.0	103	20	AA889372
40	54	100.0	103	21	AA856103
41	54	100.0	103	22	AA812509
42	54	100.0	104	19	AA851100
43	54	100.0	112	17	AA893556
44	54	100.0	115	20	AA897999
45	54	100.0	117	19	AA851102

#### ALIGNMENTS

RESULT 1	AA846211	standard; peptide; 10 AA.
ID	AA846211	
XX		
AC	AA846211;	
XX		
DT	04-APR-2001	(first entry)
XX		
DE	Human APP derived immunogenic peptide #7.	
XX		
KW	Amyloid deposit; APP; Abeta; brain; human; clearing response; nootropic;	
KW	Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;	
KW	amyloid precursor protein; Alzheimer's disease.	
XX		
OS	Homo sapiens.	
XX		
PN	W0200072880-A2.	
XX		
PD	07-DEC-2000.	
XX		
PF	26-MAY-2000; 2000MC-US14810.	
XX		
PR	28-MAY-1999; 99US-0322289.	
XX		
PA	(NEUR-) NEURALAB LTD.	
XX		
PI	Schenk DB, Bard F, Vasquez NJ, Yednock T;	
XX		
DR	WPI; 2001-032104/04.	
XX		
PT	Preventing or treating a disease associated with amyloid deposits,	
PT	especially Alzheimer's disease, comprises administering amyloid	
PT	specific antibody	
XX		

PS Disclosure; Figure 19; 143pp; English.

XX CC This invention describes a novel method of preventing or treating a

CC disease associated with amyloid deposits of amyloid precursor protein

CC (APP) Abeta fragments in the brain of a patient, which comprises

CC administering to the patient: (a) an antibody that binds to Abeta, the

CC antibody binds to an amyloid deposit and induces a clearing response (Fc

CC receptor mediated phagocytosis) against it (b) a polypeptide containing

CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent

CC that induces an immunogenic response against residues 1-3 to 7-11 of

CC Abeta. The products of the invention have neurotropic and neuroprotective

CC activity. The method is also useful for monitoring a course of treatment

CC being administered to a patient e.g. active and passive immunization. The

CC methods are useful for prophylactic and therapeutic treatment of

CC Alzheimer's disease.

XX

SO Sequence 10 AA:

Query Match 100.0%; Score 54; DB 22; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.00031;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KMDAERRHDS 10

DB 1 KMDAERRHDS 10

RESULT 2

AAB06315

ID AAB06315 standard; peptide; 16 AA.

XX

AC AAB06315;

XX

DT 03-OCT-2000 (first entry)

XX

DE Human beta-amyloid precursor protein beta-secretase cleavage site.

XX

XX Human; beta-amyloid precursor protein; beta-APP; beta-secretase;

KW subtilisin-kexin isoenzyme 1; SKI-1;

KW pro-brain-derived neurotrophic factor; PROBDNF; antilipaeamic;

KW cytosstatic; vasotropic; SKI-1 inhibitor; hypercholesterolaemia;

KW liver steatosis; Ras-dependent cancer; restenosis;

XX amyloid protein formation.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Cleavage-site 8..9

XX

PN WO200026348-A2.

XX

PD 11-MAY-2000.

XX

XX

PF 04-NOV-1999; 99WO-CA01058.

XX

PR 04-NOV-1998; 98CA-2249648.

XX

PA (RECL-) INST RECH CLINIQUES MONTREAL.

XX

PI Seidah N, Chretien M, Marcinkiewicz M, Laaksonen R, Davignon J;

XX

XX WPI: 2000-365601/31.

DR

XX

XX Novel soluble proteic fragment of subtilisin-kexin isoenzyme for

PT producing a polypeptide useful for treating hypercholesterolemia, liver

PT steatosis and amyloidosis, comprises a specific amino acid sequence -

XX

XX Example 4: Page 51; 119pp; English.

PS

XX The present sequence is the beta-secretase site of human beta-amyloid

CC precursor protein (beta-APP). The sequence may be cleaved

CC by a mammalian subtilase, specifically subtilisin-kexin isoenzyme 1

CC (SKI-1), a type-1 membrane-bound proteinase. Peptides which bind to and

CC are cleaved by SKI-1 may be used for monitoring SKI-1 activity, for

CC screening inhibitors of SKI-1 activity, or for screening enhancers of

CC SKI-1 activity. Proteic fragments of SKI-1 which bind to the SKI-1

CC catalytic site may be used as inhibitors of SKI-1 activity. They may be

CC used to treat diseases involving overexpression of SKI-1 or SKI-1

CC substrate. Such diseases include hypercholesterolaemia, high levels of

CC fatty acids, lipids or farnesyl pyrophosphate, liver steatosis,

CC Ras-dependent cancer, restenosis and amyloid protein formation.

XX

SO Sequence 16 AA:

Query Match 100.0%; Score 54; DB 21; Length 16;

Best Local Similarity 100.0%; Pred. No. 0.0005;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KMDAERRHDS 10

DB 7 KMDAERRHDS 16

RESULT 3

AAB06317

ID AAB06317 standard; peptide; 16 AA.

XX

AC AAB06317;

XX

DT 03-OCT-2000 (first entry)

XX

DE Human beta-amyloid precursor protein beta-epsilont-secretase site.

XX

XX Human; beta-amyloid precursor protein; beta-APP;

KW beta-epsilont-secretase; subtilisin-kexin isoenzyme 1; SKI-1;

KW pro-brain-derived neurotrophic factor; PROBDNF; antilipaeamic;

KW cytosstatic; vasotropic; SKI-1 inhibitor; hypercholesterolaemia;

KW liver steatosis; Ras-dependent cancer; restenosis;

XX amyloid protein formation.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Cleavage-site 8..9

XX

PN WO200026348-A2.

XX

PD 11-MAY-2000.

XX

XX

PF 04-NOV-1999; 99WO-CA01058.

XX

PR 04-NOV-1998; 98CA-2249648.

XX

PA (RECL-) INST RECH CLINIQUES MONTREAL.

XX

PI Seidah N, Chretien M, Marcinkiewicz M, Laaksonen R, Davignon J;

XX

XX WPI: 2000-365601/31.

DR

XX

XX Novel soluble proteic fragment of subtilisin-kexin isoenzyme for

PT producing a polypeptide useful for treating hypercholesterolemia, liver

PT steatosis and amyloidosis, comprises a specific amino acid sequence -

XX

XX Example 4: Page 51; 119pp; English.

PS

XX The present sequence is the beta-epsilont-secretase site of human

CC beta-amyloid precursor protein (beta-APP). The sequence may be cleaved

CC by a mammalian subtilase, specifically subtilisin-kexin isoenzyme 1

CC (SKI-1), a type-1 membrane-bound proteinase. Peptides which bind to and

CC are cleaved by SKI-1 may be used for monitoring SKI-1 activity, for

CC screening inhibitors of SKI-1 activity, or for screening enhancers of

CC SKI-1 activity. Proteic fragments of SKI-1 which bind to the SKI-1

CC catalytic site may be used as inhibitors of SKI-1 activity. They may be

CC used to treat diseases involving overexpression of SKI-1 or SKI-1

CC substrate. Such diseases include hypercholesterolaemia, high levels of

CC fatty acids, lipids or farnesyl pyrophosphate, liver steatosis,

CC Ras-dependent cancer, restenosis and amyloid protein formation.  
XX  
SQ Sequence 16 AA;

Query Match 100.0%; Score 54; DB 21; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0.00057;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KMDAEFRHDS 10  
| | | | | | | |  
Db 5 KMDAEFRHDS 14

RESULT 4  
AAR75696  
ID AAR75696 standard; peptide: 18 AA.  
XX  
AC AAR75696;

DT 21-JAN-1996 (first entry)  
XX

DE Unspecified peptide.  
XX

KM Amyloid precursor protein; APP; annexin-V; Alzheimer's disease;  
KW disease diagnosis; therapy; antibody.  
XX

OS Synthetic.  
XX

PN EP655626-A1.  
XX

PD 31-MAY-1995.  
XX

PF 10-NOV-1994; 94EP-0308309.  
XX

PR 10-NOV-1993; 93US-0149975.  
XX

PA (MCLE-) MCLEAN HOSPITAL CORP.  
XX

PI Honda T, Nixon R;  
XX

DR WPI; 1995-195688/26.  
XX

PT New peptide(s) associated with Alzheimer's disease - namely p33 and  
PT the amyloid precursor C2 fragment, useful for the prodn. of  
PT diagnostic antibodies  
XX

PS Disclosure: Page 13; 32pp; English.  
XX

CC Unspecified peptide.  
XX

SQ Sequence 18 AA;

Query Match 100.0%; Score 54; DB 16; Length 18;  
Best Local Similarity 100.0%; Pred. No. 0.00057;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KMDAEFRHDS 10  
| | | | | | | |  
Db 2 KMDAEFRHDS 11

RESULT 5  
AAE00608  
ID AAE00608 standard; peptide: 18 AA.  
XX  
AC AAE00608;

DT 02-JUL-2001 (first entry)  
XX

DE Beta-amyloid precursor protein beta-secretase cleavage site.  
XX

KM Beta-amyloid precursor protein; beta-APP; caspase; beta-secretase;  
KW cysteine protease; apoptosis; caspase expression cassette; metastasis;  
XX

KM tumour; cathepsin B; urokinase; proliferation; gene therapy;  
KW interdomain linker; cleavage site; Alzheimer's disease.  
XX

OS Unidentified.  
XX

PN WO200129232-A2.  
XX

PD 26-APR-2001.  
XX

PF 19-OCT-2000; 2000MO-US28941.  
XX

PR 20-OCT-1999; 99US-0160559.  
XX

PR 14-AUG-2000; 2000US-0225564.  
XX

PA (SCIO-) SCIOS INC.  
XX

PI Cordell B, Li Y;  
XX

DR WPI; 2001-290920/30.  
XX

PT Novel fusion polypeptide comprising first and second caspase subunit  
PT separated by cleavage site not associated in nature with caspase  
PT subunit, useful for cloning gene encoding enzymes involved in  
PT proteolytic cleavage -  
XX

PS Example 2; Page 26; 116pp; English.  
XX

CC The present sequence is a beta-secretase cleavage site of beta-amyloid  
CC precursor protein (beta-APP). This sequence is used to construct  
CC an artificially engineered chimeric cassette comprising human caspase-3  
CC with interdomain linker replaced by swedish mutant beta-secretase  
CC cleavage site. This modified caspase-3 plays a pivotal role in  
CC Alzheimer's disease. Caspases are a family of cysteine proteases, that  
CC participate in the initiation and execution of apoptosis.  
CC The present invention relates to a method for functional cloning of genes  
CC encoding proteins or enzymes involved in proteolytic cleavage. The  
CC invention is based on the use of caspase expression cassettes comprising  
CC the coding sequence of a proteolytic cleavage site flanked by sequences  
CC encoding two caspase subunits. A fusion polypeptide comprising a first  
CC and a second caspase subunit, separated by a cleavage site not associated  
CC in nature, is useful for cloning gene encoding enzymes involved in  
CC proteolytic cleavage. An expression cassette containing fusion  
CC polypeptide is used to identify a mutant cell line deficient in an  
CC enzyme of interest and is also useful for diagnosis and suppression of  
CC proliferation or metastases of a tumour cell characterised by  
CC overexpression of a polypeptide (e.g. Cathepsin B or urokinase,  
CC selectively expressed in the tumour cells). DNA encoding fusion  
CC polypeptide is used in gene therapy.  
XX

SQ Sequence 18 AA;

Query Match 100.0%; Score 54; DB 22; Length 18;  
Best Local Similarity 100.0%; Pred. No. 0.00057;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KMDAEFRHDS 10  
| | | | | | | |  
Db 9 KMDAEFRHDS 18

RESULT 6  
AAR14135  
ID AAR14135 standard; peptide: 19 AA.  
XX  
AC AAR14135;

DT 12-DEC-1991 (first entry)  
XX

DE Brain-derived protease substrate contg. beta-APP cleavage site.  
XX

KM Alzheimer's disease; chymase; multicatalytic protease;  
KW beta-amyloid precursor protein; A4.  
XX

OS Synthetic.  
 XX Key Location/Qualifiers  
 FH Cleavage-site 4.5  
 FT /note= "chymase and multicatalytic protease site"  
 XX  
 XX WO9113904-A.  
 XX  
 XX 19-SEP-1991.  
 XX  
 XX 04-MAR-1991; 91WO-US01474.  
 XX  
 XX 05-MAR-1990; 90US-0489290.  
 XX  
 XX (CEPH-) CEPHALON INC.  
 XX  
 XX Siman R, Nelson RB, Kauer J, Potter H;  
 XX WPI; 1991-295576/40.  
 XX  
 XX New Chymotrypsin-like serine protease(s) - and their inhibitors  
 PT are used to treat Alzheimer's disease  
 XX  
 XX Claim 41; Page 63; 86pp; English.  
 XX  
 XX This peptide is designed based on the sequence of beta-APP A4  
 CC cleavage site. Cleavage by proteases in the brain releases beta-  
 CC amyloid protein, the deposition of which is a feature of Alzheimer's  
 CC disease neuropathology. The peptide is used to screen for candidate  
 CC proteases which cleave between the Met and Asp residues. Two new  
 CC proteases have been isolated having this cleavage specificity.  
 CC Chymase was isolated from rat brains and multicatalytic protease was  
 CC isolated from human cerebral cortex. See also AAR14136-9.  
 XX  
 XX Sequence 19 AA;  
 SQ  
 Query Match 100.0%; Score 54; DB 12; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 0.0006;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KMDAEFRHDS 10  
 DB 3 KMDAEFRHDS 12  
 RESULT 7  
 AAY69713  
 ID AAY69713 standard; peptide: 20 AA.  
 XX  
 XX AAY69713;  
 AC  
 XX 11-APR-2000 (first entry)  
 DT  
 XX  
 XX Beta-APP alpha-secretase substrate [KM]-APP(-10,+10).  
 DE  
 XX  
 XX Nootropic; neuroprotective; beta-amyloid precursor protein; metabolism;  
 KM cleavage site; beta-secretase; neurodegenerative disease;  
 KM Alzheimer's disease.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 XX WO9964587-A1.  
 PN  
 XX  
 XX 16-DEC-1999.  
 PD  
 XX  
 XX 04-JUN-1999; 99WO-FR01326.  
 PF  
 XX  
 XX 05-JUN-1998; 98FR-0007068.  
 PR  
 XX 31-MAR-1999; 99US-0122599.  
 PR  
 XX (RHON ) RHONE-POULENC RORER SA.  
 PA (UTPA-) UNIV CURIE PARIS VI P 6 M.  
 XX

PI Rholam M, Munoz-Gimenez N, Moutaouakil M, Cohen P, Bertrand P;  
 XX  
 XX WPI; 2000-097537/08.  
 DR  
 XX  
 XX Polypeptide with beta-secretase activity, specific for wild-type  
 PT amyloid precursor protein, useful in treating Alzheimer's disease -  
 XX  
 XX Example 3; Page 24; 44pp; French.  
 PS  
 XX  
 XX Peptides AAY69702-Y69718 represent synthetic peptide substrates for a  
 CC novel polypeptide with beta-secretase activity that can cleave  
 CC specifically the natural beta-amyloid precursor protein (BAPP). Normal  
 CC cleavage of the protein occurs between amino acids Met596-Asp597 and  
 CC Val636-Ile637 (positions 4-5 and 44-45 of AAY69701). The novel  
 CC polypeptide is used to identify agents that interact specifically with  
 CC it. These agents regulate metabolism of APP, particularly they slow down  
 CC or reduce production of beta-amyloid, so can be used to treat  
 CC neurodegenerative diseases, particularly Alzheimer's disease.  
 XX  
 XX Sequence 20 AA;  
 SQ  
 Query Match 100.0%; Score 54; DB 21; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 0.00063;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KMDAEFRHDS 10  
 DB 9 KMDAEFRHDS 18  
 RESULT 8  
 AAW98002  
 ID AAW98002 standard; Protein; 33 AA.  
 XX  
 XX AAW98002;  
 AC  
 XX 21-JUN-1999 (first entry)  
 DT  
 XX  
 XX Amyloid precursor protein (aa656-678) with Swedish mutation.  
 DE  
 XX  
 XX Amyloid precursor protein; APP; human; gene targeting;  
 KM homologous recombination; transgenic mouse; transgenic animal;  
 KM animal model; Alzheimer's disease.  
 XX  
 XX Mus musculus.  
 OS  
 XX  
 XX WO9909150-A1.  
 PN  
 XX  
 XX 25-FEB-1999.  
 PD  
 XX  
 XX 18-AUG-1997; 97WO-US14507.  
 PF  
 XX  
 XX 18-AUG-1997; 97WO-US14507.  
 PR  
 XX  
 XX (FARB ) BAYER CORP.  
 PA  
 XX  
 XX Wlrak DO;  
 PI  
 XX  
 XX WPI; 1999-181029/15.  
 DR  
 XX  
 XX Modification of target nucleic acids - by homologous recombination,  
 PT used particularly for introducing a humanised amyloid precursor  
 PT protein gene into rodents for producing models of Alzheimer's  
 PT disease  
 XX  
 XX disclosure; Page 145; 209pp; English.  
 PS  
 XX  
 XX This polypeptide comprises residues 656-678 of a murine amyloid  
 CC precursor protein (APP). The invention provides a novel gene  
 CC targeting strategy that facilitates the introduction of one or  
 CC more specific mutations into any gene in a single double reciprocal  
 CC homologous recombination step. The method has been used  
 CC particularly for introducing a humanised APP gene into rodents for



CC Producing animal models of Alzheimer's disease (AD). 4 Independent  
 CC lines of transgenic mice (lines ES5007, ES5103, ES5401 and ES5403)  
 CC have been created using the gene targeting technique applied to  
 CC embryonic stem cells. In each line, the mouse APP gene was modified  
 CC to encode a mouse/human hybrid (m/hAPP) where amino acid residues  
 CC 666-770 of APP770 were encoded by human cDNA sequences instead of  
 CC mouse genomic exons (exons 16-18). Within these residues, only 3  
 CC amino acid differences exist between the mouse and human proteins,  
 CC i.e. Gly-676 to Arg, Phe-681 to Thr and Arg-684 to His. The  
 CC exon-cDNA fusion gene therefore encodes an APP containing a  
 CC humanised beta-amyloid domain. Swedish- and/or London-PAD APP  
 CC mutations have also been introduced (see also AAM97997-W98001).

Sequence 33 AA;  
 Query Match 100.0%; Score 54; DB 20; Length 33;  
 Best Local Similarity 100.0%; Pred. No. 0.0011;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KMDAEPFRHDS 10  
 |||||  
 DB 15 KMDAEPFRHDS 24

RESULT 9  
 ID AAY69717 standard; peptide; 39 AA.  
 AC AAY69717;

DT 11-APR-2000 (first entry)  
 XX

DE Beta-APP alpha-secretase substrate [KM]-APP(-20,+20).

KM Nootropic; neuroprotective; beta-amyloid precursor protein; metabolism;  
 KM cleavage site; beta-secretase; neurodegenerative disease;  
 KM Alzheimer's disease.

XX Homo sapiens.

PN WO964587-A1.

PD 16-DEC-1999.

PF 04-JUN-1999; 99WO-FR01326.

PR 05-JUN-1998; 98FR-0007068.

PR 31-MAR-1999; 99US-0122599.

PA (RHON ) RHONE-POULENC RORER SA.  
 PA (UYPA-) UNITIV CURIE PARIS VI P & M.

PI Rholam M, Munoz-Gimenez N, Moutaouakil M, Cohen P, Bertrand P;  
 XX WPI; 2000-097537/08.

DR WPI; 2000-097537/08.

PT Polypeptide with beta-secretase activity, specific for wild-type  
 PT amyloid precursor protein, useful in treating Alzheimer's disease -

XX Example 3; Page 24; 44pp: French.

CC Peptides AAY69702-Y69718 represent synthetic peptide substrates for a  
 CC novel polypeptide with beta-secretase activity that can cleave  
 CC specifically the natural beta-amyloid precursor protein (BAP). Normal  
 CC cleavage of the protein occurs between amino acids Met596-Asp597 and  
 CC Val636-Ile637 (positions 4-5 and 44-45 of AAY69701). The novel  
 CC polypeptide is used to identify agents that interact specifically with  
 CC it. These agents regulate metabolism of APP, particularly they slow down  
 CC or reduce production of beta-amyloid, so can be used to treat  
 CC neurodegenerative diseases, particularly Alzheimer's disease.

Sequence 39 AA;

Query Match 100.0%; Score 54; DB 21; Length 39;  
 Best Local Similarity 100.0%; Pred. No. 0.0013;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KMDAEPFRHDS 10  
 |||||  
 DB 18 KMDAEPFRHDS 27

RESULT 10  
 ID AAM26512 standard; Peptide; 45 AA.  
 AC AAM26512;

DT 06-JAN-1998 (first entry)

DE Amyloid precursor protein fragment APP-REP 751 (BAP del11-28).

KM Amyloid precursor protein; APP; beta-amyloid protein; BAP;  
 KM substrate; muten; secretase; Alzheimer's disease; human.

OS Chimeric Homo sapiens.  
 OS Chimeric synthetic.

FT Key Location/Qualifiers  
 FT Cleavage-site 7..8

FT Peptide /note="secretase cleavage site"

FT /label="BAP(del11-28)"

FT /note="truncated beta-amyloid protein"

FT Domain /label="Transmembrane"

PN US656477-A.

PD 12-AUG-1997.

PF 01-MAY-1992; 92US-0877675.

PR 20-SEP-1993; 93US-0123659.

PR 01-MAY-1992; 92US-0877675.

PA (AMCY ) AMERICAN CYANAMID CO.

PI Jacobsen JS, Vittek MP;  
 XX WPI; 1997-414594/38.

DR WPI; 1997-414594/38.

PT Nucleic acid encoding amyloid precursor muten(s) - comprising  
 PT reporter gene and coding sequence, for identifying compounds which  
 PT modify the activity of proteolytic enzymes which cleave APP

PS Disclosure; Fig 5A; 84pp; English.

CC This peptide sequence shows the region of amyloid precursor protein  
 CC (APP) that includes a truncated beta-amyloid protein (BAP) lacking  
 CC the native secretase cleavage/recognition site. In an attempt to  
 CC engineer an APP non-cleavable substrate for secretase, an  
 CC APP-reporter (APP-REP) protein that carries the BAP deletion has  
 CC been expressed in recombinant host cells. Deletion of these 18  
 CC amino acids, however, still resulted in the secretion of an  
 CC N-terminal APP-reporter fragment into the cytoplasm. Non-  
 CC cleavable APP substrates can be used to detect other putative  
 CC abnormal APP processing events. They can also be used to  
 CC investigate cellular post-translational modifications to APP in  
 CC order to determine the potential influence on normal secretase and  
 CC abnormal BAP 'clipping' activities.

Sequence 45 AA;

Query Match 100.0%; Score 54; DB 18; Length 45;  
 Best Local Similarity 100.0%; Pred. No. 0.0015;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KMDAEFRHDS 10  
 |||||  
 Db 8 KMDAEFRHDS 17

## RESULT 11

AAW26392  
 ID AAW26392 standard; Peptide: 45 AA.

AC AAW26392;

DT 15-DEC-1997 (first entry)

DE Amyloid precursor protein fragment APP-REP 751 (BAP del11-28).

KW Amyloid precursor protein; APP; beta-amyloid protein; BAP;

KM substrate; muten; secretase; Alzheimer's disease; human.

OS Chimeric Homo sapiens;

OS Chimeric synthetic.

FT Key Location/Qualifiers

FT Cleavage-site 7..8 /note= "secretase cleavage site"

FT Peptide 10..33 /label= BAP(del11-28)

FT /note= "truncated beta-amyloid protein"

FT Domain 20..42 /label= Transmembrane

PN US5652092-A.

PD 29-JUL-1997.

PE 01-MAY-1992; 92US-0877675.

PR 20-SEP-1993; 93US-0123659.

PR 01-MAY-1992; 92US-0877675.

PR 05-JUN-1995; 95US-0462859.

PA (AMCY ) AMERICAN CYANAMID CO.

PI Jacobsen JS, Vittek MP;

DR WPI; 1997-392937/36.

PT Screening for compounds which reduce beta-amyloid protein formation

PT - using cells which express a construct encoding a marker and an

PT amyloid precursor muten derived from APP isoforms.

PS Disclosure; Fig 5A; 84pp; English.

CC This peptide sequence shows the region of amyloid precursor protein

CC (APP) that includes a truncated beta-amyloid protein (BAP) lacking

CC the native secretase cleavage/recognition site. In an attempt to

CC engineer an APP non-cleavable substrate for secretase, an

CC APP-reporter (APP-REP) protein that carries the BAP deletion has

CC been expressed in recombinant host cells. Deletion of these 18

CC amino acids, however, still resulted in the secretion of an

CC N-terminal APP-reporter fragment into the cytoplasm. Non-

CC cleavable APP substrates can be used to detect other putative

CC abnormal APP processing events. They can also be used to

CC investigate cellular post-translational modifications to APP in

CC order to determine the potential influence on normal secretase and

CC abnormal BAP 'clipping' activities.

SQ Sequence 45 AA;

Query Match 100.0%; Score 54; DB 18; Length 45;  
 Best Local Similarity 100.0%; Pred. No. 0.0015;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KMDAEFRHDS 10  
 |||||  
 Db 8 KMDAEFRHDS 17

## RESULT 12

AAW44748  
 ID AAW44748 standard; Protein: 45 AA.

AC AAW44748;

DT 01-JUN-1998 (first entry)

DE APP-REP 751 [BAP delta(11-28)] peptide.

KW Amyloid precursor protein; APP; APP 751 isoform; deletion; substrate P;

KM epitope; Met-enkephalin; detection; secretase; beta-amyloid protein; BAP;

KW Alzheimer's disease; cleavage.

OS Homo sapiens.

OS Synthetic.

FT Key Location/Qualifiers

FT Cleavage-site 7..8 /note= "putative secretase cleavage site"

FT MISC-difference 19..20 /note= "residues 11-28 of the wild type BAP sequence

FT /note= "are deleted from between these positions"

PN US5693478-A.

PD 02-DEC-1997.

PE 05-JUN-1995; 95US-0464247.

PR 20-SEP-1993; 93US-0123659.

PR 01-MAY-1992; 92US-0877675.

PR 05-JUN-1995; 95US-0464247.

PA (AMCY ) AMERICAN CYANAMID CO.

PI Jacobsen JS, Vittek MP;

DR WPI; 1998-031744/03.

PT Amyloid precursor muten reporter molecule assay containing antibody

PT recognised marker - used to study pathways associated with

PT Alzheimer's disease

PS Disclosure; Fig 5A; 84pp; English.

CC This sequence represent the beta-amyloid protein sequence from the

CC construct APP-REP751 [BAP delta(11-28)]. The mutant sequence contains

CC a deletion of the wild type BAP residues 11-28. This causes a

CC shortening of the BAP sequence. This may affect cleavage of the BAP by

CC the "secretase" dependent on whether the "secretase" recognises the

CC cleavage site by a positional effect or by sequence. The mutant sequence

CC can be used in a method to study secretase and beta-amyloid protein

CC (BAP)-generating pathways associated with Alzheimer's disease by

CC studying proteolytic cleavage of the reporter polypeptides (e.g.

CC AAW44744 and AAW44745).

SQ Sequence 45 AA;

Query Match 100.0%; Score 54; DB 19; Length 45;  
 Best Local Similarity 100.0%; Pred. No. 0.0015;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## RESULT 13

AA042977  
ID AA042977 standard; peptide: 45 AA.XX  
AC AA042977;XX  
DT 01-MAY-1998 (first entry)XX  
DE Deletion beta-amyloid peptide (BAP) derived from APP-REP 751.XX  
KM Beta-amyloid peptide; BAP; extracellular BAP plaque;XX  
KM cerebrovascular deposit; Alzheimer's disease; Downs syndrome;XX  
KM amyloid precursor protein; APP; secretase; BAP aggregation;XX  
KM abnormal proteolytic cleavage.XX  
OS Homo sapiens.XX  
PI Key Location/QualifiersXX  
PI Domain 20..43XX  
PI US5703209-A.XX  
PD 30-DEC-1997.XX  
PE 05-JUN-1995; 95US-0464248.XX  
PF 20-SEP-1993; 93US-0123659.XX  
PR 01-MAY-1992; 92US-0877675.XX  
PA (AMCY ) AMERICAN CYANAMID CO.XX  
PI Jacobsen JS, Vitek MP;XX  
PI WPI: 1998-076482/07.XX  
PT Amyloid precursor protein fusion polypeptides - comprising APPXX  
PS fragment and marker, useful for research and drug screeningXX  
PS Disclosure; Fig 5A: 84pp; English.XX  
CC The present sequence represents a beta-amyloid peptide (BAP), withXX  
CC a deletion amino acids 11-28 (numbered according to AA042976). AbnormalXX  
CC accumulation of extracellular BAP in plaques and cerebrovascularXX  
CC deposits is characteristic in brains of individuals suffering fromXX  
CC Alzheimer's disease and Downs syndrome. BAP is a poorly soluble,XX  
CC self-aggregating protein which is derived from a larger amyloid precursorXX  
CC protein (APP). APP is expressed as an integral membrane protein, and isXX  
CC cleaved by secretase, between BAP 161ys and 171en. Cleavage at this siteXX  
CC precludes amyloidogenesis and results in the release of theXX  
CC amino-terminal APP fragment. Three major isoforms of APP exist: APP-695,XX  
CC APP-751 and APP-770. These isoforms are derived by alternative splicing.XX  
CC APP-APP 751 is a deletion construct of APP-751, which has a deletion ofXX  
CC 276 amino acids to within 15 amino acids of the BAP domain. APP can beXX  
CC used as a substrate for studying abnormal proteolytic cleavage whichXX  
CC results in the release of BAP, and also to screen for drugs that willXX  
CC inhibit such cleavage.XX  
SQ Sequence 45 AA:XX  
Query Match 100.0%; Score 54; DB 19; Length 45;XX  
Best Local Similarity 100.0%; Pred. No. 0.0015;XX  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;XX  
OY 1 KMDAEPFRHDS 10XX  
DB 8 KMDAEPFRHDS 17

## RESULT 14

AA037523  
ID AA037523 standard; peptide: 48 AA.XX  
AC AA037523;XX  
DT 01-MAR-2001 (first entry)XX  
DE Amyloid precursor protein APP residues 669-716.XX  
KM Amyloid precursor protein; APP; Alzheimer's disease; Abeta.XX  
KM Unidentified.XX  
PN WC020066181-A1.XX  
PD 09-NOV-2000.XX  
PE 01-MAY-2000; 2000WO-US11715.XX  
PF 29-APR-1999; 99US-0131579.XX  
PA (GENO ) GEN HOSPITAL CORP.XX  
PI Bush AI, Huang X, Atwood CS, Tanzi RE;XX  
PI WPI: 2001-015918/02.XX  
PT Screening for agents useful in treating Alzheimer's disease by addingXX  
PT the agent to an Abeta-containing sample and detecting inhibition ofXX  
PT oxygen-dependent hydrogen peroxide formation by the agentXX  
PS Disclosure; Fig 6; 98pp; English.XX  
CC The present invention relates to methods for identifying agents whichXX  
CC can be used in the treatment of Alzheimer's disease. These agents areXX  
CC identified for their ability to inhibit oxygen-dependent hydrogenXX  
CC peroxide formation but their inability to inhibit superoxide-dependentXX  
CC hydrogen peroxide formation. This means that they decrease theXX  
CC neurotoxicity of Abeta, the protein which is thought to cause Alzheimer'sXX  
CC disease.XX  
SQ Sequence 48 AA:XX  
Query Match 100.0%; Score 54; DB 22; Length 48;XX  
Best Local Similarity 100.0%; Pred. No. 0.0016;XX  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;XX  
OY 1 KMDAEPFRHDS 10XX  
DB 2 KMDAEPFRHDS 11XX  
RESULT 15XX  
ID AA065957 standard; protein: 50 AA.XX  
AC AA065957;XX  
DT 11-FEB-2002 (first entry)XX  
DE Human A4 amyloid precursor protein partial sequence.XX  
KM Alpha 7 nicotinic receptor; acetylcholinesterase; AChE; synaptica;XX  
KM antiparkinsonian; neurotropic; neuroprotective; Alzheimer's disease;XX  
KM motor neuron disease; A4 amyloid precursor protein.XX  
OS Homo sapiens.XX  
PN WO200173446-A1.XX  
PD 04-OCT-2001.XX  
PF 29-MAR-2001; 2001WO-GB01401.XX  
PR 29-MAR-2000; 2000GB-0007630.

PR 15-DEC-2000; 2000GB-0030660.

XX  
PA (SYNA-) SYNAPTICA LTD.  
PA (GRE/) GREENFIELD S A.  
XX  
XX

P1 Westwell M:

DR WPI: 2001-639255/73.

XX  
XX  
PR Use of alpha 7 nicotinic receptor or its functional analog to determine  
PR if a compound is capable of acting as functional analog or antagonist  
PR of acetylcholinesterase polypeptide for treating neurological disorders  
PR

PS  
PS Disclosure: Fig 1; 45pp; English.

XX  
XX The invention relates to the use of an alpha 7 nicotinic receptor (I) or  
CC its functional analog to determine whether a compound is capable of  
CC acting as a functional analog or antagonist of an acetylcholinesterase  
CC (AChE) polypeptide fragment (Synaptica peptide) on (I). If (I) is a  
CC native alpha 7 nicotinic receptor in its normal membrane environment, it  
CC is identified by means of inhibition by a blocker of (I). Methods for  
CC identifying a functional analog or antagonist of the synaptica peptide  
CC are also provided. The identified functional analog or antagonist is  
CC useful for the preparation of a medicament for treatment of a  
CC neurological disorder associated with non-enzymatic action of AChE, where  
CC the neurological disorder is Alzheimer's disease, Parkinson's disease or  
CC motor neuron disease. It is useful for inhibiting or preventing non-  
CC enzymatic activity of the synaptica peptide in vivo. The present sequence  
CC represents a human A4 amyloid precursor protein partial sequence.  
XX

SO Sequence 50 AA:

Query Match 100.0%; Score 54; DB 22; Length 50;  
Best Local Similarity 100.0%; Pred. No. 0.0017;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KMDAEFRHDS 10  
|||||||  
Db 15 KMDAEFRHDS 24

Search completed: October 29, 2002, 10:26:45  
Job time : 24.1429 secs

GenCore version 5.1.3  
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# OM protein - protein search, using sw model

Run on: October 29, 2002, 10:23:36 ; Search time 10.4286 Seconds  
(without alignments)  
92.140 Million cell updates/sec

Title: US-09-580-018-7  
Perfect score: 54  
Sequence: 1 KMDAEFRHDS 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	57	2 E60045	Alzheimer's disease
2	54	100.0	57	2 E60045	Alzheimer's disease
3	54	100.0	57	2 G60045	Alzheimer's disease
4	54	100.0	57	2 D60045	Alzheimer's disease
5	54	100.0	57	2 A60045	Alzheimer's disease
6	54	100.0	57	2 B60045	Alzheimer's disease
7	54	100.0	82	2 P00438	Alzheimer's disease
8	54	100.0	695	1 A49795	Alzheimer's disease
9	54	100.0	770	1 GRH04	Alzheimer's disease
10	47	87.0	33	2 S23094	beta-amyloid prote
11	47	87.0	695	2 A27485	Alzheimer's disease
12	47	87.0	695	2 S00550	Alzheimer's disease
13	45	83.3	747	2 JH0773	Alzheimer's disease
14	44	81.5	42	2 PN0512	beta-amyloid prote
15	39	72.2	511	2 A56750	atachain - human
16	35	64.8	428	2 B83420	probable two-compo
17	35	64.8	543	2 T48239	hypothetical prote
18	35	64.8	802	2 A83125	probable TonB-depe
19	35	64.8	900	2 E83189	protein-PII uridyly
20	34	63.0	213	2 F87669	conserved hypothet
21	34	63.0	246	2 AG1140	transcription regu
22	34	63.0	400	2 S70187	44.7K vira protein
23	34	63.0	901	2 C70179	conserved hypothet
24	34	63.0	901	2 G89810	conserved hypothet
25	34	63.0	1237	2 AE1915	hypothetical prote
26	34	63.0	1256	2 AB2042	hypothetical prote
27	33	61.1	128	2 S69856	hypothetical prote
28	33	61.1	142	2 E89026	protein F13A2.1 (1
29	33	61.1	316	2 T46000	hypothetical prote

30	33	61.1	322	2 A69963	hypothetical prote
31	33	61.1	336	2 AF2085	transcription regu
32	33	61.1	344	2 T23374	hypothetical prote
33	33	61.1	376	2 B84277	hypothetical prote
34	33	61.1	578	2 B82053	fibrin assembly
35	33	61.1	647	2 T26240	hypothetical prote
36	33	61.1	849	2 T01286	probable RNA-bindi
37	33	61.1	927	2 T38127	phosphoprotein - f
38	33	61.1	931	2 A49737	dipeptidyl aminope
39	33	61.1	1524	2 S68553	surface layer prot
40	32	59.3	55	2 C82565	hypothetical prote
41	32	59.3	113	2 AH0923	conserved hypothet
42	32	59.3	160	2 A11308	dihydrofolate redu
43	32	59.3	161	2 S30698	cyax protein - Esc
44	32	59.3	193	2 I50693	interferon - chick
45	32	59.3	213	2 A46237	actin-myosin netwo

## ALIGNMENTS

RESULT 1  
E60045  
Alzheimer's disease amyloid beta/A4 protein precursor - sheep (fragment)  
C:Species: Ovis sp. (sheep)  
C>Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 28-Jul-1995  
C:Accession: E60045  
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
Brain Res. Mol. Brain Res. 10, 299-305, 1991  
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d  
A:Reference number: A60045; MUID:92017079  
A:Accession: E60045  
A:Molecule type: mRNA  
A:Residues: 1-57 <JOH>  
A:Cross-References: EMBL:X56130  
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas  
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 54; DB 2; Length 57;  
Best Local Similarity 100.0%; Pred. No. 0.00051;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KMDAEFRHDS 10  
Db 4 KMDAEFRHDS 13

## RESULT 2

F60045  
Alzheimer's disease amyloid beta/A4 protein precursor - pig (fragment)  
C:Species: Sus scrofa domestica (domestic pig)  
C>Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 13-Aug-1999  
C:Accession: F60045  
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
Brain Res. Mol. Brain Res. 10, 299-305, 1991  
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d  
A:Reference number: A60045; MUID:92017079  
A:Accession: F60045  
A:Molecule type: mRNA  
A:Residues: 1-57 <JOH>  
A:Cross-References: EMBL:X56127; NID:q1895; PIDN:CAA39592.1; PID:q1896  
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas  
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 54; DB 2; Length 57;  
Best Local Similarity 100.0%; Pred. No. 0.00051;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KMDAEFRHDS 10  
Db 4 KMDAEFRHDS 13

RESULT 3  
G60045  
Alzheimer's disease amyloid beta/A4 protein precursor - guinea pig (fragment)  
C:Species: Cavia porcellus (guinea pig)  
C>Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 28-Jul-1995  
C:Accession: G60045  
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
Brain Res. Mol. Brain Res. 10, 299-305, 1991  
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,  
A:Reference number: A60045; MUID:92017079  
A:Accession: G60045  
A:Molecule type: mRNA  
A:Residues: 1-57 <JOH>  
A:Cross-references: EMBL:X56126  
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase  
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 54; DB 2; Length 57;  
Best Local Similarity 100.0%; Pred. No. 0.00051;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KMDAEPFRHDS 10  
|||||  
Db 4 KMDAEPFRHDS 13

RESULT 4  
D60045  
Alzheimer's disease amyloid beta/A4 protein precursor - bovine (fragment)  
C:Species: Bos primigenius taurus (cattle)  
C>Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 28-Jul-1995  
C:Accession: D60045  
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
Brain Res. Mol. Brain Res. 10, 299-305, 1991  
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,  
A:Reference number: A60045; MUID:92017079  
A:Accession: D60045  
A:Molecule type: mRNA  
A:Residues: 1-57 <JOH>  
A:Cross-references: EMBL:X56124  
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase  
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 54; DB 2; Length 57;  
Best Local Similarity 100.0%; Pred. No. 0.00051;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KMDAEPFRHDS 10  
|||||  
Db 4 KMDAEPFRHDS 13

RESULT 5  
A60045  
Alzheimer's disease amyloid beta/A4 protein precursor - dog (fragment)  
C:Species: Canis lupus familiaris (dog)  
C>Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 28-Jul-1995  
C:Accession: A60045  
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
Brain Res. Mol. Brain Res. 10, 299-305, 1991  
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,  
A:Reference number: A60045; MUID:92017079  
A:Accession: A60045  
A:Molecule type: mRNA  
A:Residues: 1-57 <JOH>  
A:Cross-references: EMBL:X56125  
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase  
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 54; DB 2; Length 57;  
Best Local Similarity 100.0%; Pred. No. 0.00051;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KMDAEPFRHDS 10  
|||||  
Db 4 KMDAEPFRHDS 13

RESULT 6  
B60045  
Alzheimer's disease amyloid beta/A4 protein precursor - polar bear (fragment)  
C:Species: Ursus maritimus (polar bear)  
C>Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 13-Aug-1999  
C:Accession: B60045  
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
Brain Res. Mol. Brain Res. 10, 299-305, 1991  
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d  
A:Reference number: A60045; MUID:92017079  
A:Accession: B60045  
A:Molecule type: mRNA  
A:Residues: 1-57 <JOH>  
A:Cross-references: EMBL:X56128; NID:92165; PIDN:CAA39593.1; PID:92166  
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase  
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 54; DB 2; Length 57;  
Best Local Similarity 100.0%; Pred. No. 0.00051;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KMDAEPFRHDS 10  
|||||  
Db 4 KMDAEPFRHDS 13

RESULT 7  
P00438  
Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C>Date: 30-Sep-1993 #sequence\_revision 19-Oct-1995 #text\_change 19-Oct-1995  
C:Accession: P00438; C60045  
R:Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Marcun, L.E.  
Biochem. Biophys. Res. Commun. 188, 905-911, 1992  
A:Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precurs  
A:Reference number: P00438; MUID:93075180  
A:Accession: P00438  
A:Molecule type: DNA  
A:Residues: 1-82 <DAV>  
A:Cross-references: GB:M83558; GB:M83657  
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
Brain Res. Mol. Brain Res. 10, 299-305, 1991  
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d  
A:Reference number: A60045; MUID:92017079  
A:Accession: C60045  
A:Molecule type: mRNA  
A:Residues: 12-68 <JOH>  
A:Cross-references: EMBL:X56129  
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase  
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match 100.0%; Score 54; DB 2; Length 82;  
Best Local Similarity 100.0%; Pred. No. 0.00076;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KMDAEPFRHDS 10  
|||||  
Db 15 KMDAEPFRHDS 24

RESULT 8  
A49795  
Alzheimer's disease amyloid beta protein precursor - crab-eating macaque  
C:Species: Macaca fascicularis (crab-eating macaque)  
C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C:Accession: A49795  
R:Podlisky, M.B.; Tolan, D.R.; Selkoe, D.J.  
Am. J. Pathol. 138, 1423-1435, 1991

A:Title: Homology of the amyloid beta protein precursor in monkey and human supports a  
 A:Reference number: A49795; MUID:91273117  
 A:Accession: A49795  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-695 <POD>  
 A:Cross-references: GB:M58727; NID:q342062; PIDN:AAA36829.1; PID:q342063  
 A:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1  
 C:Keywords: alternative splicing

Query Match 100.0%; Score 54; DB 1; Length 695;  
 Best Local Similarity 100.0%; Pred. No. 0.008;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 KMDAERRHDS 10  
 |||||  
 Db 595 KMDAERRHDS 604

RESULT 9  
 ORHUA4  
 Alzheimer's disease amyloid beta protein precursor [validated] - human  
 N:Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor Xla inhibi  
 N:Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vascular  
 protein precursor splice form APP(770)  
 C:Species: Homo sapiens (man)  
 C:Date: 30-Jun-1987 #sequence revision 28-Jul-1995 #text change 15-Sep-2000  
 C:Accession: S02260; S05194; A32277; A33260; A35486; I39452; I39451; I39453; I59562; A44  
 4668; A26853; A29302; A60805; J10036; S06121; A60355; A59011; A38384; S29076; S38252; S3  
 Nucleic Acids Res. 17, 517-522, 1989  
 A:Title: The PRA4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded b  
 A:Reference number: S02260; MUID:89128427  
 A:Accession: S02260  
 A:Molecule type: DNA  
 A:Residues: 1-288, 'V', 365-770 <LEM1>  
 A:Cross-references: EMBL:X13466  
 A:Note: alternative splice form APP(695)  
 R:Lemaire, H.G.  
 A:Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for t  
 submitted to the EMBL Data Library, November 1988  
 A:Reference number: S05194  
 A:Accession: S05194  
 A:Molecule type: DNA  
 A:Residues: 1-14, 'VW', 17-288, 'V', 365-770 <LEM2>  
 A:Cross-references: EMBL:X13466; NID:q35598; PIDN:CAA31830.1; PID:g871360  
 A:Note: alternative splice form APP(695)  
 R:La Faut, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.  
 Biochem. Biophys. Res. Commun. 159, 297-304, 1989  
 A:Title: Characterization of the 5'-end region and the first two exons of the beta-prote  
 A:Reference number: A32277; MUID:89165870  
 A:Accession: A32277  
 A:Molecule type: DNA  
 A:Residues: 1-75 <LAF>  
 A:Cross-references: GB:M24546; GB:M24547; NID:q341202; PIDN:AAIC3654.1; PID:g516074  
 R:Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.  
 Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989  
 A:Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows similarit  
 A:Reference number: A33260; MUID:89392030  
 A:Accession: A33260  
 A:Molecule type: DNA  
 A:Residues: 656-737 <DOH>  
 A:Cross-references: GB:M29270; NID:q178863; PIDN:AA51768.1; PID:g178865  
 R:Prelli, F.; Levy, E.; Van Duijn, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B.  
 Biochem. Biophys. Res. Commun. 170, 301-307, 1990  
 A:Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid of  
 A:Reference number: A35486; MUID:90321244  
 A:Accession: A35486  
 A:Molecule type: DNA  
 A:Residues: 672-710 <PRE1>  
 A:Note: 693-Gln was found in DNA isolated from HCHMA-D patients  
 R:Toshikai, S.I.; Sasaki, H.; Doi-ura, K.; Furuya, H.; Sasaki, Y.  
 Gene 87, 257-263, 1990  
 A:Title: Genomic organization of the human amyloid beta-protein precursor gene.

A:Reference number: I39451; MUID:90236318  
 A:Accession: I39452  
 A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/  
 A:Molecule type: DNA  
 A:Residues: 1-770 <YOS1>  
 A:Cross-references: GB:M33112; NID:q178613; PIDN:AA59502.1; PID:g178616  
 A:Accession: I39451  
 A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/  
 A:Molecule type: DNA  
 A:Residues: 1-530, 'QMLMPVIAPEAKYGR' <YOS2>  
 A:Cross-references: GB:M34875; NID:q178608; PIDN:AA59501.1; PID:g178615  
 R:Toshikai, S.I.; Sasaki, H.; Doi-ura, K.; Furuya, H.; Sasaki, Y.  
 Gene 102, 291-292, 1991  
 A:Reference number: A59020; MUID:91340168  
 A:Contents: annotation; erratum  
 A:Note: revised physical map for reference I39451  
 R:Levy, E.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van Du  
 Science 248, 1124-1126, 1990  
 A:Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemo  
 A:Reference number: I39453; MUID:90260663  
 A:Accession: I39453  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 656-737 <LEV>  
 A:Cross-references: GB:M37896; NID:q178618; PIDN:AA51727.1; PID:g178620  
 A:Note: a mutation with 693-Gln is presented  
 R:Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.  
 Science 254, 97-99, 1991  
 A:Title: A mutation in the amyloid precursor protein associated with hereditary Alzhe  
 A:Reference number: I59562; MUID:92022553  
 A:Accession: I59562  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 689-716, 'F', 718-737 <MUR>  
 A:Cross-references: GB:S57665; NID:q236720; PIDN:AA619991.1; PID:g236721  
 R:Kamino, K.; Orr, H.T.; Payami, H.; Wilsman, E.M.; Alonso, M.E.; Puls, S.M.; Anders  
 arakis, S.E.; Korenberg, J.R.; Sharma, V.; Kukull, W.; Larson, E.; Heston, L.L.; Mart  
 Am. J. Hum. Genet. 51, 998-1014, 1992  
 A:Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for t  
 A:Reference number: A44017; MUID:93055397  
 A:Accession: A44017  
 A:Molecule type: DNA  
 A:Residues: 687-692, 'G', 694-718 <KAM1>  
 A:Cross-references: GB:S45135; NID:q257377; PIDN:AA623645.1; PID:g257378  
 A:Experimental source: familial Alzheimer disease family SB  
 A:Note: sequence extracted from NCBI backbone (NCBI:115374)  
 A:Accession: B44017  
 A:Molecule type: DNA  
 A:Residues: 687-718 <KAM2>  
 A:Cross-references: GB:S45136; NID:q257379; PIDN:AA623646.1; PID:g257380  
 A:Experimental source: familial Alzheimer disease family LIT  
 A:Note: sequence extracted from NCBI backbone (NCBI:115376)  
 A:Note: this sequence has a silent mutation  
 R:Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.  
 Nature 325, 733-736, 1987  
 A:Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-sur  
 A:Reference number: A03134; MUID:87144572  
 A:Accession: A03134  
 A:Molecule type: mRNA  
 A:Residues: 1-288, 'V', 365-770 <KAN>  
 A:Cross-references: GB:X00264; NID:q28525; PIDN:CAA68374.1; PID:g28526  
 A:Note: alternative splice form APP(695)  
 R:Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.  
 Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987  
 A:Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascula  
 A:Reference number: A29030; MUID:87231971  
 A:Accession: A29030  
 A:Molecule type: mRNA  
 A:Residues: 284-288, 'V', 365-646, 'E', 648-770 <ROB>  
 A:Cross-references: GB:M16765; NID:q178539; PIDN:AA51722.1; PID:g178540  
 A:Note: the authors translated the codon GAG for residue 647 as Asp  
 R:Goldberger, D.; Lerman, M.I.; McBride, O.W.; Saffioti, U.; Gajdusek, D.C.  
 Science 235, 877-880, 1987

A:Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid  
 A:Reference number: A47584; MUID:87120328  
 A:Accession: A47584  
 A:Molecule type: mRNA  
 A:Residues: 674-756, 'S', 758-770 <GOL>  
 A:Cross-references: GB:M1533; NID:9178706; PIDN:AAA35540.1; PID:9178707  
 A:Experimental source: brain  
 R:Tanai, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van Ke  
 Science 235, 880-884, 1987  
 A:Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near th  
 A:Reference number: A47585; MUID:87120329  
 A:Accession: A47585  
 A:Molecule type: mRNA  
 A:Residues: 674-703 <TANI>  
 A:Cross-references: GB:M15532; NID:9177957; PIDN:AAA51564.1; PID:9177958  
 R:Dykes, T.; Weidemann, A.; Mulhapp, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Muelle  
 EMBO J. 7, 949-957, 1988  
 A:Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 prec  
 A:Reference number: S02638; MUID:88296437  
 A:Accession: S02638  
 A:Molecule type: mRNA  
 A:Residues: 672-678 <DYR>  
 R:Tanzi, R.E.; McClatchey, A.I.; Lampetti, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Neve  
 Nature 331, 528-530, 1988  
 A:Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associat  
 A:Reference number: S00707; MUID:88122640  
 A:Accession: S00707  
 A:Molecule type: mRNA  
 A:Residues: 286-344, 'I', 365-366 <TAN2>  
 A:Cross-references: EMBL:X06982; NID:928817; PIDN:CAA30042.1; PID:9929612  
 A:Experimental source: promyelocytic leukemia cell line HL60  
 A:Note: alternative splice form App(751)  
 R:Ponte, P.; Gonzalez-Demhitt, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.; De  
 Nature 331, 525-527, 1988  
 A:Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibit  
 A:Reference number: S00925; MUID:88122639  
 A:Accession: S00925  
 A:Molecule type: mRNA  
 A:Residues: 1-344, 'I', 365-770 <PO2>  
 A:Cross-references: GB:X06989; EMBL:Y00297; NID:928720; PIDN:CAA30050.1; PID:928721  
 A:Note: alternative splice form App(775)  
 R:Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.  
 Nature 331, 530-533, 1988  
 A:Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibitor  
 A:Reference number: A38949; MUID:88122641  
 A:Accession: A38949  
 A:Molecule type: mRNA  
 A:Residues: 287-367 <KIT>  
 A:Cross-references: GB:X06981; NID:928816; PIDN:CAA30041.1; PID:9929611  
 A:Experimental source: glioblastoma cell line  
 A:Note: alternative splice form App(770)  
 R:Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ashton  
 Brain Res. Mol. Brain Res. 4, 121-131, 1988  
 A:Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of three F  
 A:Reference number: A30320  
 A:Accession: A30320  
 A:Molecule type: mRNA  
 A:Status: not compared with conceptual translation  
 A:Residues: 284-288, 'V', 365-770 <VIT1>  
 A:Accession: B30320  
 A:Status: not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 122-288, 'V', 365-770 <VIT2>  
 A:Accession: C30320  
 A:Status: not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 606-770 <VIT3>  
 R:Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta, C.A  
 Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988  
 A:Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease br  
 A:Reference number: A31087; MUID:88124954  
 A:Accession: A31087  
 A:Molecule type: mRNA

A:Residues: 507-770 <ZAI>  
 A:Cross-references: GB:M18734; NID:9178572; PIDN:AAA51726.1; PID:9178573  
 A:Note: the authors translated the codon GAA for residue 599 as Gly, ACC for residue  
 8 as Val, GTG for residue 609 as Asn, AAT for residue 610 as Gly, and GGT for residue  
 A:Note: the cited Genbank accession number, J03594, is not in release 101.0  
 R:Masters, C.L.; Mulhapp, G.; Simms, G.; Potgiesser, J.; Martins, R.N.; Beyreuther,  
 Query Match 100.0%; Score 54; DB 1; Length 770;  
 Best Local Similarity 100.0%; Pred. No. 0.0089;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KMDAEFRHDS 10  
 |||||  
 Db 670 KMDAEFRHDS 679  
 RESULT 10  
 S23094  
 beta-amyloid protein precursor - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 03-May-1996  
 C:Accession: S23094  
 R:Kojima, S.; Omori, M.  
 FEBS Lett. 304, 57-60, 1992  
 A:Title: Two-way cleavage of beta-amyloid protein precursor by multicatalytic protein  
 A:Reference number: S23094; MUID:92316198  
 A:Accession: S23094  
 A:Molecule type: protein  
 A:Residues: 1-33 <KOJ>  
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas  
 Query Match 87.0%; Score 47; DB 2; Length 33;  
 Best Local Similarity 90.0%; Pred. No. 0.0071;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 KMDAEFRHDS 10  
 |||||  
 Db 4 KMDAEFGHDS 13  
 RESULT 11  
 A27485  
 Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse  
 N:Alternate names: proteinase nexin II  
 C:Species: Mus musculus (house mouse)  
 C:Date: 31-Mar-1989 #sequence\_revision 31-Mar-1989 #text\_change 13-Aug-1999  
 C:Accession: A27485; S19727; I49485  
 R:Yamada, T.; Sasaki, H.; Furuya, H.; Miyata, T.; Goto, I.; Sasaki, Y.  
 Biochem. Biophys. Res. Commun. 149, 665-671, 1987  
 A:Title: Complementary DNA for the mouse homolog of the human amyloid beta protein pr  
 A:Reference number: A27485; MUID:88106489  
 A:Accession: A27485  
 A:Molecule type: mRNA  
 A:Residues: 1-695 <YAM>  
 A:Cross-references: GB:M18373; NID:9191568; PIDN:AAA37139.1; PID:9309085  
 A:Experimental source: brain  
 R:de Strooper, B.; van Leuven, F.; van den Berghe, H.  
 Biochim. Biophys. Acta 1129, 141-143, 1991  
 A:Title: The amyloid beta protein precursor or proteinase nexin II from mouse is clos  
 A:Reference number: S19727; MUID:92096458  
 A:Accession: S19727  
 A:Molecule type: mRNA  
 A:Residues: 1-210, 'G', 212-220, 'S', 222-396, 'A', 398-402, 'T', 404-448, 'A', 450-695 <STR>  
 A:Cross-references: EMBL:X59379  
 R:Izumii, R.; Yamada, T.; Yoshikata, S.; Sasaki, H.; Hattori, M.; Sasaki, Y.  
 Gene 112, 189-195, 1992  
 A:Title: Positive and negative regulatory elements for the expression of the Alzheim  
 A:Reference number: I49485; MUID:92209998  
 A:Accession: I49485  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-19 <RES>  
 A:Cross-references: GB:D10603; NID:9220328; PIDN:BAA01456.1; PID:9220329



C:Genetics:  
 A:Map position: 16c3  
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase  
 C:Keywords: alternative splicing; amyloid; transmembrane protein

Query Match 87.0%; Score 47; DB 2; Length 695;  
 Best Local Similarity 90.0%; Pred. No. 0.21;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KMDAEPFRHDS 10  
 ||||| |||  
 Db 595 KMDAEPGRHDS 604

# RESULT 12

Alzheimer's disease amyloid beta protein precursor - rat  
 S00550

N:Alternate names: beta-A4 amyloid protein  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 13-Aug-1999  
 C:Accession: S00550; A41245; A39820; S46251

R:Shivers, B.D.; Hilbich, C.; Multhaup, G.; Salbaum, M.; Beyreuther, K.; Seeburg, P.H.  
 EMBO J. 7, 1365-1370, 1988

A:Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brain  
 A:Reference number: S00550; MUID:88312583

A:Accession: S00550  
 A:Molecule type: mRNA

A:Residues: 1-695 <SHI>  
 A:Cross-references: EMBL:X07648; NID:g55616; PIDN:CA30408.1; PID:g55617

R:Schubert, D.; Schroeder, R.; Lacombe, M.; Saitoh, T.; Cole, G.  
 Science 241, 223-226, 1988

A:Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan core  
 A:Reference number: A41245; MUID:88264430

A:Accession: A41245  
 A:Molecule type: protein

A:Residues: 18-37, 'X', 39-40, 'X', 42-44 <SCH>  
 A:Note: evidence for heparan sulfate attachment

R:Hesse, L.; Behner, D.; Masters, C.L.; Multhaup, G.  
 FEBS Lett. 349, 109-116, 1994

A:Title: The beta-A4 amyloid precursor protein binding to copper.  
 A:Reference number: S46251; MUID:94320627

A:Contents: annotation; copper binding sites  
 A:Note: rat peptides were isolated but not sequenced

R:Potempska, A.; Styles, J.; Mehta, P.; Kim, K.S.; Miller, D.L.  
 J. Biol. Chem. 266, 8464-8469, 1991

A:Title: Purification and tissue level of the beta-amyloid peptide precursor of rat brain  
 A:Reference number: A39820; MUID:91217087

A:Accession: A39820  
 A>Status: preliminary

A:Molecule type: protein  
 A:Residues: 18-32 <POT>

A:Experimental source: brain  
 C:Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques is ch

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase  
 C:Keywords: alternative splicing; amyloid; glycoprotein; transmembrane protein

F:625-646/Domain: transmembrane #status Predicted <TMS>

Query Match 87.0%; Score 47; DB 2; Length 695;  
 Best Local Similarity 90.0%; Pred. No. 0.21;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KMDAEPFRHDS 10  
 ||||| |||  
 Db 595 KMDAEPGRHDS 604

RESULT 13  
 JH0773  
 Alzheimer's disease amyloid beta protein precursor - African clawed frog

C:Species: Xenopus laevis (African clawed frog)  
 C:Date: 10-Jun-1993 #sequence\_revision 10-Jun-1993 #text\_change 13-Aug-1999  
 C:Accession: JH0773  
 R:Okado, H.; Okamoto, H.

Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992  
 A:Title: A Xenopus homologue of the human beta-amyloid precursor protein: development  
 A:Reference number: JH0773; MUID:93129227

A:Accession: JH0773  
 A:Molecule type: mRNA

A:Residues: 1-747 <OKA>  
 A:Cross-references: GB:S52417; NID:g263150; PIDN:AAB24851.1; PID:g263151

A:Experimental source: larva  
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase

C:Keywords: alternative splicing; amyloid  
 F:287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 83.3%; Score 45; DB 2; Length 747;  
 Best Local Similarity 70.0%; Pred. No. 0.56;  
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 KMDAEPFRHDS 10  
 ||||| |||  
 Db 647 KMDSEYRHDY 656

# RESULT 14

PN0512  
 beta-amyloid protein - guinea pig (fragment)

C:Species: Cavia porcellus (guinea pig)  
 C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 17-Mar-1999  
 C:Accession: PN0512

R:Shimohigashi, Y.; Matsumoto, H.; Takano, Y.; Saito, R.; Iwata, T.; Kamiya, H.; Ohno  
 Biochem. Biophys. Res. Commun. 193, 624-630, 1993

A:Title: Receptor-mediated specific biological activity of a beta-amyloid protein fra  
 A:Reference number: PN0512; MUID:93290653

A:Accession: PN0512  
 A:Molecule type: protein

A:Residues: 1-42 <SHI>  
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase

C:Keywords: alternative splicing; amyloid

Query Match 81.5%; Score 44; DB 2; Length 42;  
 Best Local Similarity 100.0%; Pred. No. 0.037;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 DAEPFRHDS 10  
 ||||| |||  
 Db 1 DAEPFRHDS 8

# RESULT 15

A56750  
 archaia - human

C:Species: Homo sapiens (man)  
 C:Date: 08-Jul-1995 #sequence\_revision 03-Aug-1995 #text\_change 21-Jul-2000  
 C:Accession: A56750

R:Radice, P.; Pensotti, V.; Jones, C.; Perry, H.; Pierotti, M.A.; Tunnacliffe, A.  
 Genomics 26, 101-106, 1995

A:Title: The human archaia gene, ARCN1, has highly conserved homologs in rice and Dro  
 A:Reference number: A56750; MUID:95301274

A:Accession: A56750  
 A>Status: preliminary

A:Molecule type: mRNA  
 A:Residues: 1-511 <RAD>

A:Cross-references: GB:X81197; NID:g773572; PIDN:CA57071.1; PID:g773573  
 C:Genetics:

A:Gene: GDB:ARCN1  
 A:Cross-references: GDB:377806; OMIM:600820

A:Map position: 11q23.3-11q23.3

Query Match 72.2%; Score 39; DB 2; Length 511;  
 Best Local Similarity 60.0%; Pred. No. 6;  
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 KMDAEPFRHDS 10  
 :|||: |||  
 Db 424 EIDGEPFRHDS 433

Tue Oct 29 11:23:40 2002

us-09-580-018-7.rpr

Page 6

Search completed: October 29, 2002, 10:31:05  
Job time : 11.4286 secs

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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 29, 2002, 10:22:36 ; Search time 5 Seconds

(without alignments)  
77.439 Million cell updates/sec

Title: US-09-580-018-7

Perfect score: 54

Sequence: 1 KMDAEFRHDS 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*  
Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	57	1 A4_PIG	Q29023 sus scrofa
2	54	100.0	57	1 A4_URMA	Q29149 ursus marit
3	54	100.0	58	1 A4_CANFA	Q28280 canis fam11
4	54	100.0	58	1 A4_RABIT	Q28748 oryctolagus
5	54	100.0	58	1 A4_SHEEP	Q28757 ovis aries
6	54	100.0	59	1 A4_BOVIN	Q28053 bos taurus
7	54	100.0	751	1 A4_SAISC	Q95241 salmisi sci
8	54	100.0	770	1 A4_HUMAN	P05067 homo sapien
9	47	87.0	770	1 A4_MOUSE	P12023 mus musculu
10	47	87.0	770	1 A4_RAT	P08592 rattus norv
11	39	72.2	511	1 COPD_BOVIN	P53619 bos taurus
12	39	72.2	511	1 COPD_HUMAN	P48444 homo sapien
13	35	64.8	269	1 T2S1_STRPT	O5512 streptomyc
14	35	64.8	900	1 GLMD_PSEAE	Q929H0 pseudomonas
15	34	63.0	478	1 GEPD_BORBU	O51581 borrelia bu
16	33	61.1	322	1 YQUA_BACSV	P54538 bacillus su
17	33	61.1	492	1 C133_DROME	O9yqb3 drosophila
18	33	61.1	500	1 STCL_EMENT	O00707 emericella
19	33	61.1	927	1 CC15_SCHPO	O09822 schizosacch
20	33	61.1	931	1 DAP1_TREAST	P33894 saccharomyc
21	32	59.3	107	1 T2AH_DROME	O9w5b9 drosophila
22	32	59.3	161	1 YZCX_ECOLI	P11291 escherichia
23	32	59.3	193	1 INFL_CHICK	P42165 gallus gall
24	32	59.3	193	1 INFL_CHICK	O90872 gallus gall
25	32	59.3	213	1 NULL_DROME	P33845 drosophila
26	32	59.3	328	1 P2Y3_MELGA	O93361 meleagris g
27	32	59.3	402	1 RDS1_SCHPO	P33693 schizosacch
28	32	59.3	502	1 YGCL_ECOLI	O46901 escherichia
29	32	59.3	780	1 TREB_YEAST	P35172 saccharomyc
30	32	59.3	1092	1 DP2L_METTH	O27579 methanobact
31	32	59.3	1159	1 DP3A_PASBU	O9cpk3 pasteurella
32	31	58.3	497	1 DHAL_ENCRU	O27640 encyrtiraeus
33	31	57.4	190	1 GP38_BPSP1	O45394 bacteriopha

34	31	57.4	351	1 VA0D_HUMAN	P12953 homo sapien
35	31	57.4	351	1 VA0D_MOUSE	P51863 mus musculu
36	31	57.4	391	1 NCAP_BRSVA	P22677 bovine resp
37	31	57.4	391	1 NCAP_BRSVR	O65708 bovine resp
38	31	57.4	391	1 NCAP_HRSV1	P24566 human respi
39	31	57.4	391	1 NCAP_HRSVA	P03418 human respi
40	31	57.4	391	1 NCAP_ORSVW	O83957 ovine respi
41	31	57.4	413	1 NODD_RHOCA	O07310 rhodobacter
42	31	57.4	431	1 PUR8_SYNY3	P74384 synecocyst
43	31	57.4	449	1 AP2C_MOUSE	O61312 mus musculu
44	31	57.4	453	1 YKK8_YEAST	P34252 saccharomyc
45	31	57.4	497	1 PSD3_SCHPO	O42897 schizosacch

ALIGNMENTS

```
RESULT 1
A4_PIG          STANDARD:      PRT:      57 AA.
ID             AC             Q29023:
DT             01-NOV-1997 (Rel. 35, Created)
DT             01-NOV-1997 (Rel. 35, Last sequence update)
DT             16-OCT-2001 (Rel. 40, Last annotation update)
DE             Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE             protein (Beta-APP) (A-beta)] (Fragment).
GN             App.
OS             Sus scrofa (Pig).
OC             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC             Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX             NCBI_TaxID=9823;
RN             [1]
RP             SEQUENCE FROM N.A.
RC             TISSUE=Brain;
RX             MEDLINE=92017079; PubMed=1656157;
RA             Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT             "Conservation of the sequence of the Alzheimer's disease amyloid
RT             peptide in dog, polar bear and five other mammals by cross-species
RT             polymerase chain reaction analysis ";
RL             Brain Res. Mol. Brain Res. 10:299-305(1991).
CC             -I- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC             INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC             G(O) (BY SIMILARITY).
CC             -I- SUBCELLULAR LOCATION: Type I membrane protein.
CC             -I- SIMILARITY: BELONGS TO THE APP FAMILY.
CC             -----
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CC             -----
DR             EMBL; X56127; CAA39592.1; -.
DR             HSSP; P05067; IBA4.
DR             InterPro; IPR001868; A4_APP.
DR             PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR             PROSITE; PS00320; A4_INTRA; PARTIAL.
KW             Glycoprotein; Amyloid; Neutone; Transmembrane.
FT             NON_TER          1
FT             CHAIN            6          48          BETA-AMYLOID PROTEIN (POTENTIAL).
FT             DOMAIN          <1          33          EXTRACELLULAR (POTENTIAL).
FT             TRANSMEM        34          57          POTENTIAL.
FT             NON_TER          57
SQ             SEQUENCE        57 AA: 6172 MW: 84209888EBA82DFA CRC64:
Query Match          100.0%; Score 54; DB 1; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.00024;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 KMDAEFRHDS 10
|||||||
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Db      4 KMDAERRHDS 13

RESULT 2
A4_URSWA      STANDARD;      PRT;      57 AA.
AC 029149;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-APP) (A-beta)] (Fragment).
GN APP.
OS Ursus maritimus (Polar bear) (Thalictos maritimus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.
OX NCBI_TaxID=29073;
(1)
RN
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
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-----
CC EMBL: X56128; CAA39593.1; -.
DR HSSP: P05067; IAB4.
DR InterPro: IPR001868; A4_APP.
DR PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR PROSITE: PS00320; A4_INTRA; PARTIAL.
KM Glycoprotein; Amyloid; Neurone; Transmembrane.
FT NON_TER 1 1
FT CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 34 57 POTENTIAL.
FT NON_TER 57 57
SQ SEQUENCE 57 AA; 6172 MW; 84209D88BA82DFA CRC64;

Query Match 100.0%; Score 54; DB 1; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.00024;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 KMDAERRHDS 10
Db      4 KMDAERRHDS 13

RESULT 3
A4_CANFA      STANDARD;      PRT;      58 AA.
AC 028280;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-APP) (A-beta)] (Fragment).
GN APP.
OS Canis familiaris (Dog).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
(1)
RN
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
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-----
CC EMBL: X56125; CAA39590.1; -.
DR HSSP: P05067; IAB4.
DR InterPro: IPR001868; A4_APP.
DR PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR PROSITE: PS00320; A4_INTRA; PARTIAL.
KM Glycoprotein; Amyloid; Neurone; Transmembrane.
FT NON_TER 1 1
FT CHAIN 7 49 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 34 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 35 58 POTENTIAL.
FT NON_TER 58 58
SQ SEQUENCE 58 AA; 6285 MW; 8469D488A2E12DFA CRC64;

Query Match 100.0%; Score 54; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.00024;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 KMDAERRHDS 10
Db      5 KMDAERRHDS 14

RESULT 4
A4_RABIT      STANDARD;      PRT;      58 AA.
AC 028748;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-APP) (A-beta)] (Fragment).
GN APP.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
(1)
RN
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN

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CC      G(O) (BY SIMILARITY).
CC      -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC      -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC      -----
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CC      -----
DR      EMBL: X56129; CAA39594.1; -.
DR      HSSP: P05067; 1BA4.
DR      InterPro: IPR001868; A4_APP.
DR      PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR      PROSITE: PS00320; A4_INTRA; PARTIAL.
KW      Glycoprotein; Amyloid; Neurone; Transmembrane.
FT      NON_TER      1
FT      CHAIN      1
FT      DOMAIN      6 48      BETA-AMYLOID PROTEIN (POTENTIAL).
FT      TRANSMEM      34 57      EXTRACELLULAR (POTENTIAL).
FT      DOMAIN      58 >58      POTENTIAL.
FT      NON_TER      58      CYTOPLASMIC (POTENTIAL).
SQ      SEQUENCE      58 AA; 6300 MW; F434209D88EBA82D CRC64;

Query Match      100.0%; Score 54; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.00024;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 KMDAEFRHDS 10
Db      4 KMDAEFRHDS 13

RESULT 5
A4_SHEEP
ID      A4_SHEEP      STANDARD:      PRT;      58 AA.
AC      Q28757;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      30-MAY-2000 (Rel. 39, Last annotation update)
DE      Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE      protein (Beta-Ap) (A-beta)] (Fragment).
GN      APP.
OS      Ovis aries (Sheep).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC      Bovidae; Caprinae; Ovis.
OX      NCBI_TaxID=9940;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Heart;
RA      MEDLINE=92017079; PubMed=1656157;
RA      Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT      "Conservation of the sequence of the Alzheimer's disease amyloid
RT      peptide in dog, polar bear and five other mammals by cross-species
RT      polymerase chain reaction analysis.";
RL      Brain Res. Mol. Brain Res. 10:299-305(1991).
CC      -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC      INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC      G(O) (BY SIMILARITY).
CC      -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC      -1- SIMILARITY: BELONGS TO THE APP FAMILY.
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DR      EMBL: X56130; CAA39595.1; -.
DR      HSSP: P05067; 1AHL.
DR      InterPro: IPR001868; A4_APP.
DR      PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR      PROSITE: PS00320; A4_INTRA; PARTIAL.
KW      Glycoprotein; Amyloid; Neurone; Transmembrane.
FT      NON_TER      1
FT      CHAIN      1
FT      DOMAIN      6 48      BETA-AMYLOID PROTEIN (POTENTIAL).
FT      TRANSMEM      34 57      EXTRACELLULAR (POTENTIAL).
FT      DOMAIN      58 >58      POTENTIAL.
FT      NON_TER      58      CYTOPLASMIC (POTENTIAL).
SQ      SEQUENCE      58 AA; 6300 MW; F434209D88EBA82D CRC64;

Query Match      100.0%; Score 54; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.00024;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 KMDAEFRHDS 10
Db      4 KMDAEFRHDS 13

RESULT 6
A4_BOVIN
ID      A4_BOVIN      STANDARD:      PRT;      59 AA.
AC      Q28053;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      30-MAY-2000 (Rel. 39, Last annotation update)
DE      Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE      protein (Beta-APP) (A-beta)] (Fragment).
GN      APP.
OS      Bos taurus (Bovine).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC      Bovidae; Bovinae; Bos.
OX      NCBI_TaxID=9913;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Brain;
RA      MEDLINE=92017079; PubMed=1656157;
RA      Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT      "Conservation of the sequence of the Alzheimer's disease amyloid
RT      peptide in dog, polar bear and five other mammals by cross-species
RT      polymerase chain reaction analysis.";
RL      Brain Res. Mol. Brain Res. 10:299-305(1991).
CC      -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC      INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC      G(O) (BY SIMILARITY).
CC      -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC      -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC      -----
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CC      -----
DR      EMBL: X56124; CAA39589.1; -.
DR      EMBL: X56126; CAA39591.1; -.
DR      HSSP: P05067; 1BA4.
DR      InterPro: IPR001868; A4_APP.
DR      PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR      PROSITE: PS00320; A4_INTRA; PARTIAL.
KW      Glycoprotein; Amyloid; Neurone; Transmembrane.
FT      NON_TER      1
FT      CHAIN      1
FT      DOMAIN      7 49      BETA-AMYLOID PROTEIN (POTENTIAL).
FT      TRANSMEM      35 58      EXTRACELLULAR (POTENTIAL).
FT      DOMAIN      59 >59      POTENTIAL.
FT      TRANSMEM      59      CYTOPLASMIC (POTENTIAL).
```

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FT  NON-TER  59  59
SQ  SEQUENCE  59 AA: 6414 MW: F43469DA8BA2E12D CRC64;

Query Match
Best Local Similarity 100.0%; Score 54; DB 1; Length 59;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY  1 KMDAEFRHDS 10
    |||||
Db  5 KMDAEFRHDS 14

RESULT 7
A4 SAISC STANDARD; PRT; 751 AA.
AC 095241;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein precursor [Contains: Beta-
  amyloid protein (Beta-APP) (A-beta)].
GN APP.
OS Saimiri sciureus (Common squirrel monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Saimiri.
OX NCBI_Taxid=9521;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver, and Kidney;
RX MEDLINE=96108492; PubMed=8532114;
RA Levy E., Amorim A., Frangione B., Walker L.C.;
RT "Beta-amyloid precursor protein gene in squirrel monkeys with
  cerebral amyloid angiopathy.";
RL Neurobiol. Aging 16:805-808(1995).
CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
  INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
  G(O).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
  WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
  RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
  NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
  PHOSPHORYLATION (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
CC -----
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  entities requires a license agreement (see http://www.isb-sib.ch/announce/
  or send an email to license@isb-sib.ch).
CC -----
CC EMBL: S81024; AAD14347.1; -.
CC HSSP: P05067; IAP.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR SMART: SM00006; A4_EXTRA; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS00279; BPTI_KUNITZ_2; 1.
KW Glycoprotein; Amyloid; Neurone; Transmembrane; Alternative splicing;
  Signal; Serine protease inhibitor.
FT SIGNAL 1 17 BY SIMILARITY.
FT CHAIN 18 751 A4 PROTEIN.
FT CHAIN 653 695 BETA-AMYLOID PROTEIN (POTENTIAL).

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FT  DOMAIN  18  680
FT  TRANSMEM  681  704
FT  DOMAIN  705  751
FT  DOMAIN  287  345
FT  SITE  740  743
FT  ACT_SITE  301  302
FT  DISULFID  291  341
FT  DISULFID  300  324
FT  DISULFID  316  337
FT  CARBOHYD  523  523
FT  CARBOHYD  552  552
SQ  SEQUENCE  751 AA: 84893 MW: 6C3E431089569049 CRC64;

Query Match
Best Local Similarity 100.0%; Score 54; DB 1; Length 751;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY  1 KMDAEFRHDS 10
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Db  651 KMDAEFRHDS 660

RESULT 8
A4 HUMAN STANDARD; PRT; 770 AA.
AC P05067; P09000; Q16011;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein precursor (Protease nexin-II)
  (PN-II) (APP) [Contains: Beta-amyloid protein (Beta-APP) (A-beta)].
GN APP OR A4 OR CVA9 OR ADL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=87144572; PubMed=2881207;
RA Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L.,
  Greschlik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.;
RT "The precursor of Alzheimer's disease amyloid A4 protein resembles a
  cell-surface receptor.";
RL Nature 325:733-736(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88122639; PubMed=2893289;
RA Ponte P., Gonzalez-Dewhitt P., Schilling J., Miller J., Hsu D.,
  Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F.,
  Cordell B.;
RT "A new A4 amyloid mRNA contains a domain homologous to serine
  proteinase inhibitors.";
RL Nature 331:525-527(1988).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=89128427; PubMed=2783775;
RA Lemaire H.G., Salbaum J.M., Multhaup G., Kang J., Bayney R.M.,
  Unterbeck A., Beyreuther K., Mueller-Hill B.;
RT "The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid
  is encoded by 16 exons.";
RL Nucleic Acids Res. 17:517-522(1989).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=97263807; PubMed=9108164;
RA Hattori M., Tsukahara F., Furuhata Y., Tanahashi H., Hirose M.,
  Saito M., Tsukuni S., Sakaki Y.;
RT "A novel method for making nested deletions and its application for
  sequencing of a 300 kb region of human APP locus.";
RL Nucleic Acids Res. 25:1802-1808(1997).
RN [5]
RP SEQUENCE OF 286-345 AND 365-366 FROM N.A.
RX MEDLINE=88122640; PubMed=2893290;

```

RA Tanzi R.E., McClatchey A.I., Lamperti E.D., Villa-Komaroff L.,  
RA Gusella J.F., Neve R.L.;  
RT "Protease inhibitor domain encoded by an amyloid protein precursor  
RT mRNA associated with Alzheimer's disease.";   
RL Nature 331:528-530(1988).  
[6]  
RP SEQUENCE OF 287-367 FROM N.A.  
RX MEDLINE=8812641; PubMed=2893291;  
RA Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.;  
RT "Novel precursor of Alzheimer's disease amyloid protein shows  
RT protease inhibitory activity.";   
RL Nature 331:530-532(1988).  
[7]  
RP SEQUENCE OF 284-289 AND 365-770 FROM N.A.  
RX MEDLINE=87231971; PubMed=3035574;  
RA Robakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;  
RT "Molecular cloning and characterization of a cDNA encoding the  
RT cerebrovascular and the neuritic plaque amyloid peptides.";   
RL Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).  
[8]  
RP SEQUENCE OF 507-770 FROM N.A.  
RX MEDLINE=88124954; PubMed=2893379;  
RA Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,  
RA Marcota C.A.;  
RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer  
RT disease brain: coding and noncoding regions of the fetal precursor  
RT mRNA are expressed in the cortex.";   
RL Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).  
[9]  
RP SEQUENCE OF 672-681.  
RX MEDLINE=88035004; PubMed=3312495;  
RA Partridge W.M., Vinters H.V., Yang J., Eisenberg J., Choi T.B.,  
RA Tountellotte W.W., Huebner V., Shively J.E.;  
RT "Amyloid angiotensin of Alzheimer's disease: amino acid composition  
RT and partial sequence of a 4,200-dalton peptide isolated from cortical  
RT microvessels.";   
RL J. Neurochem. 49:1394-1401(1987).  
[10]  
RP SEQUENCE OF 739-770 FROM N.A.  
RX MEDLINE=90236318; PubMed=2110105;  
RA Yoshikai S.-I., Sasaki H., Doh-ura K., Furuya H., Sakaki Y.;  
RT "Genomic organization of the human amyloid beta-protein precursor  
RT gene.";   
RL Gene 87:257-263(1990).  
[11]  
RP SEQUENCE OF 1-10 FROM N.A.  
RX TISSUE=Liver;  
RC MEDLINE=89016647; PubMed=3140222;  
RA Schon E.A., Mita S., Sadlock J., Herbert J.;  
RT "A cDNA specifying the human amyloid beta precursor protein (ABPP)  
RT encodes a 95-kDa polypeptide.";   
RL Nucleic Acids Res. 16:9351-9351(1988).  
[12]  
RP SEQUENCE OF 18-50.  
RX MEDLINE=87250462; PubMed=3597385;  
RA Van Nostrand W.E., Cunningham D.D.;  
RT "Purification of protease nexin II from human fibroblasts.";   
RL J. Biol. Chem. 262:8508-8514(1987).  
[13]  
RP IDENTITY OF APP WITH NEXIN-II.  
RX MEDLINE=89384866; PubMed=2506449;  
RA Oltersdorf T., Filtz L.C., Schenk D.B., Lieberburg I.,  
RA Johnson-Wood K.L., Beattie E.C., Ward P.J., Blacher R.W., Dovey H.F.,  
RA Sinha S.;  
RT "The secreted form of the Alzheimer's amyloid precursor protein with  
RT the Kunitz domain is protease nexin-II.";   
RL Nature 341:144-147(1989).  
[14]  
RP PROTEASE-SPECIFICITY OF INHIBITOR DOMAIN.  
RX MEDLINE=90211252; PubMed=1969731;  
RA Kido H., Fukutomi A., Schilling J., Wang Y., Cordell B., Katunuma N.;  
RT "Protease-specificity of Kunitz inhibitor domain of Alzheimer's  
RT disease amyloid protein precursor.";

RL Biochem. Biophys. Res. Commun. 167:716-721(1990).  
RN [15]  
RP COMPLEX WITH G(O).  
RX MEDLINE=93188965; PubMed=8446172;  
RA Nishimoto I., Okamoto T., Matsuura Y., Takahashi S., Okamoto T.,  
RA Murayama Y., Ogata E.;  
RT "Alzheimer amyloid protein precursor complexes with brain GTP-binding  
RT protein G(O).";   
RL Nature 362:75-79(1993).  
[16]  
RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 28-133.  
RX MEDLINE=99213582; PubMed=10201399;  
RA Rossjohn J., Cappai R., Feil S.C., Henry A., Mckinstrey W.J.,  
RA Galatis D., Hesse L., Multhaup G., Beyreuther K., Masters C.L.,  
RA Parker M.W.;  
RT "Crystal structure of the N-terminal, growth factor-like domain of  
RT Alzheimer amyloid precursor protein.";   
RL Nat. Struct. Biol. 6:327-331(1999).  
[17]  
RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF 287-344.  
RX MEDLINE=91104913; PubMed=2125487;  
RA Hynes T.R., Randal M., Kennedy L.A., Egenbrodt C., Kosiakof A.A.;  
RT "X-ray crystal structure of the protease inhibitor domain of  
RT Alzheimer's amyloid beta-protein precursor.";   
RL Biochemistry 29:10018-10022(1990).  
[18]  
RP STRUCTURE BY NMR OF 289-344.  
RX MEDLINE=92031488; PubMed=1718421;  
RA Heald S.L., Tilton R.F., Jr., Hammond L.S., Lee A., Bayney R.M.,  
RA Kamarok M.E., Ramabhadran T.V., Dreyer R.N., Davis G., Unterebeck A.,  
RA Tamburini P.P.;  
RT "Sequential NMR resonance assignment and structure determination of  
RT the Kunitz-type inhibitor domain of the Alzheimer's beta-amyloid  
RT precursor protein.";   
RL Biochemistry 30:10467-10478(1991).  
[19]  
RP STRUCTURE BY NMR OF 672-699.  
RX MEDLINE=94281210; PubMed=7516706;  
RA Talafofus J., Marciniowski K.J., Klopman G., Zagorski M.G.;  
RT "Solution structure of residues 1-28 of the amyloid beta-peptide.";   
RL Biochemistry 33:7788-7796(1994).  
[20]  
RP STRUCTURE BY NMR OF 696-706.  
RX MEDLINE=97128622; PubMed=8973180;  
RA Kohno T., Kobayashi K., Meda T., Sato K., Takashima A.;  
RT "Three-dimensional structures of the amyloid beta peptide (25-35) in  
RT membrane-mimicking environment.";   
RL Biochemistry 35:16094-16104(1996).  
[21]  
RP STRUCTURE BY NMR OF 672-711.  
RX MEDLINE=98359783; PubMed=9693002;  
RA Coles M., Bicknell W., Watson A.A., Fairlie D.P., Craik D.J.;  
RT "Solution structure of amyloid beta-peptide(1-40) in a water-miscible  
RT environment. Is the membrane-spanning domain where we think it is?";   
RL Biochemistry 37:11064-11077(1998).  
[22]  
RP STRUCTURE BY NMR OF 672-699.  
RX MEDLINE=20400066; PubMed=10940222;  
RA Poulsen S.-A., Watson A.A., Craik D.J.;  
RT "Solution structures in aqueous SDS micelles of two amyloid beta  
RT peptides of Abeta(1-28) mutated at the alpha-secretase cleavage  
RT site.";   
RL J. Struct. Biol. 130:142-152(2000).  
[23]  
RP STRUCTURE BY NMR OF 681-706.  
RX MEDLINE=20400065; PubMed=10940221;  
RA Zhang S., Iwata K., Lachemann M.J., Peng J.W., Li S., Stimson E.R.,  
RA Lu Y., Felix A.M., Maglio J.E., Lee J.P.;  
RT "The Alzheimer's peptide a beta adopts a collapsed coil structure in  
RT water.";   
RL J. Struct. Biol. 130:130-141(2000).  
[24]  
RP SIGNAL SEQUENCE CLEAVAGE SITE, AND TOPOLOGY.

RA MEDLINE=88296437; PubMed=2900137;  
RA Dyke T., Weidemann A., Multhaup G., Salbaum J.M., Lemaire H.-G.,  
RA Kang J., Mueller-Hill B., Masters C.L., Beyreuther K.:  
RT "Identification, transmembrane orientation and biogenesis of the  
RT amyloid A4 precursor of Alzheimer's disease.";  
RT  
Query Match 100.0%; Score 54; DB 1; Length 770;  
Best Local Similarity 100.0%; Pred. No. 0.0039;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 KMDAERHDS 10  
Db 670 KMDAERHDS 679  
RESULT 9  
A4\_MOUSE STANDARD; PRT; 770 AA.  
ID A4\_MOUSE  
AC P12023;  
DT 01-OCT-1989 (Rel. 12, Created)  
DT 01-DEC-1992 (Rel. 24, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Alzheimer's disease amyloid A4 protein homolog precursor  
DE (Amyloidogenic glycoprotein) (Ag).  
GN APP.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.  
RC STRAIN-BALB/C; TISSUE-Brain;  
RX MEDLINE=92096458; PubMed=1756177;  
RA de Strooper B., van Leeuwen F., van den Bergh H.;  
RT "The amyloid beta protein precursor or proteinase nexin II from mouse  
RT is closer related to its human homolog than previously reported.";  
RL Biochim. Biophys. Acta 1129:141-143(1991).  
RN [2]  
RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.  
RC TISSUE-Brain;  
RX MEDLINE=88106489; PubMed=3322280;  
RA Yamada T., Sasaki H., Furuya H., Miyata T., Goto I., Sasaki Y.;  
RT "Complementary DNA for the mouse homolog of the human amyloid beta  
RT protein precursor.";  
RL Biochem. Biophys. Res. Commun. 149:665-671(1987).  
RN [3]  
RP REVISIONS.  
RA Yamada T.;  
RL Submitted (MAR-1988) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE OF 289-364 FROM N.A.  
RC STRAIN-CD-1; TISSUE-Placenta;  
RX MEDLINE=89345111; PubMed=2569710;  
RA Fukuchi K., Martin G.M., Deeb S.S.;  
RT "Sequence of the protease inhibitor domain of the A4 amyloid protein  
RT precursor of Mus domestica.";  
RL Nucleic Acids Res. 17:5396-5396(1989).  
RN [5]  
RP SEQUENCE OF 1-19 FROM N.A.  
RC MEDLINE=92209998; PubMed=1555768;  
RA Izumi R., Yamada T., Yoshikai S.I., Sasaki H., Hattori M.,  
RA Sakai Y.;  
RT "Positive and negative regulatory elements for the expression of the  
RT Alzheimer's disease amyloid precursor-encoding gene in mouse.";  
RL Gene 113:189-195(1992).  
RN [6]  
RP SEQUENCE OF 281-380 FROM N.A., AND ALTERNATIVE SPLICING.  
RC TISSUE-Brain, and Kidney;  
RX MEDLINE=89149813; PubMed=2493250;  
RA Yamada T., Sasaki H., Donura K., Goto I., Sasaki Y.;  
RT Structure and expression of the alternatively-spliced forms of mRNA  
RT for the mouse homolog of Alzheimer's disease amyloid beta protein  
RT precursor.";

RL Biochem. Biophys. Res. Commun. 158:906-912(1989).  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS: APP(395), APP(563), APP(695),  
CC APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE  
CC SPLICING.  
CC -1- TISSUE SPECIFICITY: AAA(770) IS EXPRESSED IN KIDNEY. AAA(751) IS  
CC WIDELY EXPRESSED. AAA(695) IS EXPRESSED IN BRAIN, KIDNEY AND  
CC LIVER.  
CC -1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION  
CC WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC  
CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE  
CC NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF  
CC PHOSPHORYLATION (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.  
CC -1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.  
CC -----  
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CC -----  
DR EMBL: X59379; ?; NOT\_ANNOTATED\_CDS.  
DR EMBL: M18373; AAA37139.1; -;  
DR EMBL: X15210; AAA33280.1; -;  
DR EMBL: D10603; BAA01456.1; -;  
DR EMBL: M24597; AAA39929.1; -;  
DR PIR: A27485; A27485.  
DR PIR: S04855; S04855.  
DR PIR: S19727; S19727.  
DR HSP: P05067; 10CM.  
DR MGD: MGI:88059; APP.  
DR InterPro: IPR001868; A4\_APP.  
DR InterPro: IPR002223; Kunitz\_BPTI.  
DR Pfam: PF02177; A4\_EXTRA; 1.  
DR Pfam: PF00014; Kunitz\_BPTI; 1.  
DR PRINTS: PR00203; AMYLOIDA.  
DR PRINTS: PR00759; BASICPTASE.  
DR SMART: SM00006; A4\_EXTRA; 1.  
DR SMART: SM00131; Ku; 1.  
DR PROSITE: PS00319; A4\_EXTRA; 1.  
DR PROSITE: PS00320; A4\_INTRA; 1.  
DR PROSITE: PS00280; BPTI\_KUNITZ\_1; 1.  
DR PROSITE: PS50279; BPTI\_KUNITZ\_2; 1.  
KW Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;  
KW Alternative splicing; Serine protease inhibitor.  
FT SIGNAL 1 17  
FT CHAIN 18 770  
FT FT  
FT DOMAIN 18 699  
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FT DOMAIN 287 345  
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FT VARSPLIC 289 289  
FT VARSPLIC 290 364  
FT VARSPLIC 346 380  
SQ SEQUENCE 770 AA; 86752 MW; 26C50DE0890CA7A CRC64;  
Oy 1 KMDAERHDS 10  
Query Match 87.0%; Score 47; DB 1; Length 770;  
Best Local Similarity 90.0%; Pred. No. 0.097;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;



DB 670 KMDAEFGHDS 679

RESULT 10

ID	A4_RAT	STANDARD	PRT	770 AA
AC	P08592			
DT	01-AUG-1988 (Rel. 08, Created)			
DT	01-DEC-1992 (Rel. 24, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Alzheimer's disease amyloid A4 protein homolog precursor (Amyloidogenic glycoprotein) (Aβ).			
GN	APP.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
NC	NCBI_TaxID=10116;			
RN	[1]			
RP	SEQUENCE OF 1-289 AND 365-770 FROM N.A.			
RC	TISSUE=Brain;			
RX	MEDLINE=88312583; PubMed=2900758;			
RA	Shivers B.D., Hilbich C., Multhaup G., Salbaum J.M., Beyreuther K., Seeburg P.H.;			
RT	"Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brain suggests a role in cell contact.";			
RL	EMBO J. 7:1365-1370(1988).			
RN	[2]			
RP	SEQUENCE OF 289-364 FROM N.A.			
RC	TISSUE=Liver;			
RX	MEDLINE=89183625; PubMed=2648331;			
RA	Kang J., Mueller-Hill B.;			
RT	"The sequence of the two extra exons in rat preA4.";			
RL	Nucleic Acids Res. 17:2130-2130(1989).			
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.			
CC	-1- ALTERNATIVE PRODUCTS: 5 ISOFORMS: APP(395), APP(563), APP(695), APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.			
CC	-1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF PHOSPHORYLATION (BY SIMILARITY).			
CC	-1- SIMILARITY: BELONGS TO THE APP FAMILY.			
CC	-1- SIMILARITY: CONTAINS 1 BP1/KUNITZ INHIBITOR DOMAIN.			
CC	-----			
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CC	-----			
DR	EMBL: X07648; CA30488.1; -			
DR	EMBL: X14066; CA32229.1; -			
DR	PIR: S00550; S00550.			
DR	PIR: S03607; S03607.			
DR	HSSP: P05067; IAAP.			
DR	InterPro: IPR001868; A4_APP.			
DR	InterPro: IPR002223; Kunitz_BP1.			
DR	Pfam: PF02177; A4_EXTRA; 1.			
DR	Pfam: PF00014; Kunitz_BP1; 1.			
DR	PRINTS: PR00203; AMYLOIDA4.			
DR	PRINTS: PM00759; BASICPTASE.			
DR	SMART: SM00006; A4_EXTRA; 1.			
DR	SMART: SM00131; KU; 1.			
DR	PROSITE: PS00319; A4_EXTRA; 1.			
DR	PROSITE: PS00320; A4_INTRA; 1.			
DR	PROSITE: PS00280; BP1_KUNITZ_1; 1.			
DR	PROSITE: PS50279; BP1_KUNITZ_2; 1.			
KW	Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;			
KW	Alternative splicing; Serine protease inhibitor.			
FT	SIGNAL 1 17 BY SIMILARITY.			

FT CHAIN 18 770

FT DOMAIN 18 699

FT TRANSMEM 700 723

FT DOMAIN 724 770

FT DOMAIN 673 715

FT SITE 287 345

FT SITE 759 762

FT DISULFID 291 341

FT DISULFID 300 324

FT DISULFID 316 337

FT CARBOHYD 542 542

FT CARBOHYD 571 571

FT VARSPIC 289 289

FT VARSPIC 290 364

FT SEQUENCE 770 AA: 86704 MW: C26C9DB8B2D929A7 CRC64;

Query Match 87.0%; Score 47; DB 1; Length 770;

Best Local Similarity 90.0%; Pred. No. 0.097;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KMDAEFGHDS 10

DB 670 KMDAEFGHDS 679

RESULT 11

COPD\_BOVIN

ID	COPD_BOVIN	STANDARD	PRT	511 AA
AC	P53619;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Cotomer delta subunit (delta-coat protein) (Delta-COP).			
GN	COPD.			
OS	Bos taurus (Bovine).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bos.			
NC	NCBI_TaxID=9913;			
RN	[1]			
RP	SEQUENCE OF 2-511 FROM N.A.			
RC	TISSUE=Brain;			
RX	MEDLINE=97011152; PubMed=8858162;			
RA	Faulstich D., Auerbach S., Orci L., Ravazzola M., Wegehingel S., Lottspeich F., Stenbeck G., Hartner C., Wieland F.T., Tschöchner H.;			
RT	"Architecture of cotomer: molecular characterization of delta-COP and protein interactions within the complex.";			
RL	J. Cell Biol. 135:53-61(1996).			
CC	-1- FUNCTION: THE COTOMER IS A CYTOSOLIC PROTEIN COMPLEX THAT BINDS TO DIVISIVE MOTIFS AND REVERSIBLY ASSOCIATES WITH GOLGI NON-CLATHRIN-COATED VESICLES, WHICH FURTHER MEDIATE BIOSYNTHETIC PROTEIN TRANSPORT FROM THE ER, VIA THE GOLGI UP TO THE TRANS GOLGI NETWORK. COTOMER COMPLEX IS REQUIRED FOR BUDDING FROM GOLGI MEMBRANES, AND IS ESSENTIAL FOR THE RETROGRADE GOLGI-TO-ER TRANSPORT OF DIVISIVE-TAGGED PROTEINS. IN MAMMALS, THE COTOMER CAN ONLY BE RECRUITED BY MEMBRANES ASSOCIATED TO ADP-RIBOSYLATION FACTORS (ARFs), WHICH ARE SMALL GTP-BINDING PROTEINS; THE COMPLEX ALSO INFLUENCES THE GOLGI STRUCTURAL INTEGRITY, AS WELL AS THE PROCESSING, ACTIVITY, AND ENDOCYTIC RECYCLING OF LDL RECEPTORS (BY SIMILARITY).			
CC	-1- SUBUNIT: OLIGOMERIC COMPLEX THAT CONSISTS OF AT LEAST THE ALPHA, BETA, BETA', GAMMA, DELTA, EPSILON AND ZETA SUBUNITS.			
CC	-1- SUBCELLULAR LOCATION: THE COTOMER IS CYTOPLASMIC OR POLYMERIZED ON THE CYTOPLASMIC SIDE OF THE GOLGI, AS WELL AS ON THE VESICLES/BUDS ORIGINATING FROM IT (BY SIMILARITY).			
CC	-1- TISSUE SPECIFICITY: UBIGUOUSLY EXPRESSED.			
CC	-1- SIMILARITY: BELONGS TO THE ADAPTOR COMPLEXES MEDIUM SUBUNITS FAMILY. COPD SUBFAMILY.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its			

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CC -----
DR EMBL: X94265; CAA63941.1; -.
DR InterPro: IPR001392; Adap_comp_sub.
DR Pfam: PF00928; Adap_comp_sub; 1.
KW Transport; Protein transport; Golgi stack; Membrane.
SQ SEQUENCE 511 AA; 57274 MW; 6A285798P252CC7F CRC64;

Query Match
Best Local Similarity 72.2%; Score 39; DB 1; Length 511;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KMDAEFRHDS 10
Db 424 EIDGEXRHDS 433

RESULT 12
COPD_HUMAN
ID COPD_HUMAN STANDARD; PRT; 511 AA.
AC P48444;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Coatomer delta subunit (Delta-coat protein) (Delta-COP) (Archain).
GN COPD OR ARCN1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=95301274; PubMed=7782067;
RA Radice P., Pensotti V., Jones C., Perry H., Pierotti M.A.,
RA Tunaciliffe A.;
RT "The human archain gene, ARCN1, has highly conserved homologs in rice
RT and Drosophila."
RL Genomes 26:101-106(1995).
CC -1- FUNCTION: THE COATOMER IS A CYTOSOLIC PROTEIN COMPLEX THAT BINDS
CC TO DILYSINE MOTIFS AND REVERSIBLY ASSOCIATES WITH GOLGI NON-
CC CLATHRIN-COATED VESICLES, WHICH FURTHER MEDATE BIOSYNTHETIC
CC PROTEIN TRANSPORT FROM THE ER, VIA THE GOLGI UP TO THE TRANS GOLGI
CC NETWORK. COATOMER COMPLEX IS REQUIRED FOR BUDDING FROM GOLGI
CC MEMBRANES, AND IS ESSENTIAL FOR THE RETROGRADE GOLGI-TO-ER
CC TRANSPORT OF DILYSINE-TAGGED PROTEINS. IN MAMMALS, THE COATOMER
CC CAN ONLY BE RECRUITED BY MEMBRANES ASSOCIATED TO ADP-RIBOSYLATION
CC FACTORS (ARFS), WHICH ARE SMALL GTP-BINDING PROTEINS; THE COMPLEX
CC ALSO INFLUENCES THE GOLGI STRUCTURAL INTEGRITY, AS WELL AS THE
CC PROCESSING, ACTIVITY, AND ENDOCYTIC RECYCLING OF LDL RECEPTORS (BY
CC SIMILARITY).
CC -1- SUBUNIT: OLIGOMERIC COMPLEX THAT CONSISTS OF AT LEAST THE ALPHA,
CC BETA, BETA', GAMMA, DELTA, EPSILON AND ZETA SUBUNTS.
CC -1- SUBCELLULAR LOCATION: THE COATOMER IS CYTOPLASMIC OR POLYMERIZED
CC ON THE CYTOPLASMIC SIDE OF THE GOLGI, AS WELL AS ON THE
CC VESICLES/BUDS ORIGINATING FROM IT (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: UBQUITOUSLY EXPRESSED.
CC -1- SIMILARITY: BELONGS TO THE ADAPTOR COMPLEXES MEDIUM SUBUNITS
CC FAMILY. COPD SUBFAMILY.
CC -----
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CC -----
DR EMBL: X81197; CAA57071.1; -.
DR EMBL: X81198; CAA57072.1; ALT_INIT.
DR MIM: 600820; -.
```

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DR InterPro: IPR001392; Adap_comp_sub.
DR Pfam: PF00928; Adap_comp_sub; 1.
KW Transport; Protein transport; Golgi stack; Membrane; Polymorphism.
FT VARIANT 186 186 F->L (IN DBSNP:662327).
FT FT /FTId=VAR_011788.
FT VARIANT 309 309 K->N (IN DBSNP:1063124).
FT FT /FTId=VAR_011789.
SQ SEQUENCE 511 AA; 57210 MW; 4ED1F7D2D12A7E75 CRC64;

Query Match
Best Local Similarity 72.2%; Score 39; DB 1; Length 511;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KMDAEFRHDS 10
Db 424 EIDGEXRHDS 433

RESULT 13
T2S1_STRFI
ID T2S1_STRFI STANDARD; PRT; 269 AA.
AC O52512;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Type II restriction enzyme SfiI (EC 3.1.21.4) (Endonuclease SfiI)
DE (R_SfiI).
GN SfiIR.
OS Streptomyces flimbrilatus.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxId=66197;
RN [1]
RP SEQUENCE FROM N.A.
RA van Cott E.M., Moran L.S., Siatko B.E., Wilson G.G.;
RT "Characterization of the SfiI restriction and modification genes."
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: RECOGNIZES THE DOUBLE-STRANDED SEQUENCE GCCNNNNNGCC
CC AND CLEAVES BEFORE N-9.
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage of DNA to give
CC specific double-stranded fragments with terminal 5'-phosphates.
CC -----
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CC -----
DR EMBL: AF039750; AAB95365.1; -.
DR REBASE: 1655; SfiI.
KW Hydrolyase; Endonuclease; Nuclease; Restriction system.
SQ SEQUENCE 269 AA; 31044 MW; 3C48499BAA5205EA CRC64;

Query Match
Best Local Similarity 77.8%; Score 35; DB 1; Length 269;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 MDAEFRHDS 10
Db 119 MDAEFRHDS 127

RESULT 14
GLND_PSEAE
ID GLND_PSEAE STANDARD; PRT; 900 AA.
AC O929H0;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE [Protein-PiI] uridylyltransferase (EC 2.7.7.59) (PIT uridylyl-
DE transferase) (Uridylyl removing enzyme) (UTase).
```

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GN Gland OR PA3658.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas
OX NCBI_TaxID=287;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 15692 / PA01;
RA Nashimoto H.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10994043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warriner P.,
RA Hickey M.J., Britkhan F.S.L., Huftagle W.O., Kowalik D.J., Lagrou M.,
RA Garner R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reiser J., Sater M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen.
RL Nature 406:959-964(2000).
CC -! FUNCTION: MODIFIES, BY URIDYLATION OR DEURIDYLATION THE PII
CC (GNB) REGULATORY PROTEIN (BY SIMILARITY).
CC -! CATALYTIC ACTIVITY: UTP + [protein-pii] = diphosphate + uridylyl-
CC [protein-pii].
CC -! SIMILARITY: BELONGS TO THE GND FAMILY.
CC -! CAUTION: REF.1 DIFFERS FROM THAT SHOWN DUE TO A FRAMESHIFT IN
CC POSITION 285.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
DR EMBL; AB024601; AAC5913.1; ALT_FRAME.
DR EMBL; AB004785; AAC07046.1; -.
DR InterPro: IPR002912; ACT.
DR InterPro: IPR002819; HD.
DR InterPro: IPR002834; NTP_transf.
DR InterPro: IPR003607; HDC.
DR Pfam; PF01842; ACT; 2.
DR Pfam; PF01966; HD; 1.
DR Pfam; PF01909; NTP_transf_2; 1.
DR SMART; SM00471; HDC; 1.
DR Transferrase; Nucleotidyltransferase; Complete proteome.
KM TRANSFERASE: Nucleotidyltransferase; Complete proteome.
FT CONFLICT 811 811 L -> V (IN REF. 1)
SQ SEQUENCE 900 AA; 103404 MW; 7C71F31EC284E836 CRC64;
OY 2 MDAEPRHD 9
Db 400 IDDEPRHD 407

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Query Match 64.8%; Score 35; DB 1; Length 900;
Best Local Similarity 75.0%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 35210 / B31;
RX MEDLINE=98065943; PubMed=9403685;
RA Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
RA Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
RA Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
RA Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
RA van Vugt R., Palmer N., Adams M.D., Cocayne J.D., Weidman J.,
RA Uitterback T., Wathley L., McDonald L., Artach P., Bowman C.,
RA Gariand S., Fujil C., Cotton M.D., Horst K., Roberts K., Hatch B.,
RA Smith H.O., Venter J.C.;
RT "Genomic sequence of a Lyme disease spirochaete, Borrelia
RT burgdorferi."
RL Nature 390:580-586(1997).
CC -! CATALYTIC ACTIVITY: D-glucose 6-phosphate + NADP(+) = D-glucose-
CC 1,5-lactone 6-phosphate + NADPH.
CC -! PATHWAY: FIRST STEP IN PENTOSE PHOSPHATE PATHWAY.
CC -! SIMILARITY: BELONGS TO THE GLUCOSE-6-PHOSPHATE DEHYDROGENASE
CC FAMILY.
CC -----
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CC -----
DR EMBL; AE001165; AAB91531.1; -.
DR HESP; P11411; IDPG.
DR TIGR; BB0636; -.
DR InterPro: IPR001282; G6PD.
DR Pfam; PF00479; G6PD; 1.
DR Pfam; PF02781; G6PD_C; 1.
DR PRINTS; PR00079; G6PDHDSGNASE.
DR PRODOM; PD001129; G6PD; 1.
DR PROSITE; PS00069; G6P_DEHYDROGENASE; 1.
DR OXIDOREDUCTASE; NADP; Glucose metabolism; Complete proteome.
KT ACT SITE 176 176
SQ SQUONCE 478 AA; 56113 MW; 4DDBCE261161CA CRC64;
OY 1 KMDAEPHD 9
Db 249 KPDSEFHD 257

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Search completed: October 29, 2002, 10:27:31
Job time : 5 secs

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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 29, 2002, 10:23:11 ; Search time 18 Seconds

(without alignments)  
96.108 Million cell updates/sec

Title: US-09-580-018-7

Perfect score: 54

Sequence: 1 KMDAEFRHDS 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SP:archaea:\*  
2: SP:bacteria:\*  
3: SP:fungi:\*  
4: SP:human:\*  
5: SP\_invertebrate:\*  
6: SP\_mammal:\*  
7: SP\_mhc:\*  
8: SP\_organelle:\*  
9: SP\_phage:\*  
10: SP\_plant:\*  
11: SP\_rodent:\*  
12: SP\_virus:\*  
13: SP\_vertebrate:\*  
14: SP\_unclassified:\*  
15: SP\_VIRUS:\*  
16: SP\_bacteriap:\*  
17: SP\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	82	4	P78438
2	54	100.0	82	4	016014
3	54	100.0	82	4	016019
4	54	100.0	82	4	016020
5	54	100.0	534	13	093296
6	54	100.0	569	13	09PVL1
7	54	100.0	695	6	095KN7
8	54	100.0	695	11	060496
9	54	100.0	695	13	09DGJ8
10	54	100.0	751	13	09DGJ7
11	54	100.0	770	6	09PVL0
12	47	87.0	79	11	035463
13	47	87.0	607	11	099K32
14	47	87.0	607	11	099K32
15	45	83.3	693	13	0985G0
16	45	83.3	695	13	0985F9

17	45	83.3	747	13	091963	091963 xenopus ap
18	44	81.5	19	4	09UC08	09UC08 homo sapien
19	44	81.5	28	4	09UCD1	09UCD1 homo sapien
20	44	81.5	30	4	09UCA9	09UCA9 homo sapien
21	44	81.5	33	4	09UC33	09UC33 homo sapien
22	40	74.1	423	2	052379	052379 raietonia s
23	40	74.1	423	2	045693	045693 burkholderi
24	39	72.2	511	11	091M48	091M48 mus musculu
25	37	68.5	418	2	09KY96	09KY96 streptomyce
26	36	66.7	755	5	09VF30	09VF30 drosophila
27	35	64.8	428	16	09I2U4	09I2U4 pseudomonas
28	35	64.8	543	10	09LZL4	09LZL4 arabidopsis
29	35	64.8	802	16	09HML3	09HML3 pseudomonas
30	34	63.0	97	4	013778	013778 homo sapien
31	34	63.0	206	2	044945	044945 borrelia bu
32	34	63.0	210	2	093MK6	093MK6 vibrio vuln
33	34	63.0	213	16	09A314	09A314 cauliobacter
34	34	63.0	229	10	09LUF9	09LUF9 arabidopsis
35	34	63.0	240	16	092PX4	092PX4 rhizobium m
36	34	63.0	265	2	09AOL8	09AOL8 pseudomonas
37	34	63.0	329	17	09HMG1	09HMG1 halobacteri
38	34	63.0	347	12	091FD6	091FD6 chilo iride
39	34	63.0	399	12	09QB65	09QB65 wheat yello
40	34	63.0	400	2	052295	052295 shigella fl
41	34	63.0	431	2	0935K0	0935K0 salmonella
42	34	63.0	432	2	093RK7	093RK7 bacillus sp
43	34	63.0	439	2	09LS76	09LS76 salmonella
44	34	63.0	452	11	091ZK0	091ZK0 mus musculu
45	34	63.0	555	12	09QBG3	09QBG3 wheat yello

## ALIGNMENTS

RESULT 1  
ID P78438 PRELIMINARY; PRT; 82 AA.  
AC P78438;  
DT 01-MAY-1997 (TREMBLrel. 03, Created)  
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)  
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
DE AMYLOID PROTEIN (BETA-AMYLOID PROTEIN) (FRAGMENT).  
GN APP.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
CC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89392030; PubMed=2675837;  
RA Johnstone E.M., Chaney M.O., Moore R.E., Ward K.E., Norris F.H.,  
RA Little S.P.;  
RT "Alzheimer's disease amyloid peptide is encoded by two exons and shows  
RT similarity to soybean trypsin inhibitor."  
RL Biochem. Biophys. Res. Commun. 163:1248-1255(1989).  
RN [2]  
RP SEQUENCE OF 19-48 FROM N.A.  
RX MEDLINE=67120329; PubMed=2949367;  
RA Tanzi R.E., Gusella J.F., Watkins P.C., Bruns G.A., George-Hyslop P.,  
RA Van Keuren M.L., Patterson D., Pagan S., Kurnit D.M., Neve R.L.;  
RT "Amyloid beta protein gene: cDNA, mRNA distribution, and genetic  
RT linkage near the Alzheimer locus."  
RL Science 235:880-884(1987).  
RN [3]  
RP SEQUENCE OF 32-63 FROM N.A.  
RX MEDLINE=93053597; PubMed=1415269;  
RA Kamino K., Orr H.T., Payami H., Wijsman E.M., Alonso M.E., Pulst S.M.,  
RA Anderson L., O'dahl S., Nemens E., White J.A.;  
RT "Linkage and mutational analysis of familial Alzheimer disease  
RT kindreds for the APP gene region."  
RL Am. J. Hum. Genet. 51:998-1014(1992).  
DR EMBL; M29270; AAA51768.1; -.  
DR EMBL; M29269; AAA51768.1; JOINED.

DR EMBL: M15532; AAA51564.1; -.  
DR EMBL: S45136; AAB23646.1; -.  
DR HSSP: P05067; 1BA4.  
FT NON\_TER 1 1  
SQ SEQUENCE 82 AA; 8994 MW; 8DA9E42B813A070E CRC64;

Query Match 100.0%; Score 54; DB 4; Length 82;  
Best Local Similarity 100.0%; Pred. No. 0.0017;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KMDAEFRHDS 10  
DB 15 KMDAEFRHDS 24

RESULT 2  
Q16014  
ID Q16014 PRELIMINARY; PRT; 82 AA.

AC Q16014: 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE BETA-AMYLROID PEPTIDE (FRAGMENT).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93236601; PubMed=8476439;  
RA Denman R.B., Rosenzwaig R., Miller D.L.;  
RT "A system for studying the effect(s) of familial Alzheimer disease mutations on the processing of the beta-amyloid peptide precursor."  
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).  
DR EMBL: S60721; AAB26253.2; -.  
DR HSSP: P05067; 1BA4.  
FT NON\_TER 1  
SQ SEQUENCE 82 AA; 8972 MW; F534AA5B3EA9230A CRC64;

Query Match 100.0%; Score 54; DB 4; Length 82;  
Best Local Similarity 100.0%; Pred. No. 0.0017;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KMDAEFRHDS 10  
DB 16 KMDAEFRHDS 25

RESULT 3  
Q16019  
ID Q16019 PRELIMINARY; PRT; 82 AA.

AC Q16019: 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE BETA-AMYLROID PEPTIDE (FRAGMENT).  
GN BETA APP.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93236601; PubMed=8476439;  
RA Denman R.B., Rosenzwaig R., Miller D.L.;  
RT "A system for studying the effect(s) of familial Alzheimer disease mutations on the processing of the beta-amyloid peptide precursor."  
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).  
DR EMBL: S61380; AAB26264.2; -.  
DR HSSP: P05067; 1BA4.  
FT NON\_TER 1  
SQ SEQUENCE 82 AA; 8972 MW; F534AA5B3EA9230A CRC64;

SQ SEQUENCE 82 AA; 8938 MW; F534AA50E579230A CRC64;  
Query Match 100.0%; Score 54; DB 4; Length 82;  
Best Local Similarity 100.0%; Pred. No. 0.0017;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KMDAEFRHDS 10  
DB 16 KMDAEFRHDS 25

RESULT 4  
Q16020  
ID Q16020 PRELIMINARY; PRT; 82 AA.

AC Q16020: 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE BETA-AMYLROID PEPTIDE (FRAGMENT).  
GN BETA APP.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93236601; PubMed=8476439;  
RA Denman R.B., Rosenzwaig R., Miller D.L.;  
RT "A system for studying the effect(s) of familial Alzheimer disease mutations on the processing of the beta-amyloid peptide precursor."  
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).  
DR EMBL: S61383; AAB26265.2; -.  
DR HSSP: P05067; 1BA4.  
FT NON\_TER 1  
SQ SEQUENCE 82 AA; 8882 MW; F534AA5AE5D9230A CRC64;

Query Match 100.0%; Score 54; DB 4; Length 82;  
Best Local Similarity 100.0%; Pred. No. 0.0017;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KMDAEFRHDS 10  
DB 16 KMDAEFRHDS 25

RESULT 5  
O93296  
ID O93296 PRELIMINARY; PRT; 534 AA.

AC O93296: 01-NOV-1998 (TREMBlrel. 08, Created)  
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE AMYLROID PROTEIN (FRAGMENT).  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96337885; PubMed=9671674;  
RA Barnes N.Y., Li L., Yoshikawa K., Schwartz L.M., Oppenheim R.W., Milligan C.E.;  
RT "Increased production of amyloid precursor protein provides a substrate for caspase-3 in dying motoneurons."  
RL J. Neurosci. 18:5869-5880(1998).  
DR EMBL: AF042098; AAC25052.1; -.  
DR HSSP: P05067; 1BA4.  
DR InterPro: IPR001868; A4\_APP.  
DR PRINTS: PRO0203; AMYL0IDA4.  
DR PROSITE: PS00319; A4\_EXTRA; 1.  
DR PROSITE: PS00320; A4\_INTRN; 1.

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FT NON_TER 1 1
SQ SEQUENCE 534 AA; 60597 MW; FB53ECC2E66D4C92 CRC64;
Query Match
Best Local Similarity 100.0%; Score 54; DB 13; Length 534;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KMDAEFRHDS 10
    |||||||
Db 434 KMDAEFRHDS 443

RESULT 6
O9PVL1 PRELIMINARY; PRT; 569 AA.
AC O9PVL1;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE AMYLOID PROTEIN (FRAGMENT).
GN APP.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Coulson E.J., Paliaga K., Beyreuther K., Masters C.L.;
RT "What the evolution of the amyloid protein precursor supergene family
RL tells us about its function.";
RL Neurochem. Int. 0:0-0(2000).
DR EMBL; AF030341; AAF12698.1; -.
DR HSSP; P05067; 1BA4.
DR InterPro; IPR001868; A4_APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
FT NON_TER 1 1
SQ SEQUENCE 569 AA; 64753 MW; 0AB8B851863A19D CRC64;
Query Match
Best Local Similarity 100.0%; Score 54; DB 13; Length 569;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KMDAEFRHDS 10
    |||||||
Db 470 KMDAEFRHDS 479

RESULT 7
O95KN7 PRELIMINARY; PRT; 695 AA.
AC O95KN7;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE AMYLOID B-PROTEIN PRECURSOR.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CEREBELLUM;
RX MEDLINE=91273117; PubMed=1905108;
RA Podlisy M.B., Tolan D.R., Selkoe D.J.;
RT "Homology of the amyloid beta protein precursor in monkey and human
RT supports a primate model for beta amyloidosis in Alzheimer's

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RT disease.";
RL Am. J. Pathol. 138:1423-1435(1991).
DR EMBL; M58727; AAA36829.1; -.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 597 636 POTENTIAL.
SO SEQUENCE 695 AA; 78663 MW; 4F6EA0139F969D56 CRC64;
Query Match
Best Local Similarity 100.0%; Score 54; DB 6; Length 695;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KMDAEFRHDS 10
    |||||||
Db 595 KMDAEFRHDS 604

RESULT 8
O60496 PRELIMINARY; PRT; 695 AA.
AC O60496;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE POTATIVE AMYLOID PRECURSOR PROTEIN.
OS Cavia sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.
OX NCBI_TaxID=10143;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=97236426; PubMed=9116031;
RA Beck M., Mueller D., Bigl V.;
RT "Amyloid precursor protein in Guinea pigs - complete cDNA sequence and
RT alternative splicing.";
RL Blochum, Biophys. Acta 1351:17-21(1997).
DR EMBL; X97631; CAA66230.1; -.
DR HSSP; P05067; 1BA4.
DR InterPro; IPR001868; A4_APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
SQ SEQUENCE 695 AA; 78701 MW; 5196A0C4017F16AB CRC64;
Query Match
Best Local Similarity 100.0%; Score 54; DB 11; Length 695;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KMDAEFRHDS 10
    |||||||
Db 595 KMDAEFRHDS 604

RESULT 9
O9DGJ8 PRELIMINARY; PRT; 695 AA.
AC O9DGJ8;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE BETA-AMYLOID PRECURSOR PROTEIN 695 ISOROM.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Sarasa M., Rodiciose A., Sorribas V.;
RT "Cloning of full-length chicken beta-amyloid precursor protein
RT isoforms.";

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RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF289218; AAC00593.1; -.
DR HSSP: P05067; 1BA4.
DR InterPro: IPR001868; A4_APP.
DR Pfam: PF02177; A4_EXTRA; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR SMART: SM00006; A4_EXTRA; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
SQ SEQUENCE 695 AA; 78565 MW; F201ED02AEC86D95 CRC64;

Query Match
Best Local Similarity 100.0%; Score 54; DB 13; Length 695;
Pred. No. 0.017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KMDAEFRHDS 10
Db 595 KMDAEFRHDS 604

RESULT 10
O9DGJ7 PRELIMINARY; PRT; 751 AA.
AC O9DGJ7;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE BETA-AMYLOID PRECURSOR PROTEIN 751 ISOFORM.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Sarasa M., Rodolosse A., Sorribas V.;
RT "Cloning of full-length chicken beta-amyloid precursor protein
RT isoforms."
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF289219; AAC00594.1; -.
DR HSSP: P05067; 1BA4.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PRINTS: PR00759; BASICTPASE.
DR SMART: SM00006; A4_EXTRA; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS00279; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor.
SQ SEQUENCE 751 AA; 84705 MW; E78E9413A8033D84 CRC64;

Query Match
Best Local Similarity 100.0%; Score 54; DB 13; Length 751;
Pred. No. 0.019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KMDAEFRHDS 10
Db 651 KMDAEFRHDS 660

RESULT 11
O9TU10 PRELIMINARY; PRT; 770 AA.
AC O9TU10;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE AMYLOID PRECURSOR PROTEIN.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Kimura A., Takahashi T.;
RT "Amyloid precursor protein 770."
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB032550; BAA84580.1; -.
DR HSSP: P05067; 1AAP.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PRINTS: PR00759; BASICTPASE.
DR SMART: SM00006; A4_EXTRA; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS00279; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor.
SQ SEQUENCE 770 AA; 86961 MW; 5F7A1DCB2BCC583E CRC64;

Query Match
Best Local Similarity 100.0%; Score 54; DB 6; Length 770;
Pred. No. 0.019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KMDAEFRHDS 10
Db 670 KMDAEFRHDS 679

RESULT 12
O35463 PRELIMINARY; PRT; 79 AA.
ID O35463;
AC O35463;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE ALZHEIMER'S AMYLOID BETA PROTEIN (FRAGMENT).
DE BETA APP.
GN Cricetus griseus (Chinese hamster).
OC Cricetulus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetulus.
OX NCBI_TaxID=10029;
RN [1]
RP SEQUENCE FROM N.A.
RA Subbanurti K., Pinnix I., Gandhi S.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF030413; AAB86608.1; -.
DR HSSP: P05067; 1BA4.
DR FT NON_TER 1 79
FT NON_TER 1 79
SQ SEQUENCE 79 AA; 8538 MW; 37F2C6C3BFF3F597 CRC64;

Query Match
Best Local Similarity 90.0%; Score 47; DB 11; Length 79;
Pred. No. 0.041;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KMDAEFRHDS 10
Db 19 KMDAEFRHDS 28

RESULT 13
O99K32 PRELIMINARY; PRT; 607 AA.
ID O99K32;
AC O99K32;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE HYPOTHETICAL 68.4 KDA PROTEIN (FRAGMENT).
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OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MAMMARY TUMOR. WAP-TGF ALPHA MODEL. 7 MONTHS OLD, GROSS
RC TISSUE.
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC005490; AAH05490.1; -.
DR HSSP; P05067; 1AAP.
DR InterPro; IPR001868; A4_APP.
DR InterPro; IPR002223; Kunitz-BPTI.
DR Pfam; PF00014; Kunitz-BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS02279; BPTI_KUNITZ_2; 1.
KW Hypothetical protein; Serine protease inhibitor.
FT NON_TER
SO SEQUENCE 607 AA; 68391 MW; BF802214CBA7D172 CRC64;

Query Match
Best Local Similarity 87.0%; Score 47; DB 11; Length 607;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KMDAEFRHDS 10
DB 507 KMDAEFRHDS 516

RESULT 14
P97487 PRELIMINARY; PRT; 695 AA.
AC P97487; P97942;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE HIPPOCAMPAL AMYLOID PROTEIN.
GN APP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SAMP8; TISSUE=HIPPOCAMPUS;
RA Flood J.F.; Kumar V.B.; Sasser T.; Word I.; Morley J.E.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 581-662 FROM N.A.
RC STRAIN=129SV;
RA Wragg M.A.; Busfield F.; Duff K.; Korenblat K.; Capechi M.;
RL Loring J.F.; Goate A.M.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U84012; AAB41502.1; -.
DR HSSP; P05067; 1AMP.
DR MGD; MGI:88059; APP.
DR InterPro; IPR001868; A4_APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
SO SEQUENCE 695 AA; 78414 MW; 9A5FBE2ED261236E CRC64;

Query Match
Best Local Similarity 87.0%; Score 47; DB 11; Length 695;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KMDAEFRHDS 10
DB 595 KMDAEFRHDS 604

RESULT 15
O98SGO PRELIMINARY; PRT; 693 AA.
AC O98SGO;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE BETA-AMYLOID PRECURSOR PROTEIN A.
GN APP.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OX Xenopodinae; Xenopus.
OX NCBI_TaxID=8395;
RN [1]
RP SEQUENCE FROM N.A.
RA Van den Hurk W.H.;
RL Thesis (2001), Department of Biological Sciences,
RL University of Nijmegen, Nijmegen, Netherlands.
DR EMBL; AJ298150; CAC37193.1; -.
DR HSSP; P05067; 1H23.
DR InterPro; IPR001868; A4_APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
KW Signal.
FT SIGNAL
SO SEQUENCE 693 AA; 78568 MW; CAF1DF655C1AB653 CRC64;

Query Match
Best Local Similarity 83.3%; Score 45; DB 13; Length 693;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 KMDAEFRHDS 10
DB 593 KMDSEYRHDT 602

Search completed: October 29, 2002, 10:29:44
Job time : 19.1429 secs

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